

TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. 371

J014 Rec'd PCT/PTO 26 DEC 2001

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

10/030019

INTERNATIONAL APPLICATION NO.

INTERNATIONAL FILING DATE

PRIORITY DATE CLAIMED

PCT/BE00/00077

DEC 26 2001

July 3, 2000

July 1, 1999

TITLE OF INVENTION

CELL DEATH RELATED DRUG TARGET IN YEAST AND FUNGI

APPLICANT(S) FOR DO/EO/US

Contreras, Roland Henri

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.
3. ☐ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☐ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
  - a. ☒ is transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☐ has been transmitted by the International Bureau.
  - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☐ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
  - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☐ have been transmitted by the International Bureau.
  - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
  - d. ☐ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371 (c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes of the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A FIRST preliminary amendment.  
☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☒ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information: Copy of the International Preliminary Examination Report; Copy of the International Search Report; Express Mail Certificate; Sequence Disk; Sequence Listing; Version to Show Changes Made; Preliminary Amendment; Letter to Correct Name of Inventor from Isabelle Karin Luc Malcorps to Isabelle Karin Pieter Lenaerts, and 4 figures (Fig 1 1-93; Fig 2 94-157, Fig 3 158-159, Fig 4 160-161)

10/030018

PCT/BE00/00077

JAB-1521

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17. ☒ The following fees are submitted:

BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)):

Neither international preliminary examination fee (37 CFR 1.482)  
nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO  
and International Search Report not prepared by the EPO or JPO.....\$1040.00

International preliminary examination fee (37 CFR 1.482) not paid to  
USPTO but International Search Report prepared by the EPO or JPO.....\$890.00

International preliminary examination fee (37 CFR 1.482) not paid to  
USPTO but international search fee (37 CFR 1.455(a)(2)) paid to USPTO.....\$740.00

International preliminary examination fee (37 CFR 1.482) paid to  
USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4).....\$750.00

International preliminary examination fee (37 CFR 1.482) paid to  
USPTO and all claims satisfied provisions of PCT Article 33(1)-(4).....\$100.00

ENTER APPROPRIATE BASIC FEE AMOUNT =

\$ 1,040.00

Surcharge of \$130.00 for furnishing the oath or declaration later than ☐ 20 ☐ 30  
months from the earliest claimed priority date (37 CFR 1.492(e)).

\$

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	
Total claims	54 - 20 =	34	x \$18.00	\$ 612.00
Independent claims	45 - 3 =	42	x \$84.00	\$ 3528.00
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$280.00	\$

TOTAL OF ABOVE CALCULATIONS =

\$4140.00

Reduction of 1/2 for filing by small entity, if applicable. A Small Entity Statement  
must also be filed (Note 37 CFR 1.9, 1.27, 1.28).

+

SUBTOTAL =

\$

Processing fee of \$130.00 for furnishing the English translation later than ☐ 20 ☐ 30  
months from the earliest claimed priority date (37 CFR 1.492(f)).

\$

TOTAL NATIONAL FEE =

\$

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be  
accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property

\$40.00

TOTAL FEES ENCLOSED =

\$5220.00

Amount to be  
refunded:

\$

charged:

\$5220.00

a. ☐ A check in the amount of \$\_\_\_\_\_ to cover the above fees is enclosed.

b. ☒ Please charge my Deposit Account No. 10-0750/JAB-1521/MHM in the amount of \$5220.00 to cover the above fees.  
A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any  
overpayment to Deposit Account No. 10-0750/JAB-1521/MHM. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137 (a)  
or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

Philip S. Johnson, Esq.  
Johnson & Johnson  
One Johnson & Johnson Plaza  
New Brunswick, NJ 08933-7003  
USA

Signature

Myra H. McCormack  
Reg. No. 36,602  
Attorney for Applicants



10/030019  
531 Rec'd  
26 DEC 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Masure, et al.

Serial No. : UNKNOWN

Art Unit: UNKNOWN

Filed : HEREWITH

Examiner: UNKNOWN

For : Cell Death Related Drug Targets In Yeast  
and Fungi

I hereby certify that this correspondence is being deposited with the  
United States Postal Service as first class mail in an envelope addressed  
to: Commissioner for Patents, Washington, D.C. 20231 on

December 26, 2001

(Date)

Myra H. McCormack

Name of applicant, assignee, or Registered Representative

Myra H. McCormack  
(Signature)

December 26, 2001

(Date of Signature)

Hon. Commissioner for Patents  
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Dear Sir:

Prior to the examination of the above-referenced  
application, kindly amend the application as follows:

IN THE CLAIMS

Kindly cancel claim 48

Kindly amend the following claims:

1. (Amended) An isolated nucleic acid molecule  
encoding a polypeptide wherein the nucleic acid  
sequence of the nucleic acid molecule is selected  
from:



similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97%

identical to any of the amino acid sequences shown in SEQ ID NOS 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOS 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91,

93, 95, 97, 99, 101, 103, 105, 107, 109, 111,  
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 437, 439, 441, 443, 445, 447, 449, 451, 453,  
 455, 457, 459, 461, 463, 465, 467, 469, 471,  
 473, 475, 477, 479, 481 or 483;

- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139,

141, 143, 145, 147, 149, 151, 153, 155, 157,  
159, 161, 163, 165, 167, 169, 171, 173, 175,  
177, 179, 181, 183, 185, 187, 189, 191, 193,  
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447, 449, 451, 453, 455, 457, 459, 461, 463,  
465, 467, 469, 471, 473, 475, 477, 479, 481 or  
483; [and]

(f) or the functional fragment or complement thereof

for the preparation of a medicament for treating diseases associated with yeast or fungi.

2. (Amended) An isolated polypeptide which is involved in a pathway leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74,

76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96,  
 98, 100, 102, 104, 106, 108, 110, 112, 114,  
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 296, 298, 300, 302, 304, 306, 308, 310, 312,  
 314, 316, 318, 320, 322, 324, 326, 328, 330,  
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 440, 442, 444, 446, 448, 450, 452, 454, 456,  
 458, 460, 462, 464, 466, 468, 470, 472, 474,  
 476, 478, 480, 482, or 484, or encoding a  
 functional equivalent, derivative or  
 bioprecursor of said protein;

- (b) a protein having an amino acid sequence  
 which is more than 70% similar, preferably  
 more than 80% similar, more preferably more  
 than 90% similar and most preferably more than  
 97% similar to any of the amino acid sequences  
 shown in SEQ ID NOS 2, 4, 6, 8, 10, 12, 14,  
 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36,  
 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58,  
 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80,

82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,  
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 176, 178, 180, 182, 184, 186, 188, 190, 192,  
 194, 196, 198, 200, 202, 204, 206, 208, 210,  
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 230, 232, 234, 236, 238, 240, 242, 244, 246,  
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 266, 268, 270, 272, 274, 276, 278, 280, 282,  
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 302, 304, 306, 308, 310, 312, 314, 316, 318,  
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 356, 358, 360, 362, 364, 366, 368, 370, 372,  
 374, 376, 378, 380, 382, 384, 386, 388, 390,  
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 410, 412, 414, 416, 418, 420, 422, 424, 426,  
 428, 430, 432, 434, 436, 438, 440, 442, 444,  
 446, 448, 450, 452, 454, 456, 458, 460, 462,  
 464, 466, 468, 470, 472, 474, 476, 478, 480,  
 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOS 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116,





12. (Amended) A medicament comprising the compound according to claim 11.

13. (Amended) A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a medicament according to claim 12 with a suitable pharmaceutically acceptable carrier.

14. (Amended) A method for treating a yeast or fungal infection in a subject comprising the step of administering a compound according to claim 11.

15. (Amended) A method for modifying the endogenic flora of humans and other mammals comprising the step of administering a compound according to claim 11.

16. (Amended) The method of claim 14 wherein the yeast or fungal infection is an infection caused by the yeast or fungi selected from the group consisting of *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

17. (Amended) A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320,

322, 324, 326, 328, 330, 332, 338, 342, 344, 346,  
 348, 352, 354, 356, 358, 360, 362, 364, 366, 368,  
 370, 372, 374, 376, 380, 382, 384, 386, 388, 390,  
 392, 394, 398, 402, 404, 406, 408, 410, 412, 416,  
 418, 422, 424, 426, 428, 430, 432, 434, 436, 438,  
 440, 442, 444, 446, 448, 450, 452, 454, 476, 478,  
 480, 482 or 484;

(d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOS 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;

(e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOS 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; or a functional fragment or complement thereof.

18. (Amended) A nucleic acid according to claim 16 wherein the nucleic acid is derived from *Candida albicans*.

20. (Amended) A nucleic acid sequence according to claim 17 which is mRNA.

21. (Amended) A nucleic acid sequence according to claim 17 which is DNA.

22. (Amended) A nucleic acid sequence according to claim 17 which is cDNA.

23. (Amended) An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to claim 17.

24. (Amended) An isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOS 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOS 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

(a) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOS 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484; or a functional fragment thereof.

25.(Amended) An expression vector comprising a nucleic acid sequence according to claim 17.

27. (Amended) An expression vector according to claim 25 which comprises a sequence encoding a reporter molecule.
28. (Amended) A host cell transformed, transfected or infected with the vector of claim 25.
29. (Amended) A nucleic acid molecule according to claim 17 for use as a medicament.
33. (Amended) A pharmaceutical composition comprising an antibody according to claim 31.
34. (Amended) A method for treating a yeast or fungal infection comprising the step of administering an antibody according to claim 31, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2.
35. (Amended) The method of claim 34 wherein the fungus is *Candida albicans*.
36. (Amended) A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 wherein the nucleic acid probe selectively hybridises with the nucleic acid molecule.
37. (Amended) A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 wherein the nucleic acid primer selectively amplifies any of said nucleic acid molecules.

38. (Amended) A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of claim 1 or a human homologue thereof or at least one of the polypeptides of claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

39. (Amended) A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of claim 1 or a human homologue thereof and/or at least one of the polypeptides of claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

41. (Amended) A medicament comprising the compound according to claim 40.

42. (Amended) A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 with a suitable pharmaceutically acceptable carrier.

43. (Amended) A method for for treating proliferative disorders or for preventing apoptosis in comprising administering the compound of claim 40 to a subject in need thereof.



44. (Amended) A method for treating proliferative disorders or for the prevention of apoptosis comprising administering a nucleic acid molecule of claim 1 to a subject in need thereof.

45. (Amended) A method for treating proliferative disorders or for the prevention of apoptosis comprising administering a polypeptide of claim 2 to a subject in need thereof.

46. (Amended) A pharmaceutical composition comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

47. (Amended) A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.

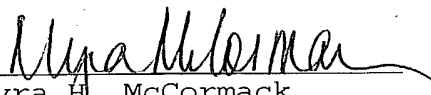
51. (Amended) An expression vector according to claim 49 which comprises a sequence encoding a reporter molecule.

52. (Amended) A host cell transformed, transfected or infected with the vector of claim 49.

REMARKS

Claim 48 has been canceled. Claims 1, 2, 10-18, 20-25, 27-29, 33-39, 41-47, 51 and 52 have been amended to better align them with U.S. Patent practice. The specification has been amended to incorporate the priority information for this Application and to include headings. These changes have been made to the substitute specification that is provided herewith. No new matter was added in incorporating the priority claims and headings. A substitute sequence listing has been provided along with a Computer Readable Form of the Sequence Listing. The undersigned hereby states that the Paper Copy and the Computer Readable Form are identical. No new matter has been added by these amendments. A version to show changes made to the claims accompanies this amendment. Favorable consideration of the remarks provided below is respectfully requested. Should the Examiner have any questions he or she is invited to contact the undersigned at the telephone number provided below.

Respectfully submitted,

  
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Dated: December 26, 2001

VERSION TO SHOW CHANGES MADE

1. (Amended) An isolated nucleic acid molecule encoding a polypeptide wherein the [Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which] nucleic acid sequence of the nucleic acid molecule is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354,

- 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435,

437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;

- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; [and]

- (f) or the functional fragment or complement thereof [a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),

- (g) the complement of any of the nucleic acid sequences as specified in a) to f),]

for the preparation of a medicament for treating diseases associated with yeast or fungi.

2. (Amended) An isolated [Use of a] polypeptide which is involved in a pathway [eventually] leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232,

234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,



modifying the endogenic flora of humans and other mammals comprising the step of administering a compound according to claim 11.

16. (Amended) The method of claim 14 wherein the yeast or fungal infection is an infection caused by the yeast or fungi selected from the group consisting of [Use of a compound according to claim 12 where the yeast or fungus is chosen from] *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

17. (Amended) A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358,



- 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; or a functional fragment or complement thereof [and,
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e)].

18. (Amended) A nucleic acid according to claim 16 [characterized in that it is] wherein the nucleic acid is derived from *Candida albicans*.

20. (Amended) A nucleic acid sequence according to [any of ] claim 17 [to 19] which is mRNA

21. (Amended) A nucleic acid sequence according to [any of] claim[s] 17 [to 19] which is DNA.

22. (Amended) A nucleic acid sequence according to [any of] claim[s] 17 [to 19] which is cDNA.

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

- (a) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484; or a functional fragment thereof [and,]

25. (Amended) An expression vector comprising a nucleic acid sequence according to [any of] claim[s] 17 [to 23] .

27. (Amended) An expression vector according to claim 25 [or 26] which comprises a sequence encoding a reporter molecule.
28. (Amended) A host cell transformed, transfected or infected with the vector of [any of] claim[s] 25 [to 27].
29. (Amended) A nucleic acid molecule according to [any of] claim[s] 17 [to 23] for use as a medicament.
33. (Amended) A pharmaceutical composition comprising an antibody according to claim 31 [or 32].
34. (Amended) A method for treating a yeast or fungal infection comprising the step of administering [Use of] an antibody according to claim 31 [or 32], or an antibody capable of binding to at least one of the polypeptides as defined in claim 2[, for the preparation of a medicament for treating diseases associated with yeast and fungi].
35. (Amended) The [Use of an] method of claim 34 [antibody according to claim 34] wherein the fungus is *Candida albicans*.
36. (Amended) A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 wherein the nucleic acid probe [and which] selectively hybridises with the [any of said] nucleic acid molecule[s].
37. (Amended) A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 wherein the nucleic acid primer [and which] selectively amplifies any of said nucleic acid molecules.
38. (Amended) A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids [as defined in] of claim 1 or a human homologue thereof or at least one of the polypeptides of [as defined in] claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

39. (Amended) A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of [as defined in] claim 1 or a human homologue thereof and/or at least one of the polypeptides of [as defined in] claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

41. (Amended) A medicament comprising the [A] compound according to claim 40 [for use as a medicament].

42. (Amended) A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 [or 41] with a suitable pharmaceutically acceptable carrier.

43. (Amended) A method for [Use of a compound according to claim 40 or 41 for the preparation of a medicament] for treating proliferative disorders or for preventing apoptosis in [certain disorders] comprising administering the compound of claim 40 to a subject in need thereof.

44. (Amended) A method for [Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for] treating proliferative disorders or for the prevention of apoptosis [in certain diseases] comprising administering a nucleic acid molecule of claim 1 to a subject in need thereof.

45. (Amended) A method for [Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for] treating proliferative disorders or for the prevention of apoptosis [in certain diseases] comprising administering a polypeptide of claim 2 to a subject in need thereof.

46. (Amended) A pharmaceutical composition [for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases] comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

52. (Amended) A host cell transformed, transfected or infected with the vector of [any of] claim[s] 49 [to 51].

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JAB-T521**CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI****Field of the Invention**

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

**Background of the Invention**

This invention claims priority from International Application Publication No. WO 01/02550 entitled "Cell Death Related Drug Targets in Yeast and Fungi", filed July 3, 2000 which claims priority from EPO Patent Application No. 99870141.1, filed July 1 1999, the contents of which are hereby incorporated by reference.

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botritis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism.

These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

5        Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. To survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has been assumed that  
10       such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a similar process of cell survival also operates in single-celled eukaryotes.

      It has been found that expression of the mammalian *Bax* gene triggers cell death in *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* with morphological changes similar to apoptosis (Jürgensmeier *et al.*, 1997).  
15       However, the mechanism of *Bax* lethality in *S. cerevisiae* remains unclear.

      Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in  
20       yeast cells and other unicellular eukaryotes.

      It is an aim of the present invention to provide nucleic acid as well as polypeptide sequences which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

25       It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases associated with yeast or fungi.

      It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

30       It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

      It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

35       It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in yeast





### Detailed Description of the Invention

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 10 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 15 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 20 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 25 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 30 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 35 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356,

- 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- 5 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 10 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 15 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 20 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID 25 NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 30 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 35 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411,

413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;

- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e); and

(g) the complement of any of the nucleic acid sequences as specified in a) to f), for the preparation of a medicament for treating diseases associated with yeast or fungi.

- Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

- As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to

determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are  
5 codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the invention  
10 from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173,  
15 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473.

The invention also relates to nucleic acid sequences from *Candida albicans*, as  
20 represented by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439,  
25 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

30 The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic  
35 reactions caused by said organisms, such as the so-called "professional diseases" in,

for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352,

- 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 5 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 10 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 15 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 20 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 25 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 30 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 35 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,

Polynucleotides according to the invention may be inserted into vectors in an  
35 antisense orientation in order to provide for the production of antisense RNA. Antisense  
RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such

5 nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in

10 diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid

15 support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the

25 yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the

30 invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as  $^{32}\text{P}$ ,  $^{33}\text{P}$  or  $^{35}\text{S}$ , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected

35 using techniques known in the art.



According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,

320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270,

272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276,

278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474 . Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.





comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional  
5 activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds which bind  
10 to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex  
15 formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

Detection of the complex formation can be performed using several  
20 approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and  
25 measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive  $^3\text{H}$  can  
30 only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound  
35 radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

5           When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

10           One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

15           Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

          This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises  
20       providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating  
25       domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the  
30       presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

          An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a  
35       protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These



binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as  $\beta$ -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an

immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, abd even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with  $^{15}\text{N}$  or  $^{13}\text{C}$  are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughout assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting, band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein trageting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Yersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughout assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention

therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds  
5 identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

10 According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

The invention also relates to a compound identified using any of the methods of the invention.

15 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

20 The compounds of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*,  
25 *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii* infections.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

30 A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the  
35 nucleic acids or polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of

said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

5 Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi  
10 selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 15 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90 or 20 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 25 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452 454, 476, 478, 480, 482, or 484;
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 30 452, 454, 476, 478, 480, 482, or 484; and,
- (d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as a medicament.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the proteins of the invention. The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')<sub>2</sub> fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to, *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium* spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic



The invention also relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof  
5 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

The invention also relates to a vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically  
10 acceptable carrier.

The invention also relates to the use of an antibody of the invention capable of binding to at least one of the polypeptides of the invention or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

15 According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention. Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with  
20 any of the above described vectors.

According to another embodiment the invention relates to a nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences described in the invention.

25 The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the  
30 invention.

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are  
35 hereby incorporated by reference.

**Table 1.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed more than fivefold in a first experiment (see Example 2). The factor by which the transcript level was affected, is expressed as the Qt value. A Qt value higher than 1 indicates upregulation while a Qt value lower than 1 indicates a downregulation. For instance, a Qt of 0.5 indicates a two-fold lower transcript level of a particular mRNA due to *Bax* expression in *S. cerevisiae*. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0,21, respectively.

**Table 2.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly in a second experiment (see Example 3). In this experiment, the Qt values were calculated using the Pathways Software (Research Genetics).

## EXAMPLES

### **Example 1. Differential gene expression analysis upon Bax-induced cell death** **Materials and media**

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTYLMuBax, after linearisation in the Ty  $\delta$  element (Zhu, 1986).

### **Cloning of mouse BAX cDNA**

Mouse *Bax* cDNA, encoding the mouse Bax- $\alpha$  protein, was cloned by Pfu DNA polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

5'-ATGGACGGGTCCGGGAGCAG-3' and  
5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.



The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

### **Plasmid constructions**

5        The 2 $\mu$  ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Clal* and *BglII*. A *BamHI-HindIII* GAL1 promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI* FLP terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty  $\delta$  element in  
10    the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

      Mouse *Bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final  
15    expression plasmid YIpUTyLMuBax.

      The plasmid YIpUTyLMuBax has been deposited in the BCCM<sup>TM</sup>/LMBP culture collection as p5CTyGALmBax with accession number 3871 under restricted use.

### **GeneFilters**

20        The Yeast GeneFilters<sup>TM</sup> were purchased from Research Genetics Inc. (Huntsville, AL, USA).

      The Yeast GeneFilters<sup>TM</sup> are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right  
25    corner and the DNA is on the labeled side of the filter.

      Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

      Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and  
30    4 are organized in the same way as fields 1 and 2.

### **The Yeast ORF target**

      The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs  
35    designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly

provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

## Results

### *Induction of Bax-expression in yeast cells*

*S. cerevisiae* cells (strain INVSc1) were transformed with the expression plasmid YlpUTyLMuBax or the parental plasmid YlpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

The Ty  $\delta$  element of both plasmids allowed a stable multi-copy integration in the genome of the yeast cell. Southern analysis of the cells containing YlpUTyLMuBax revealed the integration of 5 GAL1-controlled Bax-cassettes near Ty elements.

The yeast cells containing YlpUTyLMuBax and the yeast cells containing YlpUTyL were grown overnight in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD<sub>600</sub> of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD<sub>600</sub> of 1 was reached. Subsequently, the yeast cells containing YlpUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD<sub>600</sub> of 1. The yeast cells containing YlpUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

### *RNA isolation*

Total RNA was isolated using RNAPure<sup>TM</sup> Reagent (GenHunter Corporation Nashville, TN, USA) according to the GenHunter protocol.  $1.5 \times 10^9$  cells were concentrated in a microcentrifuge tube and 1ml RNAPure<sup>TM</sup> Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150  $\mu$ l) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was

precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH<sub>2</sub>O.

#### 5 ***First strand cDNA synthesis in the presence of $\alpha$ -<sup>33</sup>P dCTP***

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL yeast cells and incorporation of  $\alpha$ -<sup>33</sup>P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH<sub>2</sub>O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)

1 µl 0,1 M DTT

1 µl RNase Block (40 units/µl) (Stratagene)

1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)

15 1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)

10 µl  $\alpha$ -<sup>33</sup>P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 3 or 5 · 10<sup>8</sup> cpm/µg for both the INVSc1YIpUTyL and the INVSc1YIpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

#### ***Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection***

30 The Yeast GeneFilters™ were successively hybridised with the  $\alpha$ -<sup>33</sup>P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

35 The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250

mm) filled with 5 or 10 ml MicroHyb™ solution (42°C) containing 5 µl polydA (0,5 or 1 µg/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating.

- 5 Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from  
10 Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

## 15 **Example 2. Quantification of Hybridisation Signals**

- Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster  
20 corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

25

## **Statistical processing of quantification results**

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

1. The frequency of occurrence of the values in a precisely defined intensity  
30 range(data range), established between 1000 and 61000, split up in intervals of 5000.  
2. The frequency in terms of percentage.  
3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

35

Subsequently, the results of the two experiments (hybridization with cDNA from YIpUTyL containing INVSc1 cells and hybridization with cDNA from YIpUTyLMuBax

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

**Example 4 Search for homologues in *Candida albicans***

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minnesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

15

**Example 5 . Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans***

The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a

wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

#### **Example 6. Assay for High Throughput screening for drugs**

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 µl of R-compound at  $10^{-3}$  M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at  $-70^{\circ}\text{C}$ . The strains are streaked out on selective plates (SD medium) and incubated for two days at  $30^{\circ}\text{C}$ . For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at  $30^{\circ}\text{C}$  for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250,000 cells/ml. Cultures are incubated at  $30^{\circ}\text{C}$  for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20,000 to 50,000 cells/ml. Cultures are grown at  $30^{\circ}\text{C}$  while shaking at 250 rpm until a final  $\text{OD}_{600}$  of 0.24 (+/- 0.04) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at  $30^{\circ}\text{C}$  for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Table 1.

ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103



YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211

YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Table 2.

ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

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**CLAIMS**

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which  
5 nucleic acid sequence is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

- 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330,  
332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360,  
362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390,  
392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420,  
5 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450,  
452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480,  
482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence  
which is more than 70% identical, preferably more than 80% identical, more  
10 preferably more than 90% identical and most preferably more than 97%  
identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6,  
8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46,  
48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86,  
88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118,  
15 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148,  
150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178,  
180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,  
210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,  
240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268,  
20 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298,  
300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328,  
330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358,  
360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388,  
390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418,  
25 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448,  
450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478,  
480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of  
SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,  
30 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75,  
77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111,  
113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141,  
143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171,  
173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201,  
35 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231,  
233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,

- 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291,  
293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321,  
323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351,  
353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381,  
5 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411,  
413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441,  
443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471,  
473, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more  
10 than 80% identical, more preferably more than 90% identical and most  
preferably more than 97% identical to any of the nucleic acid sequences  
shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29,  
31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69,  
71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107,  
15 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137,  
139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167,  
169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197,  
199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227,  
229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257,  
20 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287,  
289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317,  
319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347,  
349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,  
379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407,  
25 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437,  
439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467,  
469, 471, 473, 475, 477, 479, 481 or 483; and
- (f) a nucleic acid sequence encoding a functional fragment of any of the  
nucleic acid sequences as specified in a) to e),
- 30 (g) the complement of any of the nucleic acid sequences as specified in a) to f),  
for the preparation of a medicament for treating diseases associated with yeast or  
fungi.

2. Use of a polypeptide which is involved in a pathway eventually leading  
35 to programmed cell death of yeast or fungi, said polypeptide being selected from :



- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

5. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or

underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.

5           6.     A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 10           (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- 15           (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20           (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

25           7.     A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 30           (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 35           (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is



10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

5 11. A compound identifiable according to the method of any of claims 6 to 9.

12. A compound according to claim 11 for use as a medicament.

10 13. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.

14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.

15

15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenous flora of humans and other mammals.

20 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,  
25 and *Sporothrix schenckii*.

17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:

30 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,  
35 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e).

5           18.     A nucleic acid according to claim 16 characterized in that it is derived from *Candida albicans*.

          19.     A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.

10

          20.     A nucleic acid sequence according to any of claim 17 to 19 which is mRNA

          21.     A nucleic acid sequence according to any of claims 17 to 19 which is  
15   DNA.

          22.     A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.

20           23.     An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.

          24.     An isolated protein which is involved in a pathway for programmed cell  
25   death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and  
35   most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348,  
 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384,  
 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424,  
 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476,  
 478, 480, 482 or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,  
 preferably more than 80% identical, more preferably more than 90% identical  
 and most preferably more than 97% identical to any of the amino acid  
 sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,  
 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,  
 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,  
 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,  
 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,  
 454, 476, 478, 480, 482 or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c)

25. An expression vector comprising a nucleic acid sequence according to  
 any of claims 17 to 23 .

26. An expression vector according to claim 25 which comprises an  
 inducible promoter.

27. An expression vector according to claim 25 or 26 which comprises a  
 sequence encoding a reporter molecule.

28. A host cell transformed, transfected or infected with the vector of any of  
 claims 25 to 27.

29. A nucleic acid molecule according to any of claims 17 to 23 for use as a  
 medicament.

30. A polypeptide according to claim 24 for use as a medicament.

31. An antibody capable of specifically binding to a polypeptide according to  
 claim 24.



35            40.        A compound identifiable according to the method of claim 39.

41. A compound according to claim 40 for use as a medicament.

42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising  
5 admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain  
10 disorders.

44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.  
15

45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.  
20

47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.  
25

48. Use of an antibody according to claim 31 or 32 or an antibody capable of binding to at least one of the polypeptides as defined in claim 2 or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.  
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## ABSTRACT

The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

**FIG. 1:**

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)

AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGAGTTCCTCAAGACTTATACTT  
CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTCGTTACAACGCTGCAGGACTCTT  
TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAAATGTGGTTGTAACCTTTT  
TAATTTTTTTCTTGAACCTTGTGAGTCGTAATAAATCGTTTCTGGGAAGTGAAGGTAAT  
AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAAGTGTGTAGG  
GACGTTTCGATACCAAAATTTCTTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT  
CGTAGCGCATACATCTGATCGAAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC  
CAGCATCAAAATTTTCATCATTAAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA  
CCTGATTGACGAACCAAGAAATGCCTTATCACATATTTATTTTGGCACTCTTCACCTACC  
TGGCCACGTCCAATGTTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGGGCCCCGAGGA  
AAAATGGGATGAATGTCAACTTTTATAAATACTCATTACTGGATTCAACAACGTATTCTT  
ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)

MPYHYLFLALFTYLATSNVVSSTQACLPGVPRKNGMNVNFYKYSLLDSTTYSYPQYMTS  
GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)

AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA  
AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTTATTCAAGATTATTTGGTTTTT  
CTAACCGCGCGCGCGCGCAGGTACCCCGCGCATCTCTTCTCTCGAAGAAAGCGGAAAAA  
ACAAAAAAGTATAAATAGTGGAGTCTTTTCCCATTTAACATTTAGAAAAAATTCG  
AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCCTTGGCGGCTTTTCTCAGTTTCG  
TGGGCTAGTACATTTTACCTAGTATGCTGGGAACCTTTTTTCCGTATTCTATTCTATTCC  
TTGCCTTACTTTTCTTATCATTTTTTATATAACCAATTTCAAAAATACTTTTTTAACGTG  
ATAGACGCATTTTGTATTACAAATTAAGAAGTCAAAATATAATATGTGAATTAATAA  
CTCCACAAGTAGGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA  
CCAAGAGCCTACCAAGACCGGATGGTTTGTGTCAGTGCAGGAAGTATGGACTCCAAGATCA  
GAGGTGGGTTGGCTTATAACGATTTTTTAACTTTACCAGGTTTAGTCGATTTTGGCGTCT  
CTGAAGTTAGCCTACAGACCAAGCTAACCAGGAATATTACTTTTAAACATTCCATTAGTAT  
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTATGGCTCTGTTGGATG  
GTATCGGTTTCATTCACCATAAAGTGTACTCCAGAGGACCAAGCTGACATGGTGCAGAAAG  
TCAAGAAGTATGAAAATGGGTTTATTAACAACCCTATAGTGATTTCTCCAAGTACGACCG  
TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTGTCAGGCTTCCCTGTCACGGCAG  
ATGGAAAGAGAAATGCAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG  
AGGACAAGTCTTTACTCGTTTCAGGATGTCATGACCAAAAACCCCTGTTACCGGCGCACAAG  
GTATCACATTATCAGAAGGTAACGAAATCTTAAAGAAAATCAAAAAGGGTAGGCTACTGG  
TTGTTGATGAAAAGGGTAAGTTTCTTCTATGCTTTCCCGAAGTGAATTAATGAAAAATC  
AGAAGTACCCATTAGCGTCCAAATCTGCCAACACCAAGCAAGTGTATGGGGTGTCTCTA  
TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG  
TCGTCATATTGGATTCTCTCAAGGTAAGTCTATTTTCCAATTGAACATGATCAAAATGGA  
TTAAAGAAATTTCCAGATTTGGAAATCATTTGCTGGTAACGTTGTCACCAAGGAACAAG  
CTGCCAATTTGATTGCTGCCGGTGCGGACGGTTTGAGAATTGGTATGGGAAGTGGCTCTA  
TTTGTATTACCCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG  
TGTGTGAATTGCTAACCAATTCGGTGTTCATGTATGGCTGATGGTGGTGTTCAAAAAC  
ATTGGTCAATATTATACCAAGCTTTGGCTCTTGGTCTTCTACTGTTATGATGGGTGGT  
ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)

MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGLAYNDFLILPGLVDFASSEVSLQT  
KLTRNITLNIPLVSSPMDTVTESEMATFMALLDGIGFIHNCPTEDQADMVRRVKNYENG  
FINNPVIVISPTTTVGEAKSMKEYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV  
QDVMTKNPVTGAQGITLSEGNEILKKIKKGRLLVVDEKGNLVSMLSRTDLMKNQKYPLAS  
KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVVILDSSQGSIFQLNMIKWIKETFPD  
LEIIAGNVVTKEQAANLIAAGADGLRIGMGTGSICITQKVMACGRPQGTAVYNVCEFANQ  
FGVPCMADGGVQKHWSYYYQSFGSWFFCYDGWYVGRYYRITR

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)

GGGAGAAGCTTATCTTACTGTAGAGAAGAAATGGGATTGCGTTACTCCATATATATTGAAA  
ATCCGTTATCTTCCCCATCATCATCGTATAAATCAATAAACGACCCGTTATTCCACTCTC  
AGCATCGATCGCAAAAAAACGTGAGCTTCATCACCTACGGTTGTAGACATTGCAAGACAC  
ATCTTTCCAGTTCCCTTCCAGATTATTTCTAGAGATTATAGGGGTAGGACCGGAAGTCTT  
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTCGAGCAACGAAGAATGTTGA  
CTGGCGACTACTTAGTCTGTGATATTTCTTTGTCTATTGGTGCAAGAGGAACGTAGGTTGA  
AATACTTGCAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC  
TGAAAAACATTTGTAAATGTACTTGATGTCTTCTTTGTCTGCTATCTAGCACCTCTCGT  
CTTTTAGTGCTTTTGTAGCGTATGATTTCTTTTAAAGAATCTGGTCTTTCTTCTTCTATTT  
TGATTGGGTATATTTCTATTTCGTGTTTCATTACTGGTCTGGGTTAATTGGGTTTTGGTTT  
GGTCCAGTTGTTTTCAAGTAGCCTTTATTTTTTTCATTGTGGTATTTTATCTTATCGATTT  
ATACTTTTTTTTATTCAAAGAAAATTAACACAGATAATCTCTTATGAGCCTAGCTACTTGT  
TTTTTCTTACAGGGCCATTGACTTATGCCCCGAACGAGTCTTACTTTACTTTTTTTTGTA  
TTTTCAATAATGTCGTGTTTCCCATGTTGTAA

YBL048W, 103 aa (SEQ ID NO 6)

MILFKNLVFLPSILIGYISIRVSLLVWNWVLVWSSCFQVAFIFSLWYFILSIYTFYFSK  
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVVPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)

GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTACGGAATCA  
CATAGCTTTTCATTTTGTTCCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC  
TACAGGGTCTGACATTTTTAACTTTCAGGTTAATGATGGTGTTCTTACTATATTCTCGAG  
TCGTACAGAAGTTAGTTTCAGATAAACTGCTTCGGTGCTGCCCACTTCTTATCATTACTTC  
AACTTTACCTTCCCTATACCTGTGTGTCCTTATTAATTCAGTTAATCCGAGGTAATAGA  
TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTTCCT  
GGAAAAGAATAACAATTAAGGCAGCCTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA  
TTAGCGCAAGAAGAAGTGTGATATAGTACTCATAGAGGCAGGCTACAGACTAGGGAAAGC  
GTGTTCAACAACAATAAGAAATGGAGACCAGTTCTTTTGAGAATGCTCCTCCTGCAGCCA  
TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC  
AATCTATCGAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAACCGGAACTGGTG  
AGAACTCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA  
CCAATGGTGCTTTGGACGATGATGTTATCCCAAATGCTATTGTTATTAAAAACATTCCGT  
TTGCTATTAAAAAAGAGCAATTGTTAGACATTATTGAAGAAATGGATCTTCCCCTTCCTT  
ATGCCTTCAATTACCACTTTGATAACGGTATTTTCAGAGGACTAGCCTTTGCGAATTTCA  
CCACTCCTGAAGAACTACTCAAGTGATAACTTCTTTGAATGGAAAGGAAATCAGCGGGA  
GGAAATTGAAAGTGGAATATAAAAAAATGCTTCCCCAAGCTGAAAGAGAAAGAAATCGAGA  
GGGAGAAGAGAGAGAAAAGAGGACAATTAGTAGGAACAACACAGATCGTCATCTAATCTTT  
CTTTGGATTCTTTATCTAAAAATGAGTGGAAGCGGAAACAATAACTTCTAACAATCAAT  
TATTCTCGACTCTAATGAACGGCATTAAATGCTAATAGCATGATGAACAGTCCAATGAATA  
ATACCATTAAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTTCTGAACCAAC  
CTTCACTTTCTGCCCAACATACTTCTTCATCGTTGTACCAAACAACAGTTAATAATCAAG  
CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGGCCTCTCC  
CACCCCAACAACCTGGACTTCAATGACCCTGACACTTTGGAAATTTATTCCCAATTATTGT  
TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT  
CCCACAAGAGAATTATCAATGTTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC  
CAAGATTTATTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC  
AACAACAAGGTCAAATGACATCTGCTCATCCTTTGCGAGCCAACTCCACTGGCGGCTCCA  
TGAATAGGTCACAATCTTATACAAGTTTGTTCACAGGCCCATGCAGCAGCTGCAGCGAATA  
GTATTAGCAATCAGGCCGTTAACAATTTCTTCAACAGCAATACTATTAAACAGTAATAACG  
GTAACGGTAACAATGTTCATTAATAACAATAGCGCCAGCTCAACACCAAAAATTTCTT  
CACAGGGACAATTTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA  
GTTCTCAATACAATTTCCGCAGACCAACCGCAACAACCTCAACCACAAACACAGCAAAATG  
TTCAGTCAGCTGCGCAACAACAACAATCTTTTTTAAGACAACAAGCTACTTTAACACCAT  
CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTATCAAATCAATTCGGTTAATCCCT  
TACTGAGAAATTCTCAAATTTACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

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TATCCCAAGCGCAACCACCAGCACAGTCCCAAACTCAACAACGGGTACCAGTGGCATAACC  
AAAATGCTTCATTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACCT  
CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTCTAATTTCTCATATC  
AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGGCAGCTTGATCT  
ATAAAGCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAACAGGGCTTGAATCGTTCTT  
TAAGCGGACTGGATTTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAAINDAQDNNINTETNDQETNQQSIETRDIDKENGVOETETGENSAKNA  
EQNVSSSTNLNNAPTNGALDDDVIPNAIVIKNIPFAIKKEQLLDIEEMDLPLPYAFNYHF  
DNGIFRGLAFANFTTPEETTVITSLNGKEISGRKLKVEYKMLPQAERERIEREKREKR  
GQLEEQRSSSNLSLDSLSKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS  
SNNNNSGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF  
NDPDTLEIYSQLLLFDREKYYYELAYPMGISASHKRIINVLCSTLGLVEVYDPRFIIIR  
RKILDHANLQSHLQQQGQMTSAHPLQPNSTGGSMNRSQSYTSLLOAHAAAAANSISNQAV  
NNSSNSNTINSNNGNGNNVIINNNSASSTPKLISSQGQFSMQPTLTSPKMNHHSSQYNSA  
DQPQOPQPTQONVQSAAQQQQSFLRQQATLTSSRIIPSGYSANHYQINSVNPPLRNSQI  
SPNSQIPINSQTLSSQAQPPAQSQTTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSQQLP  
QHTNGSVHSNFSYQSYHDESMLSAHNLNSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ  
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCTTCCACCGTCGGAAGAAACACTT  
CTGAAGTGTTAAGGTAATCGACGCCCTTGCAATTGACTGACAAGGAGGGCGTAGTAACCTC  
CAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTCCCTCTGTCTCCAATGATGAGG  
CGAAGGCTAAATTTGGTCAATTTAATGAAATTAACCCCTATTTAAGATTCACCAAGTCGA  
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTAACTAAA  
ACTTTTATCTATCTTTTCATTCTTATTATATCTCATCTCTGTACGAAGGGCCGCTCATTTGA  
TCATTTTCTCTTACATACCGTAAAGGAATGGCGTTAAAAATATATATATGAAATLGCATG  
TAATAAACTCTCTGCGAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC  
TGCGTATACGCATTCTCGTCAATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT  
TTAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC  
CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG  
TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAAATTTCC  
CTCATCCTTGCTCCAGATGCGAAAAAATTGGTCTCCACTGTGAAATCAATCCTCAATTCA  
GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA  
AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCGTTTCATCTTTTACAACAGATTCCCA  
TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAACCTCCAACCTCCGGGTACTATTA  
TCCCTAACCAGATTCTTCTCCTTCCTCAGGTTCTCCAACCTCTTCCGCGGCTCAACGAG  
ATTCTAAGGTTTCAGTTCAAACCTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC  
AGGGCAGCAATACGAATAAATTTAAAGCAAATTAATGAAGCATCTTCTCATATGACGTTGC  
GCGCATCTTCTTTAGCGCAAGATTTCGAAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC  
CCCCGCTGCTAAATGACTCAGCATTTGCCTAATAATTCAAAGAATCTTTACCTCCTGCTT  
TGCAAATGGCTTTTTATAAGAACAACCTCTGCAGGTAACACTCCGAACGGCCCCCTTCTCTC  
CAATTCAAAAAACATATTCCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC  
AACCACCATTTGCAGCAACAAGCCACGTAGCAACAAATAACAATGCAGATAGGACGAAGA  
CGCCGGTAGTAGCCACCACCAGACTATGCCATTATTGCCTTCGCCGATGCAAAATGTAG  
ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACGATA  
TTTTCGTGACTAGGTATCTGCCGATTTTTCCTATTATGTATTCCAATAACGCCACCGAAT  
TATACTCCCAATCTCAGTTGCTTTTCTGGACCGTGATGTTGACGGCATGTCTGTCTGATC  
CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT  
GCTGGATAAGAACACCTAGATCCACACATATTTGCGAAGCTTTGTTAATATTGTGCATTT  
GGCCTTTGCCTAACCAAAAAGTCCTAGATGATTGTTCTTACCGTTTGTAGGATTAGCAA  
AGTCACATGTCTTATCAATTAGGTTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA  
CTCAAACATCAATGCCAAATGCAGAAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT  
TTGCCGAACCTTTGTTGGGCGAGTATCCTTGGTTTGGCCACCAACTTCACAGACAGACTATT  
TATTAGAAAAAGCCTTATCCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA  
TTGACAATAACAACAATGATAAAAGGAACAAGAAAGACGAGCCGCACGTTGAAAGTAAAT  
ACAAACTACCGGGCAGTTTGTAGAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAAATTTGT  
CTCATATCATTTGGTTCTTCCACTTCCAGTCCTGATGGTTTATTGGAACCAAGTATCGTG

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CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACCTTTAAATTTCC  
AGAGTGACGATACTGTCAACATTTATTTTCTTTATGTTAAATTAACGTCTGTGTTGTTTG  
CATTCTACCCGAAACACCTCCTACCGATCAAATTCATATGTCACAGAGGCCTATCTAA  
CAGCTACTAAAAATGTCACTCTATTGAATAATCTTTTAGAAACACACCAATTAATTGAAC  
TGCCTATTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT  
TGACTCCTTTACTTCCTGACAAATATTTTGATTGAGCAAGGCAATCCGTGGTCACTATCC  
ATAGACTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTTGAGAATGATATTTCGA  
GAACTGCAAGTATGTTAGAAAACTGAACTTCGTACTGATCATGCATCCAGAAGTTTTTG  
TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG  
ATTTGGTTTGGTGTGTTTACGAGGCGAGAAGAAGGGAAATGGATCCCGAATATAACAAGC  
AAGCCTTAGAGAAAAGCCGCTAAGAAAAGAAAATTTTCCTCAAATGGTATCTACAATGGCA  
CTTCGTCTACGGGTGGCATAACGGACAGAAAACCTATATCCATTTGCCACTATATAACCATA  
TCTCCAGAGATGACTTTGAAACTGTAAACAAAAACAACACCAAGTGGAAACCACTGTTACCA  
CTTTAGTTCCTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAAATAACG  
GAGATTCTGACGGTCTCTATAATGGAGATTAACGGGATACCTCTTCCATGCTCGGGGAAA  
CAGGCAGCGTAAAATTTCAAAGTTTATTTCGCTAATACCTCGAATAGTAACGATTATAATA  
ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCTCTAATTCAATTTATC  
CAGTGGCTTCTGTCCCGCTTCGAATAACAATCCACAAGTACTAAGGTAGACTATTATA  
GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA  
ATCATTTTCTGCGTCCGTTCCAGGGTTAAGGAACCAACCCCGTTGGCAACTTATCTAATA  
ATGTTACATTGGGAATAGACCACCTTATCCAAGGGAGCACAGTAATTTACAAAATGTCA  
CCATGAATTATAATAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA  
TGTCCTTACGTCACCTTTGTTTTCGGTCAATATATGACAGTTGGATTCCGCGTCCGA  
CCCCGGTCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MVKDNRSDQDQDFSSAHMKRQPEQQQLQHQFSPKKQRISHHDDSHQINHRPVTSC'THC  
RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKKGSQQLQLLRQDVDEIKSKLDTLLA  
NDSVFVHLLQQIIPMGNSLLNKLNLHPTPTPGTIIIPNPDSSPSSGSPTSSAAQRDSKVSQV  
TYLSREPQLQANQGSNTNKFKANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLLND  
ALPNNSKESLPPALQMAFYKNNSAGNTPNGPFSPIQKTYSPHTTST'TVTTTTNQPPFAAT  
SHVATNNNADRTKTPVVATTTTmplLPSphanVDEFVLGDISISIEKANRLHHIFVTRYL  
PYFPIMYSNNATELYSQSQLFWTVMLTACLSDPEPTMYCKLSSLIKQLAIETCWIRTPR  
STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN  
AEKWRTRTWLGIFFAELCWASILGLPPTSQTDYLLEKALSCGDEESEEDNNDSDNNND  
KRKKDEPHVESKYKLPGSFRRLLSLANFQAKLSHIIGSSTSPDGLLEPKYRAETLSIL  
GKELDLLAKTLNLFQSDDTVNIYFLYVKLTVCCFAFLPETPPTDQIPYVTEAYLTATKIIVT  
LLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLLDPKYFDSARQSVVTIHRLYRNQ  
LTAWATSVENDISRTASMLEKLNFLVIMHPEVFEEDGIIISRMRSHLTGSIFYDLVWCVH  
EARRREMDPEYNKQALEKAARKRFSSNGIYNGTSSTGGITDRKLYPLPLYNHISRDDFE  
TVTKTTSPSGTTVTTLVPTKNALKQAEKLAKTNNGDSGDSIMEINGIPLSMLGETGSVKFQ  
SLFANTSNAGDYNNTLLDASNDISIPNSIYPVASVPASNPNPQSTKVDYYSNGPSVI  
PDL SMKRSVSTPVNHFPASVPGLRNHPVGNLSNNVTGLGIDHPIPREHSNLQNV'TMNYNNQ  
FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPV

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGGAGTACGAATTAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT  
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG  
ACCCAATTGGTGATGAAGAACATCTATTAATGACACCATTTTCAAATTAAAAGTGTTCA  
AATTATGAAAACAACATCATATAAATACGTACAAATTTTCTCTACTCGAAGTGATATAGA  
TGTATATGTGTAAGTTTACGTTTAAAGTTAGAGTCATGTAATGCTAACTGTCTCCACCGAT  
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGGTT  
ATTTTCGGCGCGCGCAAAAATATTTGGTATAATTATGGAAATACAAAAAGGGGAACCAT  
AAAGGTTGAGGAGGGGATGATAAGAGAATC'PAATAATTGTAAGTTGAGAAAAATCATAA  
TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAA  
GGAAGGCGGAGTCGGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTGCG  
AAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCGTAAATATCTAGTTTCTGCTG  
ACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTACCCCTGAGA  
AGGCCATCTTCATTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA  
TATATCAAGAACACAAGGATAAGGACGGGTTT'TGTATGTCACCTACTCAGGAGAAAATA



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CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF  
VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGFVYVTSYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)

GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCTGT  
CAAGGTGCATTGTTGGATCGGAATAGTAACCGTCTTTACATGAACATCCACAACCAACGA  
AAGTGCTTTTCAAGCATTGCTTGATTTCTAGAAAGATCGATGGTTATTCCCTCCCCCTT  
ATGCGTCCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTCGCACCTTAGCGTGCTCGCA  
ACACAAAAATAAGTAATATGCGAGTTTTAGATGTCTTGGCGATCTATGCACGTTCTTGA  
GTGGTATTTTATAACAACGGTCTTTTTTACCCTTATTCCTAAACATATAAATAGGACCT  
CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTTATTCTACTCTCTTATACTAAT  
AAAACCACCGATAAAGATATATCAGATCTCTATTAAAACAGGTATCCAAAAAAGCAAACA  
AACAACTAAACAAATTAACATGTCTATTTAACAGTCCATTTTTTGATTCTTTTGACAACA  
TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG  
CACCAAGACGTGAGTTAGCAAAACACACCCGCAAGGATTCTACTGGCAAGGAAGTTGCTA  
GACCAAAATAACTATGCTGGCGCTCTTTTATGATCCCGAGAGATGAAACCTTAGATGATTGGT  
TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGGTTTCCCTAGAAGTGTGCGAGTTC  
CAGTTGATATTTTGGACCATGACAACAACACTACGAGTTGAAAGTCGTGGTTCCTGGTGTCA  
AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCAAAATTTTGGTTTCTG  
GTGAAATTCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA  
GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA  
ACATTTAAAGCAGACTACGCAAAATGGTGTTTTGACATTAACAGTTCCAAAAATTGAAGCCTC  
AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA  
ACTAA

YBR072W, 214 aa (SEQ ID NO 14)

MSFNSPFFDFFDNINNEVDAFNRLLGEGGLRGYAPRRQLANTPAKDGSTGKEVARPNNYAG  
ALYDPRDETLDDWFDNDLSLFPSPGFGRSVAVPVDILDHDNNYELKVVPVGVKSKKDID  
IEYHQKNQILVSGEIPSTLNEESKDKVKVKKESSSGKFKRVITLPDYPGVADNIAKADYA  
NGVLTTLTPVKLPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)

AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA  
ACTAAAGTGACCTGGCTCTATAGTGTGTCCCTCTCGCGAGGACCATTGTTGCTTGCATA  
TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA  
TATATGAGTTGATGAATAAATAGTTATAAAAACTTGCTTTGGCTTCGATATATGACCGTT  
ATTTTTGACTAAGTTTAAACGAAGGAATCTAACCTCGTTCTTGTAAATTACCAAAATCTTC  
AACACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCTA  
CTTCTACTTCTGGGAAAGGCATTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA  
AAAAATAAAACGCGAAGAGCTAAAAAAGAAACCTACTATAAATAACCGATTAG  
AATCGAGTTTGTATTGAAATGGCGGTAATAAGCGTTAAACCTCGACGAAGAGAGAAGA  
TCCTACAGGAGGTAAAAACAGCTCGGTATATCAAAACGGTATTTGATTCCGGTACTACTC  
AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA  
ATAAGTACACACAACCTCAAACCAACCGCCACTGCAGTCACAACAGCCCCTATATCTAAAG  
CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTCGGCGGGACCTACTTTAAATCTTGCCA  
AGAAGCCGAATAATCTGTCTCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA  
AGCCTACTACCAAAAAGCACAAGACTTGGAGTGGTGATGGCTACGCTACCTTAAAGCCA  
GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGCTAC  
CAAGTGATTGAGATTCTCTCTTTCGAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT  
TGGATTACGAATTGAAGGAAATGCGAGAAATACGTAGCGCCAAAGAAGCCTTATCAAAA  
ACATGGGAAATCCAGCCCCACCGACCACAAGCACAACAGAAACAGTGCCCTTCTACGAAGA  
ATGACGGTGGCAAATACCAATGCCTCTGTCTCAGCTGTTTTTACTAAACACTGTGAAAA  
GATTCAAATCAGTAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACAGTC  
AAAATTCCAAAGCCAAAAAATATTTATCCAGTATTTGATGTCAACAAAATCGATAATCCTA  
TAGTAATTGAACAAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA  
AATCTTGCGCCCTCATCAGAGGGAAGGGTGAAGTTCATGTATGATTGCTTAATGGGCT  
TGGCAAGACCAACTATTGAAAAACCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG

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AAAATGACTCAGATATTAGTGGATGCCCTTTTGGCTGATGATATGGGTTTAGGTAAAACAC  
TAATGAGTATAACTTTTGATTGGACATTAATTAGGCAAACCTCTTTTGCATCAAAAGTTT  
CATGTTTCGCAATCAGGCATACCATTAAGTGGACTTTGTAAGAAGATTTTAGTCGTTTGTC  
CCGTTACTTTAATAGGAAATTTGGAAGAGAATTTGGAAGATGGTTAAATTTGTCAAGAA  
TAGGTGTTTTGACATTAAGCTCAAGGAATTCCTCTGATATGGATAAAATGGCTGTCAGAA  
ATTTTTTAAAGTGCACGAACCTTATCAAGTCTTGATTATTGGCTACGAAAACTCTTGGA  
GTGTTTCTGAAGATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG  
GCCATCGACTAAAAACGGGGCTTCTAAAAATTTTAAATACGCTGAAGAGTTTAGACATAA  
GAAGGAAGCTTTTGCTTACGGGAACCTCTATACAAAATGATCTTAATGAGTTTTCCTA  
TTATAGATTTTCATAAACCCAGGAATCCTTGGAAGCTTCGCTTCTTTCAAAGAAGATTCA  
TTATCCCTATACTAGAGCCAGAGACACTGCAAACAGATACAACGAAGAATTGTTGGAAA  
AGGGGGAAGAAAGGTCAAAAGAGATGATAGAAATTACGAAAAGATTTATTTTGAGACGAA  
CAAATGCGATTTTAGAAAAAGTACCTTCCCTCCAAAGACGGATATAATTTTATTCTGTAAAC  
CATACAGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG  
GACAATTGACGTTTCACTTCTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTAAC  
CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC  
AGGACAGCTATAGTCGTTCTTTGAACTCTGGTAAGTTAAAGGTATTAAATGACATTAG  
AAGGTATTAGGAAGGGTACCAAGGAGAAGGTCGCTAGTGTCTAACTACACTCAAACAT  
TGGATATAAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT  
CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT  
TTGGATTCTTGTTGAGTGCAAATCGGGAGGTGTAGGATTGAATCTAGTCGGTCGTTTCGC  
GACTTATTTTATTTGATAATGATTGGAATCCTTCAGTAGATTTGCAAGCGATGTCACGAA  
TTCATAGAGATGGTCAAAAAAGCCGTGCTTCATATATAGACTTGTACAACTGGGCTGTA  
TCGATGAGAAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG  
GTGACTCGGAGATGAGAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT  
TGAAGGACCTGTTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT  
CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG  
TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCCTGGATTTACAAAAGAAAA  
TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCTCG  
TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTATTCACAG  
ATTCGTTACCCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAGCCCCGCGAGATAT  
GTCTCAGAGAACAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSSVYQTVFDSGTTQMQUIPKYENKPFKPPRRVGSNKYTQLK  
PTATAVTTAPISKAKVTVNLKRSISAGPTLNLAKKPNLSSNENTRYFTIMYRKPTTKKH  
KTSWGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSLSLFTLKFAGSNEVQLDYELKE  
NAEIRSAKEALSQNMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTRFKSVTK  
QTNEHMTTVPKTSQNSKAKKYYPVFDVNKIDNPIMVNKNAAEVDVIVDPLLKFLRPHQ  
REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLKTLMSITLI  
WTLIRQTPFASKVSCSQSGIPLTGLCKKILVVCPTLIGNWKREFGKWLNLNRIGVLTLS  
SRNSPDMDKMAVRNFLKVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDGHRKNG  
ASKILNTLKSLEDIRRKLILLTGTPIQNDLNEFFTIIIDFINPGILGSFASFRRFIIPITRA  
RDTANRYNEELLEKEERSKEMIEITKRFILRRTNAILEKYLPPKTDIILFCKPYSQQIL  
AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGS DPYKSHIKDTQSQDSYSRS  
LNSGKLKVLMTLLEGIRKGTKEKVVVVSNYTQTLTDIIENLMNMAGMSHCRLDGSIQAKQR  
DSIVTSFNRNPAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDGQK  
KPCFIYRLVTTGCIIDEKILQRLMKNSLSQKFLGDSEMRNKESNDDLFNKEDLKDLFSV  
HTDTKSNTHDLICSDGLGEEIEYPETNQQTVELRKRSTTTWTSSALDLQKKMNEAATN  
DDAKKSQYIRQCLVHYKHIDPARQDELFDVITDSFTELKDSITFAFVKPGEICLREQ

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)

AGATCCTAAAACAGCACGAAGCATATTATTGCGCATAAATTTGTTCTTGTAGGATCTTTTC  
TTGACATTTTTTTTCTACTCTGCGAGAACTTCTCTTTTTTTTCTCTTAGGGACGAAAA  
CAAACAAGGGCACTTTTTTTTATCTTTTTTTTTTCTCTGTTGTTTCAAACAAAAAGAT  
TCCACCCTACATCAGTGTAAGACTGTAAAAGCTTTCTGATAAATAAGCACTTTCCAT  
ATTTTTCAACTGAAAAATAGTTTTCTTTTTTGCAGCTATTATTGACTTCATTAAAGAAATAT  
CCTTTTTTTCCCCGTTGCAATTATTTCTATAAGGGAAGCTGGAAATAGGGGGCTGGAAAA  
GATATTTGAACAGTCGCTCCAATAACCGTTCTCACCATCATTAACATTTTTGAAGGTGAA  
TACTGTTTCGGTCGATTTATGGCTAATTTGTCAAATACATTTGAAAAAGATTAAAAACAAG

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CACAAGCGGTTGAGCATACTATGTGCGCAGACAATTACATCTCTAGATCCGAATTGTGTGTA  
TTGTATTCAATAAACTTCGAGTGCAAACGAGAAGAGTTTGAATGTCGAATTCAAACGTT  
TGAATATACATTTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA  
GAATCCATCAGGATAATGCGAAACCGCTTTTTTTCATTTTTGCAGAATCTGGACTTCATGT  
AATCCATCATACCATATCATGATACTGAATTTGTCGGATGATTTGCATAAACTGATTTCTA  
TCAGCAAATCAAAAATAC'TGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT  
TGACCAATAATCCCAAACAATCCTTATATTTTTGCATTCTTACAGAACTATATAAAATGGT  
TGATTCCCTTTCTCCTTTTTTGGATTATCAATTAGATTTTTATCTAATTTTACGTATGAAT  
TCAATTCCACATACTCGCTGTTTCGCCATCCTATGGACATTGTCAATTTACAGCCTTTTGGC  
TTTATAAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTTCTACCA  
TTGAGTTTCTTCAAGATAAAACAGAAAGCCCAAAAAAAGCTAGTTTCGGTTATCATGTTGA  
AGAAATGTTGTTTTTATTCCTGTGGCTTTGTTGTTTGGCGCAATATTAATATCATTTCCAGC  
TATATTGTTTTGCGTTGGAAATTTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA  
TCTTGTCTTTTTTGCCTACTATACTTATTTGCACGTTTACTCCGGTTTTAACTGTGATTT  
ACAACAAATATTTTCGTAGAACCAATGACAAAGTGGGAAAATCATAGCAGTGTGTGAATG  
CAAAGAAATCTAAAGAAGCTAAGAACTTTGTTATTTATTTTTCTATCCAGTTACGTTCCCC  
TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTGTGTTGACCGCAGAAATAAGAA  
CTAAGGTTTTTCAATGCCTTTTTCAATATTGGCCGTTTACCTACCCATGATTCAGATTTTA  
TTATTGATACAAAGCGCTATGAAGATCAATTTTTCTACTTTATTTGTTATCAACCAACTGA  
TTCAATTTAGCATGGAAAACCTTTGTTTCCAAGCCTTGTTAGCATTGCTCAGCAGAAAATTA  
ATGGACCAAATCCTAACTTTGTCAAAGCTGAGAGTGAAATCGGTAAAGCTCAACTCAGCT  
CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAAACAGACCCCTGGGGAGCAA  
CATTTGATTTGGACGCCAACTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGGTTATGT  
TTTTCTACAATTTGGCCACTAGCTCCATTTTATCTGTTTGATAGTCAATTTGATTGTTTACC  
AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT  
ACGATAAGCCATCCTCTGTGTCTAATACCCAAAAACTGACGGTTGGTCTATGGAACCTCTG  
TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTTGACCTATATGTACC  
AGAGCTGTAATATACCAGGTGTGCGCGCTCATACTTCCATCCATACGAATAAAGCTTGGT  
ACCTAGCAAATCCAATAAACCCTCGTGGGATAAATATTTGACTATATGCTGTTTTTATTG  
AGCATGTTAGTGTTTCTTCTTCTTCTTCTAGTATTTTGAAATCTTCCCATGATG  
ACGTTGCAAATGGCATTGTGCCAAAGCATGTAGTTAACGTGCAAAACCCACCAAAACAAG  
AAGTCTTTGAAAAAATTTCCCTCCCTGAATTTAATTCGAATAACGAAAAAGAAGTCTC  
AAAGAAAAGGGTCTGCGAATGAGAAGTTGCACCAAGAACTCGGTGAGAAACAGCCTGCCT  
CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAATGATCCGTCTTCTT  
TATCCTCAGCTTCTCTCGCTTCATTATCTTCTTCTTCTTAGCAGCAAAACCGGTGTAG  
TCAAAGCTGTTGATAACGATACAGCCGGATCTGCTGGTAAAAAGCCATTGGCCACAGAAA  
GTACTGAAAAAAGAAATTTCTTTGGTGAAGGTGCC'TACCGTTGGCTCATATGGTGTTCGGG  
GCGCCACTTTTACCAGAAACAATTCCAACATCTAAAAATTACTACTTAAGGTTTGATGAGG  
ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCGAATCTTCCAACGCCACCAATAACA  
ACACCTTAGGCACGGAAAGTAAGCTTTTGGCAGATGGTGACGCCGTTGATGCACTAAGTA  
GAAAAATTGATCAAATACCCAAAATTTGCTGT'TACTGGTGGCGAAAATAACGAAAAATACCC  
AGGCCAAAGACGATGCTGCCACTAAGACTTCACTCATTAAGATGCAAAATATTAAAGCTG  
TTGTCAACGCAGCTGT'TAACGATAACCAATCGAAGGTTTCAGTGGCTACTGAACAAACAA  
AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAAACTA  
AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACAGATGCTACTC  
AGCCCCACCATCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA  
ACAATTCCTAAGACAACCGAATCCTCTTCTCTTCATCGGCGGCAAAGGAAAAACCAAAAC  
ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)

MSQTITSLDPNCVIVFNKTSSANEKSLNVEFKRLNIHSIIIEPGHDLQTSYAFIRIHQDNA  
KPLFSFLQNLDFIESIIPYHDTLSDDLHLKLSISKSKILEAPKQYELYNLSNLTNNPKQ  
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSTAFWLYKYEPF  
WSDRLSKYSSFSSTIEFLQDKQKAQKKASSVIMLKCCFIPVALLFGAILLSFQLYCFALE  
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSVNVAKKSKEA  
KNFVIIFLSSYVPLLITLFLYLPMGHLLTAEIRTKVFNAFSILARLPTHDSDFIIDTKRY  
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW  
SKVKSQYQTDWPWGATFDLDANFKLLLQFGYLVMFSTIWIPLAPFICLIVNLIVYQVDLRKA  
VLYSKPEYFPFPIYDKPSSVSNTQKLTVGLWNSVLVMFSILGCVITATLTMYQSCNIPG  
VGAHTSIHTNKAWYLANPINHSWINIVLYAVFIEHVSVAIFFLFSSILKSSHDDVANGIV

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PKHVNVQNPVKQEVFEKIPSPFNSNNEKELVQRKGSANEKLBHQLGKQPASSANGYE  
AHAATHANNDPSSLSSASSPSLSSSSSSSSKTVGVKAVDNDTAGSAGKKPLATESTTEKRN  
LVKVPTVGSYGVAGATLPETIPTSKNYLRFDEDEGKSIRDAKSSAESSNATNNNTLGTES  
KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAVN  
DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTTTDTATQPHHHH  
HHRHRDAGVKNVTNNNSKTTESSSSSSAAKEPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)

ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC  
GTCTATAAACTTCAAACGAAGGTAAGGTTTCATAGCGCTTTTTCTTTGTCTGCACAAAG  
AAATATATATTAAATTAGCACGTTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAG  
TAAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG  
GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTCGAAGA  
GATCGCACATGCCAAATTATCAAATTGGTTCACCTTACTTGGCAAGGCATATACCCATTTG  
GGATAAGGGTAACATCTTTGAATTGTGCAAAATGAAACGTATATAAGCGCTGATGTTTTG  
CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAACAAATAGAGC  
AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT  
TGGCCAATGCAGGTACCAATTCCTTAGGCAAACTAGCCGATGTCGACAAGATTGGTACCC  
AAAAAGATATCTTCCCATTTTTGGGTGGTGCCGACCATACTACTCTTTCCTGGCGACT  
ATGGTATTTCTCGTGATTTGCCTGAAGGTTGTGAAATGAAGCAACTGCAAATGGTTGGTA  
GACATGGTGAAAGATACCCACTGTGTCAGTCTGGCTAAGACTATCAAGAGTACATGGTATA  
AGTTGAGCAATTACACTCGTCAATTCAACGGCTCATTTGTCATTCTTGAACGATGATTACG  
AGTTTTTTCATCCGTGATGACGATGATTGGAAATGGAACCACTTTTGCCAACCTCGGACG  
ATGTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTCTTGG  
CTCAATACGGTTACATGGTCAAAAACCAACCAGTTTCGCCGTTTTTACCTCTAATTCTA  
AGAGATGTCATGACACTGCTCAATATTTTCAATTGATGGTTTAGGTGACCAATTCAACATCA  
CCTTGCAGACTGTGAGTGAAGCTGAATCCGCTGGTGCCAACACTTTGAGTGCTTGTAAC  
CATGTCTGCTTGGGACTACGATGCCAATGATGACATTGTAAATGAATACGACACAACCT  
ACTTGGATGACATTGCCAAGAGATTGAACAAGGAAAACAAGGGTTTGAACCTGACCTCAA  
CTGACGCTAGTACTTTTATCTCGTGGTGTGCAATTTGAAGTGAACGCTAAAGGTTACAGTG  
ATGCTGTGTATTTTACCAAGGATGAATTAGTCCATTACTCCTACTACCAAGACTTGC  
ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTCGGTTCCAACCTTGT  
TCAATGCCTCAGTCAAATTATTAAGCAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA  
GTTTTTACCCACGATACCGATATCCTAAACTTTTTTGACCACCGCTGGTATAATTGACGACA  
AAAACAACCTTAACTGCCGAATACGTTCCATTATGCGGCAACACTTTCCACAGATCCTGGT  
ACGTTCTCAAGGTGCTCGTGTCTACACCGGAAAAAATCCAATGTTCTAACGACACCTACG  
TCAGATACGTCATTAAACGATGCTGTTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT  
TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT  
TCCTAAAGGTCTGTAACGTCAGCAGCGTCAGTAACCTCTACTGAATTGACCTTCTACTGG  
ACTGGAACACTACTCATTACAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)

MFKSVVYSILAASLANAGTIPLGKLADVDKIGTQKDIFFPLGGAGPYYSFPGDYGISRDL  
PEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGLSFLNDDYEFFIRDD  
DDLEMETTFANSDDVLNPTYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHDTA  
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK  
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSVDCTDFTKDELVHYSYYQDLHTYYHEG  
PGYDIKSVGSNLFNASVKLLKQSEIQDKVWLSFTHD'TDILNFLT'TAGIIDDKNLTAE  
YVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND  
FYDYAEKRVAGTDFLKVCNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:  
859-1563 (SEQ ID NO 21)

TAACTTCTCAACATAATTATGTAAAAAATTATCTCATTAAGCCAGATAGCAAATATATCA  
CATATTGCATTGATTAATTGAGAAAAATATACATGTATCTTTTCAGTTAATTTTATTAA  
AAATAAATTATTTTCTTACTTTTTTTTCTACAGTTTGCACCATTAAACCTCTTTTCTTGCA  
TCCATACATCTTTGAACTCCATACATCTTATTTTTTTTGTGTTTTTTTTCAGTGTCTCGG  
GCATACAGGCCGCTTATCTTCATGCCGCGCCATCATCCTAGGAAACTCTTTCGGGTATGGG  
CCAAGGGCAGGCCGAAAATCCTATGTGCGTGGAGCTGATACAATCTCGGCTGGCTTGGTTT  
GTAGGGCACGGTCAATGAATGCCTGATGGGAGAAAAATTCATCTTTATGAAAAGTGATCT

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TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT  
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTTCTAA  
TGAATCAGCACGCGCTAACC GGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT  
AGTGCACATATAATAAAAAATTTCTCAAGAACAACGTTGTTTAAACGAGATAATTTCCCTCTAA  
TATACACGTACCGACACTTAGGAAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG  
GAATTTACGAAAAGGGTTTAGAAATATCAATGAAAAATAAGAAAAACCTGTAACGGAAGAA  
AGGACAGCAGGGATTTCGTTGGAATTTGTCGATATTGGCTTCGGACAACCTTTACTAACAAA  
TGGTATTATTTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAGACCTTC  
GAAATTGATGATGAACACCGTATTTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTC  
GATGGTGAAGCCGTTGGTGTATGAATTCAAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC  
GACAAACAAGGTTTCCCAATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTG  
TTGACCAAGAACGTTTCTTGTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCC  
GTCAGAGGTGCCATTGTTGGTCCAGATTTGGCTGTCCTTGGCTTTGGTCAATGTCAGAAG  
GGTGAACAAGAATTGGAAGGTCTAAGTACACTACTGTTCCAAAGAGATTGGGTCCAAAG  
AGAGCTAACAACATCAGAAAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTTCGTGATTTT  
GTCATCAGAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA  
AGATTGGTTACTCTCTCAAAGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTGAGA  
AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG  
TCTGAAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT  
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG  
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIIVGPD LAVLALVIVKKGEQE  
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT  
PQRLQKRHRQALKVRNAQAQREAAEYAQLLAKRLSERKA EKA EIRKRRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTGTTTGTCTATTCCAACATAATCATTAGCAGCACATGTCGAGCAACAG  
ATAAACACAGCAGCGGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGT'TTGTGC  
AGTGTATTACCAACTTGC GCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCTTT  
TAAACGCTTCCACGGGACATGGGTTCTAAT'TATGGAGAAGATCAAGCTTTGAAATGGCC  
CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGT'TTCAAAGACCGTGTGGTTGTC  
TATCAGTATATACTCATTGTGTTT'TTCAAAAAATCTCTGGGTTGTTTAGATGCCACTATA  
TTTCTATTTCGTATT'TATTTTATGTATACTTATTTTGCTTATTTTCTTATACTCAGGAA  
ACGTCAC'TTGGCTTGATATACTCGACGCTTATTTCTGCAAATTCAGGTCTCAAATCTGAA  
CGCGTGGAGCCCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCACATCAAAAAAC  
ATCATGGCCAATGTCAAATCACTGTACTTCTCCAAACACTGTACGACAAAAACAAAACAA  
ACAAACTCTTGTAGTAAAAAAGAAAGGGAAACTAGTAATATGGAGACACATCGTAAAAA  
AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCAGCGACATG  
GCACTAACCACATATGAATACACCAACAACAGTATAGCTAAATTGGACGCGCAGAGAGTTA  
GTAGAAGAAGAAGGAAGAAAAGGGGAAGCGGAGAGAAGAGATTATGACACATACAAACTAC  
TCATTACTCTTTGTTCTTTATTTATTCGTTGGACCTTTGTTTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)

MELAKERNGPHQKHGQCQNHCTSPNTVRQNKTNKLLLVKKKGKLVIRHIVKKMLHIRL  
VVLWSHYPEQHHGHTNHYEYTNNSIAKLDAQRVSRRRRKREARRDYDTYKLLITLCSL  
LFVGPLFLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)

ACATGACCTAATTTATAGCTTAGGGTTCTTTTTTGTCAATTCTATGCGTATGACAAAGA  
GCACCACGATGGTGATCGAAATCTCTAGGAGTAGCATACCACAGCGATATTATTTAGTAG  
TAGGCGGTTTATTATCTTTGTCCCTTTATACTGTGTGTTTCTTGCTTATTGCTTCAGTA  
GGCAGCGTATAGTATAACCAGAAAAAAGTGAAAAATAAACTAAAAAAGCACTATGAGATG  
AACGGTAAAAAATCCACCAGAGATTTGCTCACTAATAATCCTGTACCATGTCCATCAACCT  
ACATTCCGCACCCGAGTATGATCCATCTTATAAGCTGATCCAGTTGACACCAGAGTTACT  
GGATATAATACAGGATCCGGTTCAAATCACCAGTTAAGGTTTAAGTCATTGGACAAAGA  
CAAGTCTGAAGTTGTACTGTGTTTCGCACGACAAGACTTGGGTGCTGCAAGCAGCGCAAAC  
ATTCAAACACAGTTCTACTAATGAGAGAATTTGTTCTCTGAACAACCTATTACTTTTCGACG  
AAACGCTCTTGT'TTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTCGCCAAGACTG

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AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTCAGTACCAATAT  
ACAACGGAGAACTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG  
GGACCCTGGAAGAACTACTTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAAT  
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTGTTGTGATTCTTTCACAAGACTTCC  
TTTTCAAAGCACTGCATGTACTACTGATGAGCGCAATGGCAGAATCACTCGATCTACAGC  
ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAGGACATTGAGGACGAGTTCAATC  
CATACACAAGAGAAATCATTTGAAACAGTGCTGAATAAATTTGCTGTTCAAGAGCAAGAGG  
CTGAAAACAATACGTGGCGCTTGAGAATACCGTTTATAGCTCAGTGGTACGGGATTCAAG  
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGGA  
AGTCCCTTTTCCCACCTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC  
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC  
CCAAAGAACGGTTTAAAGTCCTGTTTAGGCTACAGTCACAGTGGGACTTGGAGGATATCA  
AGCCTCTAATTGAAGAACTAAATTCAAGAGGTATGAAAATAGACAGTTTCATCATGAAGT  
ATGCCCCGCCGTAAAAGACTGGGCAAAAAGACCGTGTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)

MREFVPEQPITFDETLFLGLSKPYMDVVGFakteSEFETRETHGELNLNSVPIYNGELDF  
SDKIMKRSSTKVIGTLEELLENSPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV  
LLMSAMAESLDLQHLNVEDTHHAVGKDIEDEFNPYTREIIETVLNKFVQEQEAENNTWR  
LRIPFIAQWYGIQALRKYVSGISMPIDEFLIKWKSLEPPFFPCDIDIDMLRGYHFKPTDK  
TVQYIAKSTLPMDPKERFKVLFRLQSQWLEDIKPLIEELNSRGMKIDSFIMKYARRKRL  
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)

GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAAGAAAT  
GACCCTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC  
ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAAGGTACATCCGTGCTATGGTCAGAGAG  
CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCCGGGGACGAACCAGATTCCAAGAGAAGA  
AAATAACGACCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGCGACGCTA  
CATGAACCTACTCTTTCTTCTTACATAGCTTTTCCCTTATGTATCTTTTCTGTACATTAA  
TAGACGTTCTTACAAGGTAAAATTTCACCGCGTTTAAATAGAAATGAAAAAACGTTGT  
AGAGTGAAAGAAAAGCAACAAATATACAGTTTACAAGGCAGCTTCGTATAGTAATACAGC  
ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA  
CGGATGCTTATATCCCCACGTATCTGCCCCGATGATAAGGTCTCCAATCTGGCAGATTGTA  
AAAAATTGATAGAAATGGATTCCAGACTAGATTGTATCTGACAAGAAGGAGGCTGGATA  
CGTCCATCAATTTACCTACAACACCAAGACCAAGGACCATCCCCCAATAAAGAGATGC  
TGAGGATTTACGTCTACAACACTACGGAAGCAGCCCTCGCAGCGATTCTGGCACCCACAG  
CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG  
CAAACGGAAAGCACCCATTTAGTGAGTTTTTGGAAAGGTGTCGCGGTGCGACTTTAAAAGAC  
TGAAACCGCTGGGCATGGGCAAGAAGAGGAAACCGGATTCGTCAATTGAGCCTTCCTTTGA  
ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG  
AGGATGAGGACAGTGCAGAGGCAGAACTCAGGAGGAAATTGTAGACGCACTGGAATTGGA  
ACTACGATGAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGG  
ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAAAGTACAGT  
ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT  
ATTCGATCTACAAGTACATTTTGATCAACAATCTGTTTGTACCGAACAACAGAGGCTC  
AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCTG  
GTGACGATGATGGCGTCGAGGGAAGTACTCCAAGGATAAGCCCGAATTGGGTGAAGTGA  
AGCTAGATTCACTCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCTTGATGA  
ATGTTGTGCAACCGTGAACAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA  
CAATTGATCTTTCCAAAGATACCACCTATGGTGCTACCACCTTGATGTAGATGTGTGCGC  
ACATTCTCCACCAGCCTCAACCCAGCCAAATTTACAAAAGAGGAAGAAACAGATGCTG  
AAGACACAGCAAAACTACGTGAAATCACAAAGCTTGCCTTGCACTTGAAGTCTAGTGCTC  
AAAAATACCAGTTTTCACGAAGTGTCTTTGCATCCAAGAGAAACGCTGACTACTACT  
TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCGAGGGCGACCAATACTTCAATGAAGATG  
CTGCAAGAACGAGTGACATATACAGTAACAACAACATGACAGGTCACTAATGGGCAATA  
TCTCACTACTGTACTCCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28)

MVTQTNVPVPTYPTDAYIPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRRRLDTSINLPT

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NTKTKDHPPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF  
SEFLEGVAVDKRLKPLGMGKKRKRDRSSLSLPLNLQQPEYNDQDSTMGDNDNGEDEDSDAE  
AESREEIVDALEWNYDENNVVEFDGIDIKRQKDNLRCSITIQLRGVDGGKVQYSPNLAT  
LIGMQTGSVNDVYSIYKYILINNLFVTEQTEAQDGSNDAEDSSNENNNKNGAGDDGVE  
GSTPKDKPELGEVKLDSLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYTTIDLSDK  
TTYGATTLDDVDVSHILHQPQPQPNLQKEEETDAEDTAKLREITKLALQLNSSAQKYQFFH  
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ  
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)

AGGTTTAAACGCGTTATCTTTGTTCCGAAAAAACGGAATAATATATTTTTTC  
GCGTCGCGTTCTCGCGTCTGTTTGTCTTCGCGTTCCAATGACCAAATGGGAAAGTG  
GTCGTCTTTGACGAAGGAGACGAAAACCTCTTCTAAAACGTTGGGAGAGAGATAATTACA  
TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC  
AGCCGCAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTCGCGTGTCTTCTCCT  
CTAACTGTGCACGAGGCACCCCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTT  
GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGGTTTTTTCGCGCATTTGGCAATTAGCA  
ATTTATCAGCATACTTTTCCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTTC  
TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC  
AGAGCTGCTCATTGGACTTTGCTGCGAGCTTAGACGACTTGTCTTTTGGGCATCTCTGA  
GTTGGATTTTCGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTCAGGTGCAGGCT  
TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTGTGAGGTGAGCTTTGCTAGTCTTG  
ACGGCTGTAGAGGTGTTTACATTGATGATGAGTCCCTAAGAAAATTTTTCTTTTTTTTC  
AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA  
TCATCGTCAAAGTTCTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC  
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)

MYLERWWWSCIISQSCSLDFAASLDDLFWASLSWISKSVRVGLIFSNPSGAGLDDLVMF  
RGMSFCEVSFASLDGCRGVYIDDES LRKFFFFFQYFTFR CERQMYAFKSQRSIIVKVPT  
TTRVIDLVLVNVLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)

GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG  
CCAGA ACTCTCCCGCCCTTCAGCCGCTTTTTGTTGCTGTGTATTTCAGTATATCCATCATCA  
TTTTACCTACAAGGA ACTACCTTTTATAGCCACCCTAAGTAAACAAACATTAGCTTAGC  
ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTTCTGGCATCGC  
TTTTTTACATAAGGTACCAAGGCAAGAGAAAAAGACCCGCGAAATTTTCAATTTCGAGACAT  
AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAATGAAGAAATGTGATTAGA  
CATCCTGGGGAAATTAGGTTTAAATAGGGCGGGCGCTACAGGGGTTTTCTTAACAAATTT  
CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGATAGGTATGGACTAGAACAGAAA  
GCAATTTGCAGCAAGACAATATGACTACGACGGTACCCAAGATATTTCGCGTTTCACGAGT  
TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG  
CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCATGGATATGA  
CGAGAGAGGCCTCTTGCAAAAGCACAGCATCTGCCGCGGAAGGGAAAAGTGGTAGCAGTG  
GTAGTGGCAGTGGTAGCAGTAAGCCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG  
GTGGGTCAATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG  
GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA  
ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAACCTC  
CGAAGGTGTACCAATTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT  
ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCCGTCAAACCTCCGATGTTTCG  
ACTTGTTCCTGCTTGGTTGTGCCCCGATGGTCATATCGCATCACTCTCCCTAACTTCC  
AGGACAATCTACGTGAGAACTTGCATGGGTGGTGGCCGTGGAGAACGCTCCTAGTGGGC  
CCTCGACCAGAAATTCGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTTCG  
TTGTCGAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAAGGCCTGAAAGG  
GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTTCGTGTATCATGGTTTGTGACG  
ACGATGCTCTTACGGACGTCCCTCGTCACCAAAAAAAGTATAAATTCACCAAGGTTTGT  
CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

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MTTTPVKIFAFHEFSDVAEAVADHVHQAQD GALAPKNERKHSVPNISMNALDMTREASCK  
STASAAEGKSGSSSGSGSSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVVRWGDWDIYF  
ADERLVPFSSNESNYGCAKRKILDLIDTAKYGTPKVYHIDESLIDDPQECVDNYEKLIR  
GFAGRDSVKLPMFDLFLGCPDGHIALFPNFQDNLREKLAWVVPVENAPSGPSTRISL  
TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSIVNEGAAGRVSFVDDDALTDV  
LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTAAATGGCGTAGTTCATCCGCGTTTAATTTAACTA  
GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACCTGACAGA  
CTCAGCTACCGATTAGTGTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTGGACC  
TAGTCATCCCTCCACACAAGATTTCGCTCTTAAAGTAGTGGCGCAGGCTGTTTCGCTTTTAAG  
CATAGTGCTTAATGTCGAAGGCTTTATAGATCCCAAATACTACGCCTTGAGAAATTGAAT  
GCACTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGGCGCCTGAGGCG  
GAGCGTTCGCGAAATCGGGAAAACATTATACTGGGAAAGATCACTATCTATTCTCTAAAT  
GAACTTTTAAGCAAATTAATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT  
AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAAATTTTAAGCA  
TTACAACGCATTATTATTGTTAGTGTTCGTTTCGTAGCGCAAAATGCGAACTCTTTGACGG  
TAGAGATAAAAGAGGAACTTCTAAAGCATTTAGTACTAATATGGACAATATGGCTGGAG  
GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG  
TAGACGAAGAAATTAATGAAATAAAACAGAAGGTGGGACTCCAACAGCCCATAGCATCGG  
TTGATGATAGTTTGTTCGGCCATTAAAAACGATAAAGGGTCGCGAATAACCAAAGCTTTTA  
ATGTTCAAAAAGAATACTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA  
GCACCTGTTTCATATAGCAAGGGCATGAAGGAACTGCTTGAAAATGAGTATCAGTTTATCC  
CAAACCTACTATATTATAGAAGTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA  
TCAAGTTGGTGACCGGTAGAGGAAGTGTTCCAAACCTTTTGGTTAATGGAGTATCAAGAG  
GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAACTTTTAGAATCATTACAAG  
TCTGGAGTGATGGTAAATTCTCGGTTGAGCAACGTGAAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34)

MIPSNKRNARILSITL LLLLLLVFFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA  
AMPTSTTNKGSSEVDEEINEIKQKVGLQOPIASVDDSLSAIKNDKGSRITKAFNVQKEYS  
LILDLSPIIIFSKSTCSYSKGMKELLENEYQFIPNYIIELDKHGHGEELQEYIKLVTGR  
GTVPNLLVNGVSRGNEEIKKLHTQGKLLES LQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAAAATCCAGCTTCTTTTCAAGCAATATTGTCACAAACGATGATGAGAATAGCATTGAAG  
AGGATAAGAATTTACGCTATTTCAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA  
CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG  
ATAGTAGCGGCATAGATTTTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTA  
TCGCGATGTTTGAAAATGGAAAGTAAGGAACGTAATACAAATTGACAAGTAGCCGACATG  
AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATCATG  
GAAGCAATGTGATTCCTCGATAAGTAAGCTTTTTTCTGTCTGGCGGCGAACCATTAGAG  
AACAAAAGACCGAGTTAAGAAAAAGTTTCATAAAAAACTTTTGAAAATGGATGAGTGCTCG  
TATAATGGAATAGGAACTTATGCAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC  
CAGTAATAATGGCTCGACAACCTCAAAGGAATGCATTATCTGCAGGTCTTGCTTTTGCAG  
GTAATGCAACCTCAAAATGAGTTTGATGAACATTTGCAAAATGAGGTTGAAAGAGAGAGGG  
AAATTCAAAAGAAAAAATAAAGCGAAGCTCAATCAAAAAAATCGCCAGATTTGATTA  
ATAAATCTACTTTTCAATCACGAACGATAGCCAGCAAAAAAGAGAAACATAGACAACCTAG  
ATCCAGAGTATGAAATTGTCATCGATGGCCCTCTAAGGAAAATCAAGCCCTACCATTTTA  
CGTACAGGACCTTTTGCAAAGAGCGTTGGAGAGATAAAAAATTGGTTGATGTCTTTATAT  
CTGAATTTTCGAGATCGTGAATCTGAATATTATAAAGAACAATCGAAAACGGGGACGTTT  
ATATAAACGATGAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC  
ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTGGAAG  
ATGATAACATAATGGTTATTGATAAACCAGCGGTATACCTGTTTACCCAACCTGGCCGAT  
ATCGGTTCAATACAATTACGAAAATGCTTCAAAATAATCTCGGATTTGTTGTGAACCCAT  
GTAATAGGTTAGATAGGCTTACAAGTGGATTAATGTTTTTGGCAAAAACTCCGAAGGGAG  
CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAGG  
TAGTTGGAGAATTTCCAGAAACGGAAGTAATTGTTGAAAAACCTCTAAACTGATCGAGC  
CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA



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CTGTTTTTAACAGAATCAGCTACGACGGTAAAACGAGTATTGTAAAGTGCAAACCGCTTA  
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG  
ATCCTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG  
ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAGAAAACCTGCTAAAAGTT  
GGTTCCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG  
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTTGATCTGTGGTTACATGCCATATC  
TATACGAATCAACTGAGACTGAAGAAGGAACCGAAAAGAAAAAGTGGTGCTACAAAACAG  
AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNNRLRNLFVPMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKK  
IKRTQSKKSPDLINKSTFQSRITIGSKKEKRLDPEYEIVIDGPLRKIKPYHFTYRTFC  
ERWRDKKLVDVFISEFRDRESEYYKRTIENGDVHINDETADLS'VIRNGDLITHQVHRHE  
PPVTSRPIKVIFEDDNIMVIDKPSGIPVHPTGRYRNTITKMLQNNLGFVVPNCNRLDRL  
TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVGEFPETEVIVEKPLKLIIEPRLALNA  
VCQMDEKGAKHAKTVFNRIISYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND  
EVWGNLKGKGQADFDIVITKLDEIGKRKPAKSWFHSNGGYEVLRLQEKCSICESDLYTD  
PGPNDLDLWLHAYLYESTETEEGTEKKKWCYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:  
1342-1364 (SEQ ID NO 37)

TAT'TCCGACTAGAAAAAATTAATTTTCTAACTACAAAAAATTCCTGCATATATGTAA  
GGATGTAAACAGGAAATGTATGGGTCACATATTAATAGCTTGT'TTTACTCCATAAAAGAGT  
CTGATATTTCAGAAAAAACACCCATACATGTTGAAAAATAATGCAT'TGTGAAAAAAGTGG  
TTGAAAAATGTATGCGATCTAGGAAAACTGAATTTTCTTAGGTTGTCTGCTCCTCCTCT  
AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATTCCTCTGT'TTCCCTCTAGCTGAGG  
GAAACAGAACTGGTAGCAGTTCGTTCCGGCCAGGCCGCGTGAGCCTATACCACCGAATAT  
TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAATGTATA  
GGTTACGCAGTAGACTATTTAATATATACCTTTTATTTTAGCAGTGT'TTCGAAAAATACA  
GCAAGAGAATAAGCAACAAGATGTCCTGCCGTCCTCAAGTGTCCTCAAGTATGTTAAATAATT  
AAACGATGTCACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA  
AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTTA  
GAACAACGGATCACCATTTTACACGTTAAAGACCGAGTAGAAATAACCAATAAATTTGTGT  
GGGAAAATATTATAC'TTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCT'TTTGCGGTCTT  
ATTTAT'TCATTCGCTCCCTTTCGAATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC  
CAGGGTACCTCACTTGT'TTACCCTTTTACACAGTTCATAATATTTTGTAGGATTTTGAA  
TTTCTGTTTTTACTAACATGTGACACGAAATGTTTTTCATTTTGGTTTATAACAGACTT  
TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCACGTCAAGGCCGGTAAGGGTTTGATTA  
AGGTCAACGGTCTCCAATCACTTTGGTTGAACCAGAAATCCTAAGATTCAGGTCTACG  
AACCATTATTGTTGGTTGGTTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA  
CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG  
TCGCTTACCACCAAAGTACGTTGACGAACAATCCAAGAAGCAATTGAAGAAGGCCTTCA  
CCTCTTACGACAGAACTTTGTTGATCGCTGATTTCTAGAAGACCAGAACCACAAAGAAATTCG  
GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF  
SNIDIRVRVTGGGHVSQVYAIRQAIAGLVAYHQYVDEQSKNELKKAFTSYDRTLLIAD  
SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:  
709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC  
CTTTTTCGGGTTAATTCCTCCGCGCTTTCGTTAGACTATTTTGCAAGGACCCAAATAGGAG  
ACGATCTGGAGGCTTCTACAAAACAGCGTGCCGTTTTGATGGCATGAGCAGGGGGCGCAAA  
GGAAACACCGGTAAATCGCGCAAGACCTTGT'TGGCCACGTAGCCTCAAAGGTTGAATTGA  
CACTTGTCTACAGAACTTGAAAAGTACAAAAGGAGGTCACATAAAACAGTAAGCTTGAGA  
AGCTTTTAAGATATGGTGCGAATCGTTACAGAATATTCCTTGCAAGAAATAATGGCGGGTCC  
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGTAATGTGA  
TGTGTGTTTCGACTGGAAAGCGGAGAACATTATGAAGTAAAGGACAATCAGCACGCCTTC

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CAGACTTTTAAGAAACATTGATGGAGCCATTGATATCGGCACCGTACCTAACAACAACAA  
AAATGTCTGCTCCTGCTACGCTTGATGCTGCCTGTATTTTTTGCAAGATTATTTAAAGTA  
TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG  
TACATATACATAAAGCAGAATACTAACAATCGATCCGCTATGCAACAGGCGAAATTCAT  
CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG  
AAGGTCATGCTTTAATCATTCCTAAGTACCATGGTGCGAAGTTGCATGACATCCCGGACG  
AATTCCTTACCGATGCTATGCCGATTGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA  
CTTATAATGTGTTGCAGAATAATGGTAAAATTGCGCATCAAGAAGTCGACCACGTCCACT  
TCCATTTGATTTCCTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGCCAGCCCAAG  
AAACGGACTTCGATAAGTTGGGCAAGCTACACAAGGAATTGCTTGCCAAACTAGAAGGCT  
CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTTTKMSAPATLDAACIFCKIIKSEIPSFKLIETKYSYAFLDIQPTAEGHA  
LIIPKYHGAKLHDIPDEFLLTDAMPIAKRLAKAMKLDTYNVLQNNGKIAHQEVDHVHFHLI  
PKRDEKSGLIVGWPAQETDFDKLGLKHLKELLAKLEGSD

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTGGAGACTTTGTGTTGTAGCTTAGAATTTCTTCCACTATATGAAAGCCAAG  
ACCTCTTCTCCTCTTTTCGACACTTCGTTTATTTCCACTTTCCCTTATTTAGTATTCATCG  
TTCAGAATGCTTTCTTTATTTTACGACGGTTACCACACCCGTACACCCTTATCTCATTTC  
ACCAGTACCTTTCTTTATTAGATTCACTCTTATTTTATTTTAGGATTTTATAGGTCAATTGTA  
CGACGCGTGTGCGACCATGGAAAAGGTGTCGACGCTGCGATGCTATCCATTACCCGTCAT  
TCATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTATATATATATGAGAGTTA  
ACGAATGTAATATTTCTGAATGTTAAATAATTGTTATCCGTCATTATTGTTTCACTTCTC  
TCTTTGAAATTTTCGCTTGTTTTCTGTTTTTCATCTTATATTTTACTTCAATCCTAAGATAG  
TCATATCGACTTAATTCCAAATGAGAGCTAAGTGGAGAAAGAAGAGAAGACTAGAAGACTTA  
AGAGAAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRAKWRKKRTRRLKRRKRRKVRARSK

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2:  
909-1268 (SEQ ID NO 43)

CATGCGGACCTTGTGTGTTTTGTTTCTAGATTGTTTTATTTTATGATTGTTGAAGATAT  
AAACCACTGTATAGTTGTATAAGATAGGATAATGATGGTGCACCTGAAAATAAACTTACTA  
GCTCTTTAATATTGCAACGGCTTGTAACGGGCGCCATGATGACATTTCAGAATTATACCAC  
TACTATATGAAAAAATGAAAAGAGGGCCCTGCTTTGAACCCGTACATTTTATTTCTATAATA  
TTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA  
ATTTTCCACCATGGATTTCAGCACCCAAACATTTGAATTTTTTTTTCATGTCCGATTGTGAAA  
TTTTACTGAAGATGAGGGTAAATAGAGGCCTGCAATCGTCATCATATGAGAAATGGATAT  
ATTGAAAATCTACTCACATCTCTTTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA  
AGAACCAAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA  
TAATGTGCTATGGAAGAAAAAAGTCTCCTTTAATGTCTGCAGGATAAATAATCAAGTGGT  
CTGAAGAAAATTTACAGCTACAGTATTACTGCAAACCTTGCAGGCAAATATCAGAGAGAT  
CTCACCAGCTACAAC'TTGGTAACAGAAATTTATAAGTTTATGGCACTTGTTAAAATTGTT  
TGGAAGTTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCACATGTGAACATTT  
TTTTTTGGATAATGCATTGCACAGACGCTATTAGTGTATACGAGAATCTAAAAATTTGAA  
ACTGGCTCATAAAAACAGGAACCTTTTACTAACAGTTATGATTTTTTGTTCCTTTCTT  
ATCAATAGGCCGGCGTTAAAGCTTACGAACCTAAGAACCAAATCCAAGGAACAATTAGCTT  
CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTTGAAGGTCCAAAAGTTGTCCAGAC  
CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA  
ACGAACAACAAAGAGAAGCTGTTAGACAATTA'ACAAGGGTAAGAAGTACCAACCAAAGG  
ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAATTCGAAGCTTCCC  
AAGTTACCAGAAAAGCAAAGAAAGAAGCAAATCGCTTTCCACAAAGAAAGTACGCTATCA  
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE  
QQREAVRQLYKGGKYQPKDLRAKKTRALRRALTKFEASQVTEKQKKQIAFPQRKYAIIKA

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YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC  
AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA  
TGTGGTTAGAACAAACATCCAGATGGAGTCACAAATGAATATCAAGGGCCTCGTAGCGATG  
ACGAAGACGATGAAGACAGTGAAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA  
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATAAAGGGTTTCTTT  
AAGTAATGTCATGTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC  
GATGCCCAGTGGAAAAGTTTAAAGTGAAAAATTTTCAACACATACAAGTTTAATAAGTT  
GGTTTTGATGCAAATAGCATTACTAAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG  
TGATTTTGTATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTGC  
CAGATACCCCCAAGGATCAATGTGCGCATTGCGAATATAGCATTTCAAATTGTGAATGCTG  
AAACATTAGTATGCCATTATGGGACCAATTCTTTACCGAGCATTGAAGTAAACGGGACGA  
CAAAGAGTTTGGAGAGTGCAATGGTGAATTTGGACAAGGATATTCATGACGTTATTGGTA  
ACGACGACTTTGTTCTTGTTCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC  
GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG  
ACTTATGGAAGGAATTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA  
AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAAATGCAGCCAAAATA  
CGAAGGATTTGGACGAAATAGTTAGAAATATTGGAAGTTTCAATCCCAACTGAAGAGGCAG  
GCTCTGTTCCAGAGATATACTCTCTTTTAAAAAGGACAACGGATATATTAATACAATTGC  
ACAAAAAGTGTACTTCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC  
ACACCGATATTAGAGCGTTTTTTGCAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC  
CGCCCCGACACAACCTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTAGACCAG  
TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCCTAACGTTAATAAATACTGGA  
GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTGTCTTCC  
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC  
TGGCAAACACTAAGCAACCAAGGGTGGTGGAAACATGTCTTGGAGCTTCAACCTTCTTCCA  
CCGGAGTACTCGATAAGGCTCAAGAAATTTTATCGCCTTTCCCTCAAAGTAAAAACAAAC  
CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACCTTTCAAAGACGTACTG  
CATGTTTTAGATGTTCTTTTCCGGCACCATCAAATAGTCAAATACATACTGCCAACTCAA  
ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACCTCGGGATCTTCAA  
GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGGCCCTGAGTTCAACATGATTG  
CTAACACACGCCAGCAGCTTTAACATACAATAGAGCTCATTTTCCTGCAATTACGCCAT  
TGTCGCGACAAAATTCATTGAACATGGCACCATCGAACAGTGGGTCGCCGATAATTATAG  
CGGATCATTTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATATTA  
ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAAATAACAACA  
TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA  
ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA  
ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTTCCAATATCGGTATGGGAGGAT  
GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTTCACGTGCACGTATCATA  
ACTTTGCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGGCGATG  
CAAGTGAACCAATCATTTACATAGATTTCATCAACATTTGGACCAGCGTCGCGTACTCCCA  
GTAATAACAATATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTTCGCACCGATGGGA  
ACGATAACAAAGTTCGTGATATTAGTTTGTATGGAATTTATGTCACCACCGTTATCGATGG  
CAACAAAGTCAATGAAGGAGGGAGATGGGAATGGTAGCTCGTTTAAACGAGTTCAAAAGTG  
ACAAAGCTAACGTTAATTTTTCCAATGTTGGTGATAATAGCGCTTTCGGTAATGGTTTTA  
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVLELQVAHLPDTPKQDCRIANIAFQIVNAETLVCHYGTNSLPSIEVNGTTKSLESA  
MVQLDKDIHDVIGNDDFVLVSLYSTWHIRVTLPRQARDDGFILTSYLQHPKVFDLWKEFD  
RWCNVNHEILGQKKAISNNNCNTKSISINAANKTKDLDEIVRILEVSIPTEEAGSVPEIY  
SLLKRTTDILIQHKKCTSPEDMESVLTKPYDSHTDIRAFLQEKSKILYMNLPDPTTQS  
ELESWFTQYGVPRVPGFWTVKNIVEDTSNVNNNWSLNNSPYVEDQDSISGFVVFQTHEEAT  
EVLALNGRSILSNLANTKQPRVVEHVLELQPSSTGVLDKAQEILSPFPQSKNKPRPGDWN  
CPSCGFSNFQRRRTACFRCSFPAPSNSQIHTANSNNNVNSSRNNLNRRVNSGSSSNISNTA  
ANHPYGAPEFNMIANNTPAALTYNRAHFPAITPLSRQNSLNMAPSNSGSPIIIIADHFSGN  
NNIAPNYRYNNNNNNNNNNNNNNNNMTNNRYNNNNNINGNGNGNGNNSNNNNNNNNNNHH  
NGSINSNSNTNNNNNNNNNNNNNNNNCNSNIGMGCGSNMPFRAGDWKCSTCTYHNFACNVV  
CLRCGGPKSISGDASETNHYIDSSTFGPASRTPSNNNISVNTNGGSNAGRDTGNDNDKGRD

ISLMEFMSPPLSMATKSMKEGDNGSSFNFKSDKANVNF SNVGDNSAFGNGFNSSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCC'TTCCGTTGATCT'TAGATTCT'TAGAGGTT'CATGAAGCTAGAAAGCGAC  
TTGAACAAAGTCATCCTT'CAAGAATCGAAATCT'CAAGAGAAAAACAAATTTAATGTAGA  
TTGTCCACTATC'TCATGTAAATATACATAACAGGTATT'CCTGAGCGTTCGAAAATTAGAC  
TG'TACTTTTCTGATGCGCTCCCGTACACCT'TTGACATATACAAACATCCGCACATTTTAT  
AGCTTTCT'TTCTAGAATTT'TTCCACGCGCTCTCGATCAATGAAGTCTTAAAAGTAAGT  
ACCCCTAACTTTTTTCCAGGCAAGGCTGGCCTCATTACCC'TACCCGAAAGTTTCACTTTA  
CCCCATGGCAGATGGACGATATTTTAAACAAGACGAAACTGACCTCGTCTTCTATAAACT  
GGACTTCTAAGCAACTCTCATT'TATCTTATATCCGT'TCCATTTTGTACTAAAAGAACCAG  
ACCACATCGATTCAATCGAAATGAGAGCCAAGTGGAGAAAGAAGAGAACTAGAAGACTTA  
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRAKWRKKRTRRLKRKRRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:  
995-1354 (SEQ ID NO 49)

TATTGACGTTTCGCTCTCAGGTCCACCGTGT'TCTCAAAAGATACTTTTAAACCTAAAAC  
ACACGAAATCATATTATGATAATTCAGAATGATAGTGTGGTACTGTGTCAATTGACTGTT  
CAAGACTGAAGAGGATCTTTGAT'TTGTGTTACTCAACAAATAATCTTACGAAAACCTTT  
CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTAC  
ATTTAATTTTTTATACATAATAGGTAGCTTAAATTGTAAAGTCGCAAAAAAAATGGCA  
GCGCAGCCTCTCCGGGTGAACCCACGACAACCTTACCTGGCACTCCATGCACTAACGGGC  
GGGTTTGGGCAGGATTCCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT  
GTAATATAATGTTAAGCATACGCTGTGCTGATTAGCACTATTATTGACCGTAGAATAGGTAC  
AGTGAGACAGTATATTCGAAATGGTATGTTTGAGATGAACAAAATAATAAAGACTGACAA  
CTGCAGAACAGAGAGGATCATAGCAACCTAGTGCAAGAAAGAGCCTCGAAGCGTTAACT  
TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG  
TAATCAAGTATATCGGATTATTTCGCAAGCAAAAGAAATCAAGGAAAAGAAAGTGAAAATAGC  
ATACATCTTTAAATTCAGAGGTTTGTCTGAATTTTAATAGGGAAGTTTACGTTATGATTG  
TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATTCTCCTAATTTTTTTTATTGTAAA  
AAAGCCTTCCAACGAAATAAATTAGTTATTGGTTTTTTTCTCTGTTACGAGGGATATAT  
GATGCCTGTGCTTGTAGTTTATTATAAGTGCTAATAAAATACTAACGTTAATAAAAATT  
TGGAATATTATTTTCAATTTTTTATCCTATTAAATAGGCCGGTGTAAAGCTTACGAACTAAG  
AACCAAATCCAAGGAACAATTGGCTTCTCAATTTGGTTGACTTGAAAAAGGAGTTGGCTGA  
ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG  
TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAGAGAAGCTGTTAGACAATTATA  
CAAGGGTAAGAAGTACCAACCAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG  
AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGC  
TTTCCCACAAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKVQKLSRPSLPKIKTVRKSIACVLTVINE  
QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTCCTTTAAAGGGATATATAACAGATTCT'AAAACTGACAGAAATATTTTCGAGT  
GAAGAAGAAGCGTTAAATATTGGATCTTTCCGCAGTTCTACTCTGATACATTTTTGAAGT  
AGGAGAGTCATTTAGAAGGCGTATTGCTCAATAGTAGAAAGCAGGCCTGTGCACATGAAT  
TAATTAATAAATATAAAGGTAGTGATTAGACGACACATGTCCATAGGTAACCTGTCTATAA  
TTTTGAACAATTTCCCTTCTTTTCTTTTTTTTTTTTGGGTGCGGCGATATGTAGCTTGTT  
AATTTACACATCATGTACTTTTCTGCATCAAAATATGAAAGGCGATAGTAGCTAAAGAAA  
ATACCGAGAAATTTCCTCGAAAAGTTGACGACAAAAGAAAGGCATAAAAAAGTAATTTGAA  
AATATTTTAAAACTGTTTTTAACCCATCTAGCATCCGCGCTAAAAAAGGAAGATACAGGAT  
ACAGCGGAAACAAC'TTTTAAATGATGGAACTCCTACAGACAATATAGTTCCCCCTTTTC  
ACAATTTTGGTAGCTCGACACAATATAGTGGTACCTTGTCGAGAACTCCCAACCAATAA  
TAGAGCTAGAGAAGCCAGTACTCTATCCCCATTGTCAAGAGGAAAAAAATGGACGGAAA  
AGTTAGCCAGGTTCCAAAGAAGTAGTGCTAAAAAGAAAAGATTCTCACCTTCTCCTATTT

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CCTCCTCTACATTTTTCGTTCTCACCCAAATCTAGGGTCACTTCTTCAAACCTCTTCTGGCA  
ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC  
ACCCTCACAGAACATCGTCTTTTGCCAAGACCTAATTCGAATCTCTTTTCACGCAAGTAATA  
GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAAATTTATCAGATAATATACCAC  
CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAAAAAATCCTTTTGA  
ATGCTTCTTGTACGTTATGTGACGAGCCTATTTCCTAACAGAAGAAAGGGAGAGAAAAATTA  
TAGAGCTTGCATGTGGCCACTTAAGTCACCAAGAATGTC'TTATTATCTCTTTTGGCACCA  
CTTCAAAGGCAGACGTTTCGTGCGCTATTTCCCTTTTGTACCAAATGTAAAAAAGATACTA  
ACAAAGCCGTTCAATGCATTCCAGAAAATGATGAACCTAAAGGATATTCTAATTTCTGATT  
TTTTGATTTCATAAGATTCCCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCCCTC  
CTTATTCACCACTCTTGCCCTCCTTTTGGGTTATCCTATACACCTGTTGAAAGACAAACGA  
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATA'TTGGCTGCACCCCCCAAGGAAA  
GAAACCAAATTCACAAAAAATCAAAC'TATACATTTTACATTCACCCCTGGGGCACA  
GAAGAATTCCGTCCGGAGCAAAC'TCTATCTTAGCAGACACCTCTGTAGCGTTGTCAGCTA  
ATGATTCTATTTCTGCTGTTTCCAATTTCGGTAAGAGCAAAGGATGACGAAACCAAAACAA  
CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATCTTTTGAACAATTTCCAGGAAGAAT  
TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATGATGA  
TTTCCAAAGATGGTCAGAGATATATAAATGCTGGTGTTTCTTATTGGAAGACGCA'TTGT  
TAATAGAGAGAAGTGGATAACGATGTTGATGTTTGGAAATTAGACTAAAGAATTTAGAAG  
TATTTACACC'TATTGCCAAC'TTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA  
CCT'TAAATAAACAACATTGCGCCGATTTATCAGATCTTTACATTGTTTCAGAATATAAATT  
CTGACGAAAGCACAACTGTACAGAAATGGATATCAGGTATATTGAATCAGGATTTTGTAT  
TCAATGAGGACAATATCACT'TCGACCC'TGCCTATTCTTCCCATTATAAAGAAC'TTTCAA  
AAGATGTTGGT'AATGGTAGGCACGAGACGAGTACCTTTCTAGGTTAATCAATCCTTAACA  
AAGTTGTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA  
CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTCGACAGTATACAATCTGTTCTAA  
CCACGATAAGCTCAATTCTTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT  
TACAGATCGATTTTACGAAAT'TGAAGGAAGAAGACAGT'TTAATTGTTGTTTATAACAGTC  
TAAAGCTTTAACCATTAAATTTGCGCGT'TTGCAGT'TTTGTTTCGTTGATCGAAATAATT  
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC  
TCAAATCAAAGAGTTCCCTCGACACAATTTTCACCTATTTGGTTGAAAAATACTCTATATC  
CCGAAAAATATTCATGAACATTTGGGTA'TTGTGCTGTATCAAATAGTAATATGGAAGCAA  
AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTT'TGGAAGAAGAAGGCCCA  
ATGAATTGAAGATTAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTGATGAAC  
TAGTCGAGGCCAGCTCCTGGACTTTTGT'TTTAGAAAC'TCTTTGCTACAGTTTCGGTCTAA  
GTTTTGATGAACATGATGACGATGACGAAGAGGATAATGATGATTTCGACCGATAATGAAC  
TTGATAATAGTT'CAGGATCACTGTCCGATGCTGAATCTACAAC'TACTATTTCATATTGATT  
CTCCATTTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG  
AGGGTGAACATAGCAATATAGAAAAC'TTAGAACTGTGCTTCTTCAGTACAGCCAGCTC  
TGATTCCCTAATATTAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAATGAAA  
ATGAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA  
CCAGACGCAGTTCA'TTCTCGAGTCTTATAGAGAGCGGTAATAACAAC'TGTCCCTCCATA  
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTLSRTPNQIIELEKPSTLSPLSRGKKWTEKLARFOR  
SSAKKKRFSPSPISSTFSFSPKSRVTSSNSSGNEDGNLMNTPSTVSTDYLPQHPRHTSS  
LPRPNSNLFHASNSNLSRANEPPRAENLSDNIPPKVAPFGYPPIQRTSIKKSFLNASCTLC  
DEPISNRRKGEKIIELACGHLHQECLIIISFGTTSKADVRLFPFCTKCKKBDTNKAVQCI  
PENDELKDILISDFLIHKIPDSELSITPQSRFPYPYSPLLPPFGLSYTPVERQTIYSQAPS  
LNPNLILAAPPKERNQIPQKKSNYTFLHSPLGHRRIIPSGANSILADTSVALSANDSISAV  
SNSVRAKDDETKTTLPLLSYFIQILLNNFQEELQDWRIDGDYGLLRVLVDKLMISKDGQR  
YIQWCFLFEDAFVIAEVDNDVDVLEIRLKNLEVFPIANLRMTTLEASVLKCTLNKQHC  
ADLSLDLYIVQNINSDESTTVQKWISGILNQDFVFNEDNITSTLPILPIIKNFSKDVGNR  
HETSTFLGLINPNKVVEVGNVHDNDTVIIRRGFTLNSGECRQSTVDSIQSVLTTISSIL  
SLKREKPDNLAIILQIDFTKLKEEDSLIVVNSLKALTIKFARLQFCFVDRNNYVLDYGS  
VLHKIDSLDSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVAVSNSNMEAKKSILFQ  
DYRCFTSFGRRRPNELKIKVGYLNVDYSDKIDELVEASSWTFVLETLCYSFGLSFDEHDD  
DDEEDNDDSTDNELDNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI  
ENLETVASSVQPALIPNIRFSLHSEEEGTNENENENDMPVLLLSMDMDKGIDGITRRSSFS

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SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA  
GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCCTACACATATCTCTCTTC  
AAGATTATCGTGTATGCTAATGCTAGAAAGTAATATATCGCGTCAGGACTCTGTCTCCACAA  
CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGGCTGTGGCAAACC  
CTGATTACAGACCCAGAATGATATCCTTCTCTGTAGTTTTGTAGATGTCATATATGTACGT  
TTATGGAACAGCATTTTAGAAAAGTATTACCCAGCTTATCACTTCGTTTTTTTTTTCTTT  
CCGTGTACTCGCTACACGTAGAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG  
ACGTTCAATTAAGACTCAGTTAAGATTGCCTTGAGAATAAACAAAAGTAATCACAGTTAAC  
TATTGAACAAGAGTGCACCTATGACTTCACTTTCTTCACAGCCAGCGTACACGTTGGTTT  
TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTTCAGAAAGCTCTTGAAA  
AGGGATCTGATGAACAAAAAATTGACACGATGAAATCAATTTTAGTTACAATGCTGGAAG  
GAAATCCAATGCCTGAATTGTTGATGCACATAATAAGATTTGTCATGCCTTCTAAAAATA  
AGGAATTAAAAAAGCTTTTGTACTTCTACTGGGAAATTTGTTCCCAAAGTAGCTGAAGATG  
GAAATTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTGCAACATC  
CTAATGAATATATTAGAGGTAACACATTAAGGTTTTTAACGAAATTGAGAGAGCCGAAC  
TCTTAGAACAGATGGTTCCCTCTGTCTTAGCGTGCTTGGAATACCGTCATGCATATGTTT  
GTAAGTATGCAATCCTAGCAGTTTTCTCCATTTTCAAGGTCAGCGAACATTTACTTCCCG  
ATGCTAAAGAAATCATCAATTCGTTTCATAGTAGCTGAAACTGATCCAATATGTAAAAGAA  
ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAAATGCCTTACACTATTTAGAGAACA  
ATATTGCTGATATAGAAAACCTAGACCCCTTTATTACAAGCTGTCTTTGTTCAATTTATCA  
GACAAGATGCAACACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTTGATGGAAC  
TGCTTTGACCAACGACTTCCGATGAAGTCATCTTCGAGACCCGATTAGCCCTAACTGTGT  
TGTCTGCCAATCCAAATGTCTTGGTTCCCTGCGGTAAACAAATTGATTGACTTGCCGTC  
AGGTTTCTGATAATAACATTAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA  
ATAACGTAGGTGCTTTGGAAGAGTTAACCCTGGATATTTTGAGAGTCTTGAATGCAGAAG  
ATTTAGACGTTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGCCACATCCAGAAATG  
CTGAAGATGTTGTTGAGCTTTTGAAGAAAGAGCTGCAAAACAACCGTAATAAACCAGATC  
AAGACAAGGCAATGTCAGTACAGACAATTGTTAATAAAAACTATTTCGTACCGTGGCTGTAA  
ACTTTGTAGAAATGGCAGCAAGTGTTGTTTCGCTATTATTAGATTTTCATCGGTGATTTAA  
ACTCGGTGCGGCCAGTGGTATCATTGCCCTTTATCAAAGAAGTGATCGAAAAATACCCAC  
AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA  
AAGCTTACCGCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC  
AACATTGTTGGAAGCACATTTCGTAACAGCGTAGGTGAAGTTCTTATCCTTCAATCAGAAA  
TCAAAAAGTTAACACAAAACCAAGAACACACCCGAAGAAAATGAGGTTGACGCTACCGCCA  
AGCCAACTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTGATG  
TGAAGACTTCTCAAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTGCCC  
GGTTTGTTTTAAAGTGGTGATTCTACACAGCTGCCATTCTGGCCAACACCATCATTAAC  
TTGTTTTTAAATTCGAAAACGTTTCCAAGAACAAAAGTGTCAATGCTCTAAAGGCGG  
AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGGAGAAA  
AAATTGATGAAGATTCTTTAGAGAGAGTTATGACATCTATTCTATTATTATTGGATGAAG  
TTAATCCTGAGGAAAAGAAGGAAGAAGTTAAACTTCTGGAGGTTGCATTCTTGGACACCA  
CCAAATCCTCATTCAGAGACAAATTGAAATTGCAAGAAGAACAAGCATAAGAGAGCAT  
TAAAAGACAGTTGCAAAAACATCGAACCAATTGATACGCCGATTTCTTTTCAGGCAATTTG  
CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACCTGGCAA  
TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTTGAAGCTGAAGAAGATAG  
TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGTATTACAAACAATCAAT  
TTGACGTCGTATTAGATGTTCTTCTTGTAAATCAAACGAAAGAAACATTGAAAAACCTAC  
ATGTGCAATTTGCAACTCTTGGTGATTTGAAGATTATTGACACACCACAGAAGACCAACG  
TGATTCTCATGGCTTCCACAAATTCAGTGTACTGTCAAAGTTTCTCTGTGCTGACACAG  
GTGTCATTTTCGGTAATATTATTTATGATGGTGCGCATGGTGAAGATGCTCGTTATGTTA  
TTTTAAACGACGTTTCATGTTGACATTATGGATTATATCAAACCAGCCACTGCTGACGATG  
AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAACAAAATATCGGTCAAATCAC  
AATACCAACAGATTGCATGCTTATTGAGAGAACTGGTCAAGGGAACTAATATGGGTATTC  
TAACACCATCAGAGTCGTTGGGAGAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG  
CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCAACCTGTGTATCGAAAAGGATTCCAAAA  
CCAATGATGTCATAGGTTATGTTTCGTATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC  
TAGGTGACAGAGTGGCATTGATTGCTAAGAAGACCAATAAACTTGCTCTCACTCATGTTT

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GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFDPSPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPEL  
LMHIIRFVMPSPKSKNELKKLLFYFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG  
NTLRFLLTKREAELLEQMVPVSLACLEVRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN  
SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT  
PALKAQYIELLMELLSTTTSDEVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSNNI  
KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL  
LKKELQTTVNNPDQDKAMQYRQLLIKTIRTAVNVFVEMAASVVSLLLDFIGDLNSVAASG  
IIAFIKEYIEKYPQLRANILENMVQTLDKVRSKAYRGALWIMGEYAEGESEIQHCWKHI  
RNSVGEVPILQSEIKKLTQNQEHTENEVDATAKPTGPVILPDGT YatesAFDVKTSQKS  
VTDEERDSRPPIRRFVLSGDFYTAAILANTI I KLVLFENVSKNKTVINALKAEALLILV  
SIVRVGQSSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLLEVAFLDTTKSSFKR  
QIEIAKKNKHKRALKDSCKNIEPIDTPI SFRQFAGVDSTNVQKDSIEEDLQLAMKGDAIH  
ATSSSSI SKLKKIVPLCGFSDPVYAEACITNNQFDVLDVLLVNQTKETLKNLHVQFATL  
GDLKIIDTPQKTNVI PHGFHKFTVTVKVSSADTGVIFGNIIYDGAHGEDARYVILNDVHV  
DIMDIK PATADDEHFRMTMWNAFEWENKISVKSQ LPTLHAYLRELVKGTNMGILTPSESL  
GEDDCRFLSCNLYAKSSFGE DALANLCIEKDSKTNDVIGYVRIRSKGQGLALS LGDRVAL  
IAKKTNKLALTHV

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)

AAACTTTGTTCAAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACTTATTTT  
ACTGCATGTGGATAAAAGTTTTCGAATCGTTTGCAGGCAAATGTAACTATTACTTTTT  
AATGATTCTGATACTCTTTGATTCCATTCTGTCACTACTTTTTCTGCATTTGAAACGCT  
AATTAAGTATTTCTTGGCCCTGCTTCTTTTCTTTTGATTTCTTTTTTTATTCTCAAGTT  
TTTAATTTCTGGAGAATCTCTTTTTTTGTTTATTTTGTAAACACAGTTAGTGGAGCCTTG  
TAGTATCGAGAGTAGACTATCTTTGGAAAGCAATGCGAGTTGAGAGATTGTGGAGTGTAC  
TACAGAACCAATATTAACACAATCTTTCTCTCAAACGTAAACACCGAGTTTTTTTCCCA  
CCAATCGTGAATCCGATAGCATATACTTTTGTCTAGAAATTTCAATAAACACAGAATAA  
CGAAGAGTGCTAAGGGACAAATGCAAAACCTCCGTGTGATTCTGTCCTCCGATATGTATAATC  
AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT  
CTCCGCAAATTGACAGCCAGCACGTCCCAAAAGTTACCTTATAGAATAAATCCTACAA  
CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA  
ACTTGATGCATCTATCTGGTCCGTCTGACTATAGATCGATGCATCAAAGTCTTATACATC  
CATCTTATATCATCCCTCCGCATTCAAATGAAAGAAACAATCAGCTTCTTCAACAGAC  
CTCAAAATGCTCATGTTAGTATTCACCTTCCGTGGTATTCCCCCTAAAAAGTTATTCCA  
TATCTTATGCACCTTATCAAATAAATCCCCCTTTACCAAATGGACTTCCGAACAGAGCA  
TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA  
CCAGTGTTACTACTGCACCTCCTTCTTTTCAAAACAGTGCTGATACCGCTAAAAATTCAG  
CTGATAATAATGATAATAATGATAATGTAACCAAACCTGTTCTTGATAAAGACACCCAAC  
TCATAAGTAGTTCAAGCAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACCG  
CTCAAAAGGCATTTAGACAAAAGGAAAGAAAAATACATCAAGAATCTCGAACAAAAATCAA  
AGATATTTGACGATTTACTAGCAGAAAATAAATACTTCAAATCATTAACGATTTCATTAA  
GAAATGACAACAACATTTTAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT  
TAAGAAGTGAGTATGATGTCTTATGTAACGAAAACAACATGTTGAAGAATGAGAATAGTA  
TAATAAAAAATGAACACAACATGTCAAGAAATGAAATGAAAACCTAAACCTTGAGAATA  
AACGCTTCCACGCTGAATATATACGAATGATCGAGGATATTGAAAATACTAAAAGAAAG  
ACAAGAACAACGAGATGAAATAGAGCAACTAAAAAATAAAGATCCCTGGAGGAA  
TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)

MQNPLIRPDYMNQSSSMATYNASEKNLNEHPSPQIAQPSTSQKLPYRINPTTTNGDTD  
ISVNSNPIQPPLPNLMHLSGSPDYRSMHQSPHPSYIIPPHSNERKQSASYNRPQNAHVS  
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQSI SLNKEYIAEEQLSTLPSRNTSVTTAP  
PSFQNSADTAKNSADNNDNDNVTKPVPDKDTQLISSSGKTLRNTRRAAQNRRTAQKAFRQ  
RKEYIKNLEQKSKIFDDLLAENNNFKSLNDSLRNDNNILIAQHEAIRNAITMLRSEYDV  
LCNENNMLKNENSI I KNEHNMSRNENENLKENKRFHAEYIRMIEDIENTKRKEQEQRDE  
IEQLKKKIRSLEEIVGRHSDSAT

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YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)

CCGACAGTACGACTTAAAAAACAAAAACAACGTCCAGGTGGAAAAAGCTGCCGCAAATGG  
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT  
AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG  
TTTCTACAAGTATTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT  
TAAATCTACACAGTTGCCATATCGTTTATCGCCTTATTCTTCAGAAACATTTTCATCAACTA  
CTCTGGTGCATTTATTTTCATGTTAGTTACCATATATACCGGCCGGCCGCATCGGGGTTTTT  
TGATTGAAAAAATTGGTATATTTTTCAGTACACATATAAATAAAACCCTCAATTTGCCTCT  
CCAACCGTTATACTATTCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG  
GGATTTTTCATCTAATACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT  
GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCAGTTTATGATTC  
TAACCATCAACGAATTAAAAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA  
ACATGTTGAAGGATTATTGTTTTGTGATCTTTTGTGTTACAAGCTAATAAGTAATTTTTTTT  
ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCA  
GAAGATTGTTTCGTTGGTTATTGGACTCACCATTTTTGAGGGGTACCGTAGAAAAGGAAG  
TCACAAAGGTCAAACAATCGATCGAAGACGAACATAATAGATCGGACTCTCAGTTAATGA  
ATTTCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA  
AATTGAACGACTTGATACCACATACCCAAATGGAAGGAAGGAAAGGTCTCTGGTCCGTTT  
ACCACGGTGGTGATGATTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG  
CCAATCAATTACATCCCGATGTCTTTCTGCCGTACGTAAAATGGAATCCGAAGTGGTTT  
CTATGGTTTTAAGAATGTTTAAATGCCCTTCTGATACAGGTTGTGGTACCACAACCTTCAG  
GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC  
GTGGAATCACCGAACAGAAATAATTGCTCCCGTAACCTGCACATGCTGGGTTTGACAAAG  
CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG  
TGGACCTGGGAAAAGTGAAAAAATTCATCAATAAGAACACAATTTTACTGGTCCGTTCCG  
CTCCAAACTTTTCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAAAATAGCACAAA  
AATATAAACTTCCTTTACACGTGACAGTTGTCTAGGTTCCCTTATTGTTTCATTTATGG  
AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA  
TATCATGTGACACTCATAAATATGGATTTCACCAAAAAGGCTCGTCAGTTATAATGTATA  
GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT  
ATGGCTCTCCTACATTAGCAGGGTCCAGGCTGGTGCTATTGTCGTAGGTTGTTGGGCCA  
CTATGGTCAACATGGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG  
CAATGAAGTTTAAAAAATACATCCAGGAAAACATTCAGACCTGAATATAATGGGCAACC  
CTAGATATTTCAGTCATTTTCATTTCTTCAAAGACCTTGAACATACACGAACCTATCTGACA  
GGTTGTCCAAGAAAGGCTGGCATTTCAATGCCCTACAAAAGCCGGTTGCACTACACATGG  
CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG  
TGCAAGAGTTGAAGAGCGAATCAAATTTCTAAACCATCCCCAGACGGAAGTACGCTCTAT  
ATGGTGTGCGCGGGAGCGTTAAAACTGCTGGCGTTGCAGACAAATTGATTGTGGGATTCC  
TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPIHLLREEGDFQAQFMILTINELKIAIHGYLRNTPWYNMLKDYLL  
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVKEVTKVKQS  
IEDELIRSDSQLMNFQPLPSNGIPQDDVIEELNKLNDLI PHTQWKEGKVS GAVYHGGDDL  
IHLQTIAYEKYCVANQLHPDVFPVRKMESEVSMVLRMFNAPSDTGCGTTTSGGTESLL  
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK  
KFINKNTILLVGSAPNFPFGIADDIEGLGKIAQKYKLPLHVDSCLSFIVSFMEKAGYKN  
LPLLD FRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPWTGGLYGSPTLA  
GSRPGAIVVGCWATMVNMGENGYIESCQEIVGAAMKFKKYIQENIPDLNIMGNPRYSVIS  
FSSKTLNIHELSDRLSKKGWHFNALQKPVALHMAFTRLSAHVDEICDILRTTVQELKSE  
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTTGTCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCTGTGGAGCAGAT  
TCCTTGGAACCTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGCTGT  
TCTTCGACTGGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT  
TCAGACATTATCCTTATGGTTTTAGCGTAATTGCTTAATTTTGATTCTTCAAAGTATA  
TATATTTAGAAGAGAGGAAATTATTTTTCTCATGTCCTTTTAAATCCCTTTGGGTGGCG  
AAAAAAGAATGTAAAAAATTTTGCCCTTCGTTTACAGTGATAAATATACGGAGGGGCT  
CTATGATAAAGGTAGTAGTAAATCATTGAATTGTTGAACAAGCATTGACAGATATGATAA



CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAGTTACTA  
TAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTGCGTCCTCGTATGCCCAAG  
CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATTCATGGTTATGAAGTGAGAAGAA  
TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCACCTCCAGACAGGAG  
CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTGAGCATTGCTTTTAA  
CCAACCTCCAGATTCCACTGGGGTCCCTCATATTTCTAGAGCATACAACGTTGTGTGGGT  
CTGTTAAATATCCAGTTAGGGACCTTTTTTCAAAATGCTAAATAAATCTCTAGCTAATT  
TCATGAACGCTATGACAGGTCCAGATTATACATTTTTCCTTTTCCACTACGAACCTC  
AAGATTTGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC  
AAGAAGATTTTGGATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCAGACCCGGAGA  
GTAACATTGTTTTCAAAGGTGTTGCTATAACGAAATGAAAGGTCAAATATCAAATGCCA  
ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG  
GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA  
ATTACCATCCCTCCAATGCAAAAACTTTCACGTACGGTAACTTGCCATTGGTGGATACGT  
TAAAGCAATTAAATGAGCAGTTTCAAGTGTACGGGAAGAGAGCTCGAAAGGATAAGTTGT  
TAATGCCATTTGATTTAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA  
TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTTGTGGAGCGCCACAGG  
ACACATATGATACCTTTTTGTTAAAGTACTGGGGAATTTATTAATGGATGGCCATTCTT  
CTGTAATGTATCAAAAATTAATAGAAATCAGGAATTTGGTTTGGAGTTCTCCGTAAATTCAG  
GTGTTGAACCAACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGGCGTGAGTGATA  
TTGAAATATTTAAAGACACTGTAAATAATATTTTCAAACCTGTTGGAAACAGAACATC  
CTTTTGACCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTAAGAAGGATC  
AAAAGGCTGACTTTGGACTTCAATTACTCTATTTCTATACTACCTGGTTGGACAAACAAAA  
TCGATCCTTTTGAGAGCTTGTGTTTGGAGACGTTTTCGAAAGATTTAGAGGTAACTTAG  
AAACGAAAGGTGATACCTTTATTTCCAAGATTTAATCCGTAAATATATCGTTTATAAACCTT  
GTTTCAACGTTTTCATTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC  
AAACAAGACTGAGAGAAAAAATTACTGCCTTGGATGAACAAGACAAGAAAAACATCTTTA  
AACGTGGTATACTGTTACAGGAGAAACAAAATGAAAAAGAGATTTATCCTGTTTACCTA  
CCTTACAAATAAAAAGACATCCCAAGAGCTGGTGATAAATATTCATCGAACAGAGAATA  
ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC  
TAAATGACATAATACCTTTTGAACCTCTTCCACTACTTACCTTTATTTGCTGAATCGTTAA  
CTAACCTAGGGACAACAACAGAATCCTTCAGTGAAATAGAAGATCAGATAAAATTACATA  
CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCTAACACCACAGAGCCTCGCC  
TGATTTTTCGGGTTTGACGGATGGTCTTTAAATTCGAAGACCGACCACATTTTGAATTCT  
GGTCTAAGATCTTACTAGAACTGATTTCCATAAAAACAGCGATAAATTGAAAGTTCTTA  
TCCGCTTATTAGCATCTTCAAACACATCTTCTGTAGCAGATGCCGGTCATGCATTTGCAA  
GGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCTCAATGGTA  
TTGAGCAACTACAAATTTATAAATAGATTGCACAGCTTGTAGACAATGAAGAACTTTCC  
AAAGAGAAGTTGTCGACAAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA  
TGAATTTTTTTATCACCTCAGACTCTGATGTTCAAGCGAAAACAGTAGAAAGCCAAATTT  
CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG  
ATTATCCTCTTATTGGATCCAAATGTAAACATACTTTGATAAAATTTCTTTCCAGGTCC  
ATTACACATCCCAAGCTTTATTGGGTGTGCCGTATACACATAAGGATGGCTCTGCACTTC  
AAGTTATGTCAAATATGCTAACATTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG  
GTGCTTATGGTGGTGGTGTCTTATAGCGCCTTAGCGGGTATTTTCAGTTTCTATTCCT  
ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC  
TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC  
AAGTAGACGCACCTAAAAGTCCCAAGGAGAAGGCGTGACGTATTTGATGAGCGGTGTTA  
CAGACGATATGAAACAAGCAAGAAGGGAACAACCTTTAGACGTATCTCTCCTGGACGTTT  
ATAGAGTCGCCGAAAAATATCTACTAAACAAGAAGGGGTGAGTACGGTCATTGGACCTG  
GAATCGAGGGGAAGACTGTTTACCATAATGGGAGGTGAAGGAAGTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQAVRKYPVGGIFHGVEVRRILPVPELRLTAVDLVHSQTGAEHLHID  
RDDKNNVFSIAFKNPDPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSLANFMNAMTG  
PDYTFNPFSTVNPQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG  
VVYNEMKGQISNANYFWSKFQQSIYPSLNNSGGDPMKITDLRYGDLLDFHHKNYHPSNA  
KTFITYGNLPLVDTLKQLNEQFSYGKRRARKDKLLMPIDLKKDIDVKLLGQIDTMLPPEKQ  
TKASMTWICGAPQDITYDTFLLKVLGNLLMDGHSSVMYQKLIESGIGLEFSVNSGVEPTTA  
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIEQLELSKKDQKADFG

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QLLYSILPGWTKIDPFESLLFEDVLQRFGRDLETKGDTLFDLIRKYIVHKPCFTFSIQ  
GSEEFKSLDDDEEQTRLREKITALDEQDKKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI  
PRAGDKYSIEQKNNTMSRITDTNGITYVRGKRLNDIIPFELFPYLPFAESLTNLGTTT  
ESFSEIEDQIKLHTGGISTHVEVTSDPNTEPRLIFGFDGWSLNSKTDHIFEFWSKILLE  
TDFHKNSDKLKVLRLLASSNTSSVADAGHAFARGYSAHYRSSGAINETLNGIEQLQFI  
NRLHSLLDNEETFQREVVDKLTLELQKYIVDTNMMNFFITSDDVQAKTVESQISKFMERL  
PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVPHYTHKDGSAQVMSNML  
TFKHLHREVREKGGAYGGGASYSALAGIFSFSYRDPQPLKSLETFKNSGRYILNDAKWG  
VTDLDEAKLTIQQVDAPKSPKGEVTVFMSGVTDDMKQARREQLLDVSLLDVHRVAEKY  
LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1612 bp, CDS: 500-1612 (SEQ ID NO 61)

CTTTTCTCAGCACCTGTCCAGAGACATAACATCACATCGCCCCAGTAAATGCA  
TACGCAAGATAAGATACAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT  
GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA  
TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCCCT  
GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT  
GAGGCTGTAATGCTTACCGTTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCCCCATACAC  
ATTTTTTCGGTAACCTGCGGCATATAGATGAAAGTTGAAATGAATATTCAAAAGAATATATA  
TAATAATGCAGGAGATCAAGGAAGAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA  
AATAAAAAGTAAGCAGGAGAATGAATCGTGTTGGTATAGACGTAGATCATATGATAGGGG  
TCCTGCTTCTGGCCGTAGTGGTGGTGTGTTTGGGTGGCGCTTCGTGTTTGACTAATGAAT  
TGCTCGAGACAAACGCGTACAATAAACCTTTCTTCCTTACTTATCTAAACATATCATCGT  
TTGCTCTTTATTTGACGCCAGATCTATGGAGGATAATCCAATCAAGAAGGAAGAGCTTGC  
AGGAACGGACAGAACGAACATTACCTATTACACACACAAGAATCTTTTTCAGAGTTCCCTAC  
CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG  
TGAAGGATACAAATGAGGTTGAGTCTGCTATTTTGGCGTCTTGTGGTTCGTGGCAAATTTGG  
CGGCTAACGCTGCTTTGTGCTATACCACAGTGGCTTCGTCAACAATTCTTTCATCGACAT  
CCTCATTTTTTACCTTATTTCTTGCCACTAGTCTAGGAATAGAACTTTTTTCGACAAAAA  
AACTGCTGGGGTTATTTGTGCTTTGTTTGGGAATTATCTTAATTGTGATGCAATCCTCGA  
AGCAACAGGATTCTGTGAGTGCTTCCCTCTTTTGGTAGGTAACACTTTAGCACTGCTGG  
GGTCATTGGGTTACAGTGTCTATACAACCTTTTGAATAACGAAATATCATCCAAAGGTC  
TCAGACTAGACATTACAGATGTTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT  
GGCCAATTTTAATAATCCTGGATATAACACATATGGAACTTTTGAACACCAAGTAACCT  
TCCACATTTCTTTTCTTGTCATGTAAATTGTATCATTATCTTTGTTAGTGACTATTTTT  
GGTGTAAGCCCTCATTTTGACATCACCTTTGGTGGTTACCGTTGCCTTAACTTTTACTA  
TCCCGTTAGCCATGTTTCGCTGATTTTGTATGGCGAGAGGCATTTTTTACGCCTTGGTATA  
TCATTGGTGTTATTTTCATTTTTGTTTCATTCTTTCTAGTTAACCATCGGGGAGAATCTG  
CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIDVDHMGVLLAVVVVFWVGASCLTNELLETNAYNKPFFLTLYLNISFALYLTP  
DLWRIIQSRKSLQERTERTLPIHTQESFSEFLPLLSSTPSTSSNLSSIADTKVKDTMRL  
SLLFCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFTKKLLGLFV  
SLFGIILIVMQSSKQQDSVSASSFLVGNLALLGSLGYSVYTTLLKYEISSKGLRLDIQM  
FLGYVGIFTFLFWPILIILDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL  
TSPLVVTVALTFTIPLAMFADFVWREAFFTPWYIIGVIFIVSFVFLVNRHGESAVEKDCA  
AVEKGPILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2: 983-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAATTGAGAACGATATTATTAATTCTAGTATATTTTAGGAACAGCA  
GGCCATTATATCCAAAACCTTTTTTAAATAGCATCCACATCACTTACTGGCGTACAGTTT  
CGTGTCTGGCAACAAAAAGTACATTTAATTTCAATGATTAAAAAGACATTAAACATCCG  
TACATTACGCACCCATGCATGCTATCTGAAAATATTCTACATGCTGCTTTTAGAAATTTG  
AAGCGGCATATGGTGTTTCTTGGCGAGACGCGCGCTCAGGGGAACCTGCGATTCCGAAAG  
ATGCCCTTTCCAGTCCCATATGCCCATCCCAAGATCATGCCCGGAGAGCAAATGTCGCC  
CCAGCCAGGTCGGACACATCTGTCACTTCCAGCACTAAGTATTGTCAAAGCTAGGGTTAAT  
TGAAGATAGCTCTACATGTTATTAGTAGAGTTTTTAAACGTTGAGATACTAGTGAACGTA  
TACACAAGAGCGGATAAAAGATGTCTTTAGTTGTCCAAGAACAAGGTTCTTCCAACACA

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TTTTACGGTATGTTTATTATTACTAGTGAGCTATGACAAAATCGGCTAAAAACTTAAAAA  
TATGACAGACAAGAAAGGAAATTCATTCACCTCTTTAATCGTGGCGATTATTCGCTAACG  
ACGTGATTAAATATAATAATGATGTTCCCGGGCTGGACTAAGAACGTAATAATAAGGCTG  
ATGAACAAATTTATGGTTTATGCATCAAAAAGGAACATGAATTTGGCATAAGCGCACATA  
ATTACGGAACATTGCAATAGCGGTCGGAGGTAAAGTACCGGGAATGCTTTACAATGAATC  
AGCTATTGGCGGATATTGACCAACCAACACTAAAATTTTATATCCTGCTCCGATTTTGT  
CTTGGCCGTGAAATCCATTATGCACATTTTTTACTAACGTTTATCAATAAGTTCGGTTTC  
CCGTCTAAATTTTTTTTACGCAGTTTGTGTAACACTAACGTTGACGGTAACATTAAGATCG  
TTTACGCTTTGACCCTATCAAGGGTGTTGGTTCGTCGTTACTCCAACCTGGTCTGTAAGA  
AGGCTGATGTTGATTTACACAAGAGAGCTGGTGAATTGACCCAAGAAGAATTGGAAAGAA  
TTGTTCAAAATTATGCAAAACCCAACTCACTACAAAATCCCAGCTTGGTTCTTGAACCGTC  
AAACGACATCACTGATGGTAAGGACTACCACACTTTGGCTAACAACGTCGAATCCAAAT  
TGAGAGATGACTTGGAAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT  
GGGGTTTGCCTGTTAGAGGTCAACACACCAAGACCACTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEQQSFQHILRLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE  
LTQEELERIVQIMQNPHTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR  
AHRGIRHFWGLRVRGQHTTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAAAGTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC  
GACAGGTCGATGACTTGTAGGGCTCTTGCAGACTCTTCTCTACGCCAAAATCATTTTTTA  
AAACAGGGCAGACTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAAGAGGC  
CACACTGAGGCCGGTGTCGATTTGTGTAAACTAAGTGGACTAAGTCCCGTCGCTGTTATT  
GGCGAATTGGTTAACGATGACGAACAAGGAACATGATGAGATTAAATGACTGCCAAGCG  
TTTGGTAAGAAACATGGCATTCCCTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG  
AAATAATCTGGTGAACATTTTCTCCATTCTATCTATCACAACAGACTCACACATATATAC  
ATGTATATATTTGTAACCTTTGTATATATCTTTTGTTTTTTTGACCTTTTTCTTCTCTATG  
TTTTTCAGCCATACAAAAATATGGGATTTTGTAGCAAGAGAAAAAGTACATCTAAAAAAG  
TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA  
TGAACAGGATTTTCGGATATGGGAACAAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA  
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCCAGTTAGATACTC  
AAATCGCCCAGTTAAACTTCCAGCTGCAAAATATTCAAAAGAATTTGCAAAAGATCAAACA  
ACAAGCAACCCTCGTTAAGAAAACAGGCTTTTGAAGATTTTAAATAAACGTAAACAGTTAG  
AAAATATGAAGGATTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCCAGTTAACAA  
ATGATAACTTTACAGAACAATGATCACTATAAACGCCTAAAGCAAAACAAACAATGCCA  
TGAAGGCTCAATACGGCAAGATAAAATATCGACAAACTACAGGACATGCAGGATGAGATGC  
TGGATTTAATAGAACAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAATAACAGTG  
GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG  
AGGATTTCACTTTGCCAACCAGCGAAAACATTAGGTAACGATATGCCCAGTTACTTAC  
TAGGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAACTTAGATACTGAAGACA  
AAAATAAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHLKKVVIGGSQDWLKHYSYKLFKAIMNRIFGYGNKSHDQLLQESNQSMNQA  
QQSLSNRISQLDTQIAQLNFQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL  
DSQSWSMTQAQLTNDNLQNTMITINALKQTNNAMKAQYKINIDKLQDMQDEMLDLIEQG  
DELQEVLMNNNSGELDDISDAELDALAQEDFTLPTSENSLGNMPSYLLGANAPP  
AFIDEENLDTEDKNKALESAQ

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:  
916-1295 (SEQ ID NO 67)

GGCAAATCAATTAATAATTCCTTTTCTCTCTACCTTTGCTAATATTA AAAACCATAGTTGT  
AAAGGGTACTTAATGCTATATTCTGTTAAGTTTCCTATTTCACCTTGTTTTTCCAATT  
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAATCATTTTCCACCCACACATATATT  
ACCCTTTTTTTGGGTGAAGAGAAGTAGTATTTTGTTTTTTCATGGGAGTGGAAGTCCTTTC  
AAAATAATCCGAGCAGTAGTGCTGTCTAGGCGGAGATTATTGAAAGTCGGCATTGGCTG  
CAGCTAGCGTTTTTGTTTTTTGGTACTACCTGTCAAACCCGGCGTCTGCCTAGATTGCGCGG  
AGGGTACGTTGAAACTTTTGCCTTTCCACGTCAGTTTATAATATCAAAAGCAGCAATATA

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CACATTTAATGGTTTGCCCTTAGTGACTATTAGGGCGTTTTTGGTGAAAAGAAAGAGTCGC  
TCAAAGAAATCAATATAACCATGGCTAAATTTTTGAAAGCAGGTAAAGTTGGTACGTAAA  
TTTAACAGAGCAAACGCTCTAATTAAGATATCGAATAAAAGGGGACTTTTCAGGTGCATAA  
GATGGGAAATTTGTACAATCTGAGGGACAAACAATATGGAAAGCAGTACATGATTGTATTG  
TCATTGTAGGAGGTACCAATTGTGCCAGTAAAAAAGAGAGGGCCCGGGGAGCACCACATT  
CACGACCAATCGTGTGCTGATCTGCAAAAAAGGCACATGGAATAATGTAATTTATCAGTGTTC  
AACACTGAGTTGAACAGATAGCTATCTAATCAATGTTAACTTTCCAGGGAACAAAAAGCT  
AAATCCACTTCTCTTTTATTTCAAAATATCATTAGAAATAGAAAAATTTACTAACAAATT  
TTCGTATTATCGTAGCTGTCGTTGTTTCGTGGTTCGTTACGCTGGTAAGAAGGTTGTGATCG  
TTAAGCCACACGATGAGGGTTCTAAATCTCATCCATTCGGTCACGCTTTGGTTGCCGGTA  
TTGAAAGGTACCCATCAAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTCGCTAAGAGAA  
CTAAAAATCAAGCCATTTCATCAAAGTCGTCAACTACAACCACCTATTGGCAACCAGATACA  
CCTTGGATGTTGAAGCTTTCAAGAGCGTTGTATCTACAGAGACTTTTGAACAACCATCCC  
AACGTGAAGAAGCCAAGAAGGTTGTAAAGAAGGCATTTGAAGAAAGACATCAAGCTGGTA  
AAAACCAATGGTTCTTCTCCAAGTTGAGATTCTAA

YDR471W, 136 aa (SEQ ID NO 68)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFHALVAGIERYPKSVTKKHGAK  
KVAKRTKIKPFIKVVVYNHLLPTRYTLDVFAFKSVVSTETFEQPSQREEAKKVVKAFEE  
RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69)

TAACAATAGAAAAAATACACACACATTAGATTGGAATTAGAGCTTAAGTGGTACAAACT  
AGGGCTAATAAAGAGGTAACGGTCGGTTCTCTACTAAGGTTTCGTATTGTGTGGCACCAGAT  
GTTAAGCACTTTTAAGCGGAATAAAGTTCGAGTGGAATTTTATGTTTAGTTAGGTTTACC  
TTGAATTTTTTTAAAAAAGAGTCAGACAGGCTCGCTCTTTCCTACTAAATATTAGG  
AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACCTCCAAATTTAT  
CTTACAAAGAGCTATTAGTATCTTGGTTCTTCTATTTTCTTCGATTATTGGTGATTTTTTC  
CCGCTCTAGCCAAATCCGAGCGTTCCATCGATTTT'TTGGGGAAAACAGCACATGCAATA  
AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAATCTCT  
TTTGCATATTTCTATTATAGATGAGACGAGAAACGGTGGGTGAATTTTCTTCCAGTAGCG  
ATGATGATATTTCTTTTGGGAATTAGGCACCAGGCCCTCCAAGGTTTACTCAAATACCGCCAT  
CATCAGCAGCATTACAAACACAAATTTCCCACTACTTTGGAGGTTACAACGACCACATTAA  
ACAATAAACAGAGTAAAAATGATAACCAACTGGTTAACCAACTGAATAAAGCTCAAGGTG  
AAGCAAGCATGCTTCGTGATAAAAAATAAATTTTGAACATTGAAAGGGAAAAGGAAAAGA  
ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT  
TAAACAAGAATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG  
GAAAAATCGAAAAGGGAAGTTATTACGAATGTAAAACCACCGTCAACAACATTTATCAACAA  
ACACAAACACTATAACGCCAGATTTCGTCTCTCAGTTGCAATCGAAGCAAAACCTCAATCAC  
CACAATCAAAAAACGTAAGATAAGTGATAATTTACTGAAAAAATATGGTTCCCTTAA  
ACCCAAATAGGATTATTTCCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCATC  
AAATAATAGGCGCTGACCTGAGCACAATAGAAATATTAAATAGATTGAAGCTTGACTACA  
TCACAGAGTTTAAATTTAAGAAATTTTCGTACATTGCTAAAGGAGCCCCCATAGGGAAGTCCA  
TAGTTTCTCTACTTTTGGGATGTAAAAAGAGCTTGACCCTCGACAGGTTTCATAGATACTT  
TGCTAGAGGATATAGCTGTTTTGATCAAGGAAATATCAGTTCATCCAAATGAATCGAAAT  
TAGCTGTCCCATTCTCGTTGCATTGATGTATCAGATTGTACAATTTTCGTCTTAGTGCCA  
CTCATAATTTAGCACTGAAGGATTGTTTTCTTTTATTTGCGATTTAATAAGAATCTATC  
ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCCTCAGA  
TTTTCCAATATGAACGTGATAGACTATTTGATAATTTTCGTATTTCCTTTGATCTCCTAGAAG  
GTATATTAAAGGTACTGCAGTCGCATCCTTAAGCAAATTTATATGGAATTTT'TGATGAAA  
ATATTCTAAAATCATTTGAATTTGTCTACAACTAGCACTAACCATTTTCATACAAGCCAA  
TGGTAAATGTAATATTTAGTGCAGTCGAGGTCGTTAATATTATCACTAGTATAATATTAA  
ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA  
TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGGCGACGTATATAATGAAA  
ATGTGGATGATACTACAACCTTTCATATGTGCAAGTACCATGACTTTTTTGGGTTAATCCGAA  
ATATAGGTGATAATGAATTTGGGAGGATTGATATCAAAGCTGATTTTATACTGACCGATTGC  
AAAGTGTCCCAAGGGTAATTTCTAAAGAGGATATTGGGATGGATAGCGACAAATTCAGTG  
CCCCATAATAGGTTACAAGATGGAATAATGGCTTTTGAAGTTAAAAGATGAAGTTTAA  
ATATTTTTTGAATAATTTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA  
TGCTCATCCACTCCTCTAAATTCCTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG

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TGGGACAAGACTCCCCGAACCTTGGACCTCAGATGCCATCTTATTGAACATACTTTAAACCA  
TAATATATAGGCTATGGAAGACCATTTCAAACAATTGCGTGAAGAACAATCAAGCAGG  
TAGAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA  
CAGCAAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA  
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCCTTTGAGGATTTACCAGAATATATCG  
AAGAAGAATTGAAGATGCAATTGAATAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG  
ATGAGAAAATTTCAAGAAATGGCAAGAACTATTTCTTGAGTCAAAATCATTTCGATCTAACCA  
CACTAGAGGAGGCCGATTTCATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)

MRRETVGEFSSDDDDDDILLELGTTRPPRFTQIPSSAALQTQIPTTLEVT'T'TTLNNKQSKN  
DNQLVNQLNKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELQVKHLQELAKLKQELQK  
LEDEKKFLQMEARGKSKREVITNVKPPSTTTLSTNTNTITPDSSSSVAIEAKPQSPQSKKRK  
ISDNLKKNMVLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK  
NFVIAKGAPIGKSIIVSLLLRCCKTLTLDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV  
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVPIHESNMNLHVEPQIFQYELI  
DYLIISYSFDLLEGLRLVLQSHPKQTYMEFFDENILKSFEFVYKLALTI SYKPMVNVIFS  
AVEVVNIITSIILNMDNSSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTTL  
HMSKYHDFGLIRNIGDNELGGLISKLIYTDRLQSVPRVISKEDIGMDSDKFTAPIIGYK  
MEKWLLKLKDEVLNIFENLLMIYGD DATIVNGEMLIHSSKFLSREQALMIERYVGQDSPN  
LDLRCHLIEHTLTIIYRLWKDHFQKQLREEQIKQVESQLIMSLWRFLVCQTETVTANEREM  
RDHRHLVDSLHDLTIKDQASYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKQFQM  
ARTILES KSFDLTTLEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)

CTCTTTAAATATTCTATGTACTTTGTGCAAACATCATTGTCATCACATAAATGCATTCCCT  
ACTATTACTAACTTGAACCTTCACTTCACTGGAAGAACTGGGTATTCAAGGTAAAGAAAT  
CATTTGTTTTTGCGCCAAGTTTCGTCTGACAAAGAAATTTTTTATTATTATTTCCCACTTTTC  
ATCGAAGGAAACGCGTCAAATCCATTCGTTACTACGCGCAATCTGCGTTATTTCTTTT  
CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCCTTTTGATGTTAAATTA  
AAGCGACTGAATGAAGTGCACACATTTTTTATTCTTCTTGATTTTTCTTTCTTTTGT  
TTTGCTTTCTCTTCTGTGCGACAACGCTCTCAACTGTACTCACCATTAGTATTTCTCGAAGGC  
TTTAGCAGACTTGTGAATAATTAATTGCCCACTTTGATCAAGAAAGATATTCGCAGCACA  
ATACAATAATAACATTTCAAATGGCAATCAATGGTAACAGTATTCCTGCCATAAAGGATA  
ATACCATCGGTCCATGGAACTAGGTGAAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC  
AGCTTGCTCGTAATGGATCCACAGGACAAGAGCGGCAGTTAAGGTAATATCAAAAGCAG  
TATTAATACCGGTAAATGTGACGGTACTTCGATTGTTGGCTCCACCACCCAGATGCTC  
TACCATATGGTATAGAACGCGAAATAATCATTATGAAGTTGTTAAACCACCCAAATGTGT  
TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTTAGAAATACGCGG  
AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCTCTGCCAGAGCATGAAGCTA  
TCAGGTTTTTTAGACAAATTATTATTGGTGTGTCGTAATGCGTTGGGTATTGTCC  
ATCGTGATCTAAACCGGAAATCTATTATTAGATCATAAATATAACATCAAGATTGCAG  
ATTTTGGTATGGCTGCTTTGGAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC  
CACATTATGCTGCACCAGAAATTGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG  
TGTGGTCATGCGGTGTGATCCTATTCCGCCCTTCTTACTGGTCGGTTACCCTTTGACGAGG  
AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCCTT  
CTGATGATGAAATTTTCGCGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC  
CTGAAAGAAGAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA  
GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCACGCCAT  
TATCAGAAAGTAATTTCTTCTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC  
ATGGAAGAGATCCTGAAGGAATTAAGGAAAACTAAGAGAACCTGGCGCTAATGCAGAAA  
AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAAGC  
AACAGCAAGTTAAGAAGAGGCAGTCAATTAGTAGCGTTTCTGTTTCCCCATCTAAAAAG  
TATCGACAACCTCCACAACGCAGAAGAAATAGAGAAATCTTTAATTAGTGTAACATCTTCTC  
GTAAAAAGCCAATATCCTTCAACAAATTCAGTGCCTCCAGTGCCTCCTCCAGCAATCTAA  
CTACACCCGTTCTTCAAAACGCCCTTTCAAAAACCTTCTCTTCAAGAAGAAATTATCTA  
CAATCGTTAACCAATCTTCTCCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA  
ATGTGGAAGAAGTCAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAGAACAAAAGAT  
CTTCTAGATCTATCAAGAGAATGTCATTGATACCAAGCATGAAACGTGAATCGGTGACAA  
CAAAATTAATGTCAACATATGCGAAATTTGGCAGAGGATGACGATTGGGAATACATTGAGA

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AGGAAACAAAGAGAACGAGCTCAAATTTTGCAACTTTGATAGATGAAATTTTGTGAGTACG  
AAAAGTACGAACAAATAAGGAAAGAGAAGGAAGAGCTAGAACGTAAAGTGAGAGAAGCAA  
AAGCACGTGAAGAGCTGGAACGTAGAAGACGTAAACAAGAAGAAAAAGAACGTGCAAGAA  
AATTACTAGAAAAGGAAGATCTGAAAAGAAAACAGGAGGAACCTCAAGAAGCAAATTTGAAA  
TTGATATAAGTGTCTAGAGCAAGAGCTGTCCAAACACAAAGAGGAAAAAATCGGATGGTA  
ATATTAGATCTATCTCTGCTCCTATGGAAAATGAAGAGAAAAATATCAATCATTTGGAGG  
TTGATATTGACAATATTTCCGTCGCCGCAACTTTTCTTTACAAACTAGACCTGTGTCAA

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAACCTGAGGAAGTAAGTCCAGTGGAACCAA  
AGAGAACAGAAAATGAAAGACTTACAACAGAAAAAGAAATTTTAGAAACTATCAGAAGAT  
CAAAATTTCTTTGGGTTTCATCATTTTAATATCGATAAAGAGTTGAAATTTGTCTAAAATGGAAT  
ATCCAAGTATAATTGCACCACAAAGATTGTTCAGAGGAGCGAGTGGTGTTCAGATTCTTAATG  
ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAGGATA  
GTACCGCAACAACCTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG  
TACCACAATTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAGGCTATCTGTCC  
TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTTTGGTTGATATTTTGAAAAACGGTA  
ACCTTGATGTCAATAACCAACAAAGCCAAAGAATTTCCAACACCAAGAAGTGCGGATGATT  
CAGAATTTCTTTTGAACCTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTTCGAACG  
ATGAGAGATTGTCGATGTCGGTGATTCCACTATCAAAGACAAATCCGCGTTAAAGCTGA  
ACTTTGCAGATCGTTTTTAATGGATCGAACGAAGCGAAACAACTGATAACTTACATCTTC  
CGATCCTTCTCCGCTTAATGGTGACAATGAATTGCGTAAACAGAATAGCCAAGAGGGTG  
ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG  
AAAAGGAAGAAGAAAAAGAGGAAAAAGGAAGAGAAAAAGCCAGAACAACACAAACAAGAAG  
AGGATCAAGAAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG  
TGCAAAAAAATTAGGGAAAAAATGCTGGCTCGCAGGCAAAAGGATCATTCAAAGATCACT  
TAAAAGAGCATAAGCAGGATAAAAAATACAGCAATTGGAAATGGTTCCTTCTTTAGAAAAT  
TCTCAAAATCTTCGGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT  
TTAATGGTTTTAGAGAAGCTGTTGCGTGGTTGGACTCAGTATGGTTTAAAAAATATAAAAT  
CGCACCCCAACAATCTGACCTTAACGGGTAAACTATCGAGTGATAATATATCTCTACTAC  
GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA  
AGAAAGTTTCTGTTTCAAGCTGTCAAAGTTGGTCAATGAAGTTGAGAACGTCC  
TGAATAAGGAAGCGCTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINGNSIPAIKDNTIGPWKLGETLGLGSTGKVQLARNGSTGQEAAVKVISKAVFNTGNV  
SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN  
LLVERGPLPEHEAIRFRQIIIGVSYCHALGTVHRDLKPENLLIDHKYNIKIADFGMAAL  
ETEGKLLLETSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT  
LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLQKYPsirDSKS  
IRGLPREDTYLTPLESNSSIDATILQNLVILWHGRDPEGIKEKLREPGANAECTLYALL  
YRFKCDTQKELIKQQQVKKRQSISSSVSPSKKVSTTPQRRRNRESLSVTSSRKKPISE  
NKFTASSASSSNLTTPGSSKRLSKNFSSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK  
RASIFSTTKKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS  
SNFATLIDEIFEYKEYEQIRKEKEELERKVREAKAREELERRRRKQEEKERARKLLEKED  
LKRKQEELKKQIEIDISDLEQELSKHKEEKLDGNIRSIAPMENEKKNINHLEVDIDNIL  
RRRNFSLQTRPVSRDLPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS  
FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNVSQLKDSTATTAP  
VSDGRLRKISEIRVPQFTRKSRHFSSESNKRLSVLSMYSTKESFTNLVDILKNGNLDVNNQ  
QSQRIPTRSADDSEFLFETVNEEAETGNSSNDERLYDVG DSTIKDKSALKLNFADRFN  
GSNEAKQTDNLHLPILPPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSHTKEEENE  
EKEEKKPEQHKQEEDEKREKVDDMEPPLNKSQKIREKNAGSQAKDHSKDHLKEHKQD  
KNTAIGNGSFFRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNLTL  
LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKKVSFSKAVKKLVNEVENVLNKEGVL  
QK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATGCGTAACCATTTTGTACTACCGCTTCGTATGCTTTCTTGCACTTTGTG  
GAGCTACTCATACAATAGCTTATAATCTGTGTAGTCAAACCTATATACTAGGCAAATTACT  
AGTAAATGCAGTATTCATATGTCCTCAAACCGTTTTTTGCAGTATGTTATTGATCCATCG  
AATCAAAATTTTTCACCGCCAAGAGAAAAAAGATCTTACTATTTTGTGCTTATGAAAAAA

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TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAATTGGC  
ACATCCTTGGTTGACACTTGTCTATTTATTTAAAAGGTTTAAAAAGTAGTGTTCAGCAGT  
TCTATCATATTTTTTTTATTTAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA  
TTTAGGGTGGCGTTAAATAAACGAGAGAGCCCAAAAATATAACCAAGATAAAGAAAATCA  
ATCATAAAGTGAATTCAAAAATGTCATCGCAAAACCTCAATGATAATCCAAAAAATACAT  
CCTCAGCAGCTGAAGATAAGAAGAAACAACTTCATCCTTAAAGTTGGCACCAATACCAA

CCACATCGCCATGGAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC  
TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTTCGGGGTCAATTAAATTA  
CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA  
CAAATTCAAAGTCAGGAAAGAACTCTAAAAATCTAAGACTAATAAAAAAATGAAAAAGC  
GTGGCAAAATATAATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT  
CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA  
ACATACATTCAAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGATAACAAACAACA  
ACAATTCACCAACGGTAGACAATCAAGAAATTTATCAAAACAGGAATGGCAAAACAAGAT  
ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAAATAATT  
ATCAGGCTAGACCTGAATATATTCCCAATGCCAGCCACTGGTTGAACAACAATTCAGAA  
ATAGCTATAAACAACCTGTCATACTTCCGTCAACAGCAGTATTATAATAACATCAACTATC  
AACAACAATTGCAAACACCATATTATTACTCAATGGAACCTATTTTTAAATCTATCGAA  
GTATCAAAAACCAAATTTGAATTTCTATTTTAGTGAAGAGAACTTGAAAAACAGATGAATTTT  
TAAGATCTAAATTCAAAAAAGCCAAATGACGGATTTATCCCCATGAGTTTGATAGGGAAAT  
TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA  
GAGAAGTTTTTACAACATAAAGAAACAAACCATTGGAATTTGCCCTTGGGAAGCATAGAAG  
GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAACCTATTTTATTAGGCGCG  
AAAATTGGGCTGAATACGCTATGGAAGTAATTTTGATGAAAATGATGACGAAACGAA  
AATACAACATTGAGAAACTATTGGGACCGAACGATTTAGACAATTATTCTTATATGGGCT  
ATCCAAACTTCTTTCCAGTAATGAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG  
AAATTAGCAGGCAGTTTGAACAAAACTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLNDNPKN'TSSAEDKKKQ'TSSLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT  
AKPSKNGSGSIKLT'SNTKWTPITPSVIIISGSKD'TNSKSGKNSKNSKTNKKMKRKGKYNND  
INKKDFNGQ'TNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKRITNNNNSTNGR  
QSRNYQNRNGK'TRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNNNSRNSYKQLS  
YFRQQQYYNNINYQQQLQTPYYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLRSKPKK  
ANDGFI PMSLIGKFYRMVNL'SLGGDPNLLILASMREVLQHKETNHLEIALGSIEGAQKNMA  
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNDLDNYSYMGYPNFFPS  
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCTGTTCCCTGTTCCCTGTTCCAGTAGAATCTGAGACGGC  
TTT'TGTGCCATCAGCATTCACAGCACCACCGTGCCAACAAAGAAGAAATCAAAAAATAA  
AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTTAATGAAGGCAGAGATAAGTCATC  
TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC  
CTCTGATTAACCTTCCTGGTTAGTCTTTTGGTTTTGTTCATAGCAAAATTAAATATATA  
TATATAAGCTTGCTTTCCCTTCAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA  
CCGAGACTTTTTTTTCAAAGGCACGCGTGTCTTTTTTTGTTAAGACAATAGATATTTTAGC  
ATTGAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA  
GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT  
TTTGCTGTTTGGCTTCTTTACGTTGGCTGAAAACAGCGCAAGAGCTACGCGGGATCAG  
ATTACTCGTTCTAACAGAGAAGAAATTTAAATCATTTCATCGAATCTCATCCGTTAGTCC  
TCGTGAGTTTTTTGTCTCCATGGTGTGTTGCATCTCAGATCTTACGCCCTCACTTAGAAG  
AGGCCGCTCTATTTTTAAAGGAGCATAACGTCCCGAGTTGTTCAAATTGATTGTGAGGCTA  
ACAGTATGGTTTGCCTGCAACAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA  
ATGGTTCGTATTTTGTATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC  
AGTACATGATTTCAGCTATACGAGGCTTCTGTCAATTTATTTAAATTCCGAAGATGAAATCC  
AACCATACTTTGAAAAATGCAACTTTACCAGTAGTAATAAACAGAGGCTTGACAGGCTTGA  
ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTTTATCCCTTC  
TAGATTGAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATTCGTGT  
TTGATGGAATGTAGACTCTTTGGTTCGAAATTCGGTTGCTCTAACTCAGTGGTTAAAAAG



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CTGGTGCTAAACGTGCTCAATTTCAGAAAGAAGAGAAAGTTTGAATTAGGTCGTCAACCAG  
CCAACACAAAAATTGGTGCTAAGAGAATCCACTCTGTGTCAGAACTAGAGGTGGTAACAAGA  
AATACAGAGCTCTAAGAATTGAAACCGGTAACTTTTCTTGGGCTTCTGAAGGTATCTCCA  
AGAAGACCAGAATTGCTGGTGTGTTTACCATCCATCCAACAATGAATTGGTTAGAATA  
ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTCAGACAATGGTTCG  
AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAAGCTCAAGGAAGAAGAACTGTTG  
CCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT  
CTTCGGTTGAATCTCAATTTCAGCGCCGGTAGATTATACGCTTGATCTCTTCCAGACCAG  
GTCAATCCGGTAGATGTGATGGTTACATCTTGAAGGTGAAGAATTAGCTTTCTACCTAA  
GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)  
MGISRDSRHKRSATGAKRAQFRKKRKFEGRQPANTKIGAKRIHSVRTRGGNKKYRALRI  
ETGNFSWASEGISKKTRIAGVVYHPSNNELVRTNTLTAAIVQIDATPFRQWFEAHYGQT  
LGKKKNVKEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD  
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81)  
ACCCATATATGGGAGGACAACCTCGCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG  
TAGAAGCGGAAAGAGAAGGAGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT  
GGATTTCCGAGACATCGTTGGCATTTGGGCCCCGTCCAATTAAATCTTTTGGCCTGAAAAG  
AGATCCATGACGGATGGGGCCGGGGCAATACTATGGTTTCGAGCGGTGGCCAGTCTGGAAG  
AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTTCGGGGAGGTTA  
TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATTT  
TTTCATGGCTCGGATTACTTCCGTACTGCTGGCTAAAATCGAAATCTCGGCCTGCTGAGA  
GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA  
ACATAAGAACCGGAACACGTCATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC  
GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC  
GTCAGCAGCAGCAGACCAGCGTGGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG  
CTGCGCTTGCCCATGCCCAGACATATAGCATACATGTGGTATCAGCATGTGATGCCACGCC  
GGTTGCCAGTAGAGGGCCCGCTGCTATGTGAAAATGGCTGGCGTAGCATTGTACCAGGACA  
GGCTCTTCTTACCCGCGCAGTTCCCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA  
CCAGCCCAGAAGATGAACTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG  
CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAGAGTGAAGGTTATCTTGCAGGAGA  
TGGATACGCTACCAGGGCAGCCGCCATTAAAGGCTGCGCGACTTCCCGCAAATGACCAAGG  
CTATGGGCATAGCATTGATGCAGCAAGATGAGCAAGCAGCTGCCCTGGCGTTGTTTGGAC  
GACAGCCCCCTAGTGATAAAGAACGAATGGTCACTACCGCTACTACTGGCTGGTGTCCTTT  
GGCATGTTCCCGGGCCAGCGCAGGCGGACGCTGTGCTGGCGGAGTTCCGTCAAAGTTATC  
GCGGGCTGCCGCTGCTGGATGCCGAACCTAGTGATAAAGAGAAGAGGATTTGAAATCAACA  
CATAA

YER153C, 254 aa (SEQ ID NO 82)  
MLTITKRLVTTDVRSRILLSSLNGKMSDALALLRQQQQTSDVDVELLHHTMLARAAALAHAD  
TIAWMWYQHVMFRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNRDRRTSPEDEL  
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPGQPPLRLRDFPQMTKAMGIALM  
QQDEQAAALALFGRQPLVIKNEWSLPLLLAGVLWHVPGPAQARRVLAEFRQSYRGLPLLD  
AELVIKRRGFEINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83)  
GGACTAGAAGCCAAAAGCCAGAGGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC  
TGTTAAGGGGATATGTTGCAACTTGCAGGGGGCGGCACAAAATAACATAGAAACGTAGTA  
AAGAGGGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAAACCCATTGACGTAGAAAT  
TGAAAGAAGGAAAGGTATACGCAAGCATTAATACAACCCACAAACACAGACCAGAAGCAC  
TCTAGACGGAGAGTAACCTAGATCTACAGCCCTTGGAATCGTTTGGTCAACTTTGAGGT  
TCCGGTCTGCTCCCCCTCTTGATCTGAAAGGTCTTTCTCTAAATCTATATTAACGTATAA  
ATAGGACGGTGAATTGCGTTCTACTTCTCAATTGCGTTTGATCTTATTTAATCTCTCTC  
TAATATATAGAAAAAAAACCATCTGATTATTCGATAATCTCAAACAAACAACTCAAAAC  
AAAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAGGATTCCGGTGAAAAAGCTT  
CTGAAGCTTTGAAGCCAGACTCTCAAAGTCATACGCTGAACAAGGTAAGGAATACATCA  
CTGACAAGGCCGACAAGGTCGCTGGTAAGGTTCAACCAGAAGACAACAAGGGTGTCTTCC



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TGGTAATTTTACCTTACTTTACCGACATCGAACCTGATCTCTTCCCCAAGTACATTTCTA  
GCAATTTGCCGTTGGCTTACTTCTTTTATACTTCTGAGGAAGAATTGGAAGATTACACTG  
ATCTTTTTCACGCAGTTAGGTAAGGAAAATCGTGGCCAAATAAATTTTCATTGCATTAACT  
CTACAATGTTCCACACCACGTTAGATTCTAAATATGAGAGAACAGTTCCCATTATTTG  
CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACCAGAAGAAGAGT  
ACGCGAAATTAGAAAAACCACAACCCTAGACAGAGATATGATCGTTTCAGTTGGTAAAG  
ATTACCGTGAAGGTACTGCCAAGCCAATTGTTAAGTCAGAAGAGATTCCAAAAGAACAAA  
AGTCCAATGTTTATAAAATAGTTGGGAAGACACATGACGACATTGTTTCATGATGATGACA  
AGGATGTCTTGTCAAATATTACGCGACATGGTGTATTTCATAGTAAAAGGTTTGGCGCTA  
TTTACGAAGAAATTGCAAATGTCTTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTGA  
TCGCCGAAGTGAATTCAGGGGCAAATGATATCTTAAGTTTTCCTGTGACAGGATATCCAA  
CCATTGCTTTGTATCCTGCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAA  
ATTTGGAAGATGTTTTCGAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGG  
CAATTTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC  
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)

MQVTRFISAIVSFCLFASFTLAENSARATPGSDLVLTEKKFKSFIESHPLVLVEFFAP  
WCLHSQILRPHLEEAASILKEHNPVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG  
QVYRGVKITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV  
ALDLAEDYVFLSLDSEDKSLSIHLPNTTEPILFDGNVDSL VGNSVALTQWLKVVLIPYF  
TDIEPDLFPKYISSNLPPLAYFFYTSEELEDDYDFTQLGKENRGQINFIALNSTMPHH  
VRFLNMQRFPLFAIHNMINNLKYGLPQLPEEEYAKLEKPOPLDRDMIVOLVKDYREGTA  
KPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVKYATWCIHSKRFAPIYEEIAN  
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFE  
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)

GGGGCAAATGATATCTTAAGTTTTCTGTGACAGGATATCCAACCATTGCTTTGTATCCT  
GCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTT  
GAATTTATCAAGGAATCAGGTACACATCAGATTGACGGCCAGGCAATTTATGATAAATTG  
CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA  
ATAAATAAAGCATATATAATGCACATTTTTTAACATCTGATTACTCGCATCGTTTCTGGAA  
GAAAATAGCTAATATTCTGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA  
TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA  
CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTTCGTTTTCAATCACATTCTAG  
TTTACAGTAATTGAGTCTCGATGATGTTTAAATTTTACCTTTTCGTCACCTTTTTTTTCCA  
CCATTCTTGCAGGTTCCCTGTGATGTTTGAAGAAATCGGTATTATCAAGAGAATACCGGTAG  
AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTTATTATACAGGATCTT  
TATTAGAATCGGGAAGTGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG  
AACTTGGCGTTGGCAGAGTAATTAAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG  
GCGAAAAAGAAAGCTGCAAATTCAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCAG  
CGCTCATTCTCCTCAAGTGCTGATTTGGTGTTTGATGTGCAATTGGTAGACGTGAAATCAG  
CCGCCTAG

YDR519W, 135 aa (SEQ ID NO 78)

MMFNIYLFVTFSTILAGSLSDLEIGI IKRIPVEDCLIKAMPGDKVKVHYTGSLLESSTV  
FDSSYSRGSPIAFELGVGRVIKQWDQGVAGMCVGEKRKLQIPSSLAYGERGVPGVIPP  
DLVFDVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)

CGAGCTTGCCAGCATTTCCAATGCCATCGTATTGTACTCAATGGTGAAACTTACCACCAT  
ATTGTTAAAAGCTATTATTTATGATTTTACTTACCAAACATTGAAAGGAGACTGAACAC  
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA  
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATTTCTAACGCA  
TGCATCCTGAGCAATGAAATCATGCAACCTTAACATTTGAGGTTAATATATGAGAAATTAAC  
TAGCGTTGAGGAGGTACTGCAATTTAAAAGACCGAAGAAATTATCGATGCAAGGAAAAATG  
GGTCTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAAATATCACAT  
ACTTTCGCCTTCTATCTCGATGCGTTATTACAAGAAAATAGTTTTACTAACAAATTAACA  
AAAATTAATAATAGTGTAATAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCAGCCA

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AAGGTGTCCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT  
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTCG  
AATATGTTTTCCGGTCGTGTCCACGGTGAAGAAGACCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRKGFGEKASEALKPDSQKSYAEQGKEYITDKADKVAGKVQPEDNKGVFQGVHDSA  
EKGKDNAEQGESLADQARDYMGAAKSKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCCTTTTTTCGGCAGAGTCGTGGACACCTTGGAAGACACCCT  
TGTTGTCTTCTGGTTGAACCTTACCAGCGACCTTGTCGGCCTTGTCAGTGATGTATTCCT  
TACCTTGTTTACGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTTCAC  
CGAATCCTTTTTCTACCTGCGTCAGACATTGTTGTATTTAGTTTTTTTTTGTTTTGAGTTGT  
TTGTTTGAGATTATCGAATAATCAGATGGTTTTTTTTTCTATATATTAGAGAGAGATTAA  
ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTTA  
ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG  
ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGCTAGAGTGCTTCTGGTC  
TGTGTTTGTGGGTTGTATTAATGCTTGCGTATACCTTTCCTTCTTTCAATTTCTACGTCA  
ATGGGTTTTTTTTCTTCTCTTTTCCCTTTTCCCTTTTCCCTTTTCCCTTTTCCCTTTTCT  
ATGTTATTTTGTGCCGCCCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT  
ATTCTAGTCTTGCTATTTTTTACCGCCTCTGGCTTTTGGCTTCTAGTCCTTGTCCTCAAGAG  
CCAAGGGCCCCGTCAACACGTCGTCATTGCTACCGCCAGCTGGCACCCACACATCACCGAC  
CCTTTTTTTTCCATTTTTCGGCTGGGCGGTTAGTGGGATCCGCCCCGCTCCCGGAGATTTTCA  
CTTGGATTTGCGCGTCCCCCTTTTTTTTCTTCATTCTCTGACTCCCCCTACCTTCTCCCACT  
TTTCTGTGTATCAAGAGGAAAAGAAGGAGAAAAGGAGAACTCCGAAAAATACCGAACAAG  
AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSFNFYVNGFFSFLFLFLFLFPLSLRIFYVILCRPLQVATYPLNRCQQYSSLAIF  
TASGFWLLVLVPRAKGPSTRRHCHYRQLAPTHHRPFFSIFGWAVSGIRPLPEIFTWICASP  
FFLHSLTPPTFSHFSVYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCTTCCGTACGTCACAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT  
CTATCCTTTTGCATAATATTTTCGTCACCATTTATCTTGTGCGGTGTTTTTATTTAAAC  
AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAAATCAAAAAAATGGCTTTCATG  
GATCGAGTATTTGTTTGTGCAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC  
TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCTCTCGGA  
AGAGTTAACTTCACGCGGGTAAATCACTTGTGATGCGGTATATTCTCTATACGGCTAATA  
GATGAATCAGGGTGTTTTTAAAGTGCGTATAAACCCCTTTTGCTATTTTTCGTTTATATAATT  
GGCGTTGATAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT  
AAAAATACAAAAAGTTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC  
TGCTTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGGTCCTC  
CAAACGAGGCCCCCTCGGTGCTTTTATCTGGTTGCATCGTTTATCGATTAACGAACCCA  
TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG  
AGAGGCCCCAGGACGCTAGTTCTTCGTGCTTGTCTTCATCGCCGCCAAAGATCAGAAAGT  
ACAACAAAGTTTTTTTATAATTACGCATGGGATAATGTTAACCTCAAGGAGTATCTGAGTG  
GTTTAAGAGGGCAATCTGGCCTTGCGGGCAGTAGCTCATCAAGTAATATCTTGGGCACTC  
GCCAAAGAGCTCAGTCCACAAGTTCCCTTGAAGTCTTTAAAGGGGTCTCCTCACCCCTCTT  
CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGGTTCGT  
TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCGTGACATATAGCATGGAATCCGTTA  
TTGACGACGCAAAAATTATAGTGATTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA  
CCATTTTCAACCCGACGAGTGAGTTATCAGAAACTGTTTGTGTAGATAACTCATGGCCCCG  
ACAAAGTGGATTATTTCTATTTTCAGTACCCAACAAAGCCGTAGCTATTGGTTTCAGCCACCC  
CTATAAATATTTCCATTGTACCTCTTTTCGAAAGGTTTGAATTTGGGCTCAATCAAAGTCG  
TATTATTTTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGGC  
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA  
ATGGTTGCTTTGTAAATAACCCCTTTTTTTCAGCCTGATCATTCATTCCAAGACAAGTGGG

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AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACCTGTGTGCAAGATTGTGATG  
TCCGCTCTAACATTAAGGTTTCGCCATAAGCTCAAATTTTTTCATCATCCTAATTAACCCAG  
ATGGTCATAAATCTGAGTTAAGAGCGTCCTTACCGATTCAACTTTTTATTTCACCATTTG  
TGGCACTTTCAATAAAACCATTGTCATCCTCGAATTTGTATTTCGCTTTTTTAGCACCCTA  
ACCAGAAAGACGAAAACTCATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG  
CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCCCTACCA  
TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG  
GTTCTTTTCACTCGCACGGCTGTGGAACGTCTGGAACATGTACTCCTTTGGGAAGCGAAT  
GTTTCGACTGTGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA  
TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCTGCCGCTTCCA  
GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCACGGAGAGAATCTTAC  
CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC  
CTGTTTTTACTTTCAAGATCCCCAGCCCCAAGCGTGTGAGCCCATGAAGTGTACCAGTGC  
CCTCGGGCTTAAATTATCCAGAGACTCAAACCTGAACAAGGTTCCATCGTATGGCAAGG  
CAATGAAATATGATATCATTGGTGAGGACCTTCTCCTTCCCTACCTTGTGCGATACAAA  
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCCAGGAACCTTTCGACAACATTGTCAT  
CTTCTATACCAACTAGCTTTTTCATTCCTCTAGTTTATGAGTAGCACTGCTTCCCCATTT  
CCATAATTAAATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACACTTAATGAGT  
TAACCTTCGAAAACCTTCGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC  
GGAGGGCTACTTCTTTAGCTGGGTATTATGGGAGGTTTTCTATCAAAGGGTAACAAACGAT  
AG

YFR022W, 733 aa (SEQ ID NO 88)

MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPNEAPSVLLSGCIVLSINPEMQIKSIS  
LRLYGKIQIDVPLERPQDASSSSLSPPKIRKYNKVFNYNVNDVNLKEYLSGLRGQSG  
LAGSSSSSNILGTRQRAQSTSSLKSLKSSSPSSCTLDKGNVDFPFSAILPGSLPESVES  
LPNCFVITYSMESVIERSKNYSDLICRKNIRVLRTISPAAVELSETVCVDNSWPKVDYSI  
SVPNKAVAIGSATPINISIVPLSKGLKLSIKVVLFFENYQYCDFFPPVISENRQVTELNL  
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNVCVDQCDVRSNIKV  
RHKLKFFIILINPDGHKSELRASLPILQFISPFVALSIKPLSSSNLYSLFSTTNQKDENS  
SQEEEEYYLFSRSASVTGLELLADMRSGGSVPTISDLMTPPNYEMHVDRLYSGSFTRTA  
VETSGTCTPLGSECSTVEDQQQDLEDLRILRTKIRNQRDNLGLPPSASSAAASRSLSPLL  
NVPAPEDGTERILPQSALGPNSSVPGVHSNVSPVLLSRSPAPSVSAHEVLPVPSGLNYP  
ETQNLNKVPSYGMKYDIIGEDLPPSYPCAIONVQPRKPSRVHSRNSSTTLSSSIPTSF  
HSSSFMSSTASPIIINGSRSSSSGVSLNTLNELTSKTSNNPSSNSMKRSPTRRRATSLA  
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAAAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT  
ATTTTGACTCTGTGGAGCATACAGCTACCATAAATAGGATTGTGGGGACAAATATGGAA  
TGGATCAAAACGTTCTTAGGATTGTGGTGGTAAAACCTTGTAATAATCCAAGCTGAGATCTT  
AAATCCAGCAAACCTTCGCCCATATTTATTCTTTTATAACAGAAGAAGAGACTATATTCT  
CAAACCTCGTATATTTATATACATATCCTCCAAACAACTCCCAAGTTTCACTTTCCCTG  
GATTTACCTTGGCATTCCCTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA  
TGATATCACAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA  
AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC  
GAAAAAACAATATTACAATCATGTGGGTGCTGCTGCTGCATCTGCTGCTGGTTATGACA  
GGCAGATCACTATCTTTTCCCCCGAGGGTTCGTTTATATCAAGTAGAATATGCCTTTAAAG  
CGACTAATCAAACATAAACTCACTAGCGGTCAGAGGTAAAGATTGTACAGTGGTGA  
TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAACCTACTGTTTCGTATATTTTTT  
GTATTTCAAGAACAAATTGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG  
CCCTAAGAGCCAAGGCTGAGGCTGCAGAAATCCGTTATAAATATGGTTATGATATGCCAT  
CGGTATGATTGGCTAAGAGAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA  
TGAGACCATTAGGTGTTATACTCACATTTGTTTCGGTAGATGAAGAATTGGGTCCCTCCA  
TTTACAAAACCTGACCCTGCAGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA  
AACAACAGGAGATCACAACAACTTAGAAAACCATTTCAAAAAGAGTAAAATCGACCATA

TCGGGATGGTGGGTTGTTCTGTACCCCCGATTACACCCGCTCTGCCATTTCATTTTATC  
GTTTTTCGTCTTTTCTTTCAATGTATTGATAATTAACGTGTCTATGTGATGCTATTGGTAT  
ATAGCCTTTCTGTATATCCCTCTAACAAATTACAAAGTATTCTGTTTAAAGCAAGTG  
CTAGAAGTGACTCGGTTCTCTTAGGAAATTCTAAACGAGATTTCTTATTGGTGATTG  
TAACAATTGATGAGATACTTCACTAGCCACCTTAACTTTACGGACCTTCTTTTGAACGA

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TGCTTCGAATGACAACGCCTTTTTGATATATAATATCCAATTTTCATTATAGGGAAATTTT  
CAACTCTTACCCGCCCTGCTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC  
GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTCACAGTGTAGTCAG  
TCCGCATAAGAGCATTTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG  
AAAAGAACAAAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCCTGGATAAAGAAT  
TCGTCCCCACTGAAAAGTTACTGAGAGAAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA  
AAAAATCCACTAATGTAGAGATCAGCAAACCTCGTGAAGAAAATGATTAGCTCTTGGAAAG  
ACGCAATTAATAAAAAATAAGCGTTCAGGCAAGCACAGCAGCATCATCAAGATCATGCCG  
CAGGCAATGCAGAGGACAAGACAACCTGTAGGTGAGTCCGTGAATGGTGTTCACAGCCGG  
CCTCCTCCCAGTCAGATGCCATGAAACAAGACAAGTACGTCAGCACTAAACCAAGAAATA  
GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA  
AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA  
CTGCAAAGGCCATAGAAAAGTGAATGAATAAAGTTAACAACCTGTGACACCAACGAAGCCG  
CTTACAAAGCCAGGTATCGTATAATTTATTCAAACGTCATATCAAAGAATAACCCAGATC  
TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCTTAGCTACATGCGATGCCA  
AGGATCTGGCACCAGCGCCCTTAAAGCAAAAAGATAGAAGAAATTGCCAAGCAAACTTAT  
ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT  
GTAAAGAGAAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATGA  
CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDDKEFVPTEKLLRETKVGVEVNKFKKSTNVE  
ISKLVKKMISSWKDAINKNKRSRQAQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA  
MKQDKYVSTKPRNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESHPQSIILHTAKAIES  
EMNKVNNCDTNEAAYKARYRIIYSNVI SKNNPDLKHKIANGDITPEFLATCDAKDLAPAP  
LKQKIEEIAKQNLNAQGATIERSVTDRFTCGKCKEKKVSYQLQTRSADEPLTTFTCTCE  
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT  
GGTCAGATATACTTTCGCATGGGTCAATACCATGGTCAACCCAACCAGTTCTTCTTTGCG  
TTTTCAAAAGTTGTATAATATTCAAAAACGCTAACTGATAATTTGGGTGAGGTTTCGAAA  
GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCCAGATGTTAACTGCAGTCA  
TTTTGTTTTTCTTGGTCTTTTACCTCGAATAGGTTTTCTTGTTTTTGTTATTTGTTTTCTTT  
TTGGACCCTATGTTTATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG  
GGATCTGCCACTGGTAACTTCAAAATAGACAAGACGAAAAAACGGTGAAAATGGGTGATA  
GAAATAATACAGAAGTAGATGTTGAATTAGATTAAACTGAAGATATATAATTTATTGGAA  
AATACATAGAGTTTTTTGTTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT  
CTGATTTTTTCTTTCAGCCAACCTTGGAGACGAATCTAGCTTTTGACGATAACTGGAACATTT  
GGAATTCTACCCTTACCCAAGATCTTACCGTAACCGGCTGCCAAAGTGTCATAAATGGA  
GCAGTTTCTTAGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC  
CACAATTTGTCCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTGCTTGTGGAAGTAT  
CTCATACCAACCTTACCGAAATAACCTGGATGGTATTATCCATGTTAATTCTGTGGTGA  
TGTTGACCACCGGCCATACCCTTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT  
TTACCGGCTGTACAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDQFNNTTSSSDFFFSQLGDESSFDDNWNINWSTLTQDLTVTGCQSVNNWSSFLRSR  
FQVLVSLVFWDDQCPQFVQVDWLPMSLLLEVVSHTNLTEITWMVFIHVNSVVMMLTTGHT  
STTGVLVSLTDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:  
1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC  
GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG  
AATTGAAATCTACGATACCTTGATGTTGACATTTATAGCACTAGTCCCAGGAAACCTTTTC  
GAAAAACACAGCAAAAACAAGAGTACTGTAACCAATGTAACATCTGTACACCAGGGACCC  
ACACATTACCAAAATCAAAATTATTTTTCTAATGCCTGTTATTTTTCTTATTTTTCTCT  
GGCGCGTGAATAGCCCGCAGAGACGCAACAATTTCTCTCGCAGTTTTTTCGCTTGTTTAA  
TGCGTATTTTTCCAGATAGGTTCAAACCTTTTCATCTGTATCCCGTATATTTAAGATGGCG

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TTTGCTTTCTCCGTTGATTTTTTTTCCTTCTTAGTGATTTTTTTTGCATTAAATCCCAGAAC  
AATCATCCAATAATCAAGAATGCCTTCCAGATTCTACTAAGACTAGAAAAGCACAGAGGTC  
ACGTCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT  
TTTTTTAGTGTTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAATGTCAAT  
CAGCTAAGTGTAATCAACATATTTCTTTGTGTTTTGATTGCGAATTTGTATTACCATCT  
CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAAA  
CTGAGCAAAAAGAAAGTGTGCATAGCCTTTGTCTACTTCTCCTTTATTATACCATGATA  
TTCAGAACAGTCATACTGTCTACTCATTTTTACGGCTATAAAAGGTAACTTTCATTTAGAT  
TATGGAAGCACTAATTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG  
AGTTACCACGTTTCTTTTGTTCGATAAAAATGTCCAGTTGAAAACCTGTTTTACTAACGA  
TTTAAAAATTGTATTTTCATTACAATATTTTTTTTGTACAGCCGGTAAAGGTCGTATCCGT  
AAGCACAGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT  
AACATGGATAAAATACCATCCAGGTTATTTTCGGTAAGGTTGGTATGAGATACTTCCACAAG  
CAACAAGCTCATTTCTGGAAGCCAGTCTTGAACTTGGACAAATTGTGGACATTGATCCCA  
GAAGACAAGAGAGACCAATACTTGAAATCTGCTTCTAAGGAAACTGCTCCAGTTATTGAC  
ACTTTGGCAGCCGGTTACGGTAAGATCTTGGGTAAGGTTAGAATTCCAAATGTTCCAGTT  
ATCGTCAAAGCTAGATTCTCTCAAGTTGGCTGAAGAAAAAATCAGAGCTGCTGGTGGT  
GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MPSRFTKTRKHRGHVSAGKGRIGKHKHPGGRGMAGGQHHHRINMDKYHPGYFGKVGMR  
Y FHKQQAHFWKPVLLNDKLWTLIPEDKRDQYLSASKETAPVIDTLAAGYGKILGKGRIPN  
VPVIVKARFVSKLAEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGTCTTTTACAATTCCTG  
GGAGTTTGGCTATTGCTACCCCTTGGTCTTAGCACCACTTTTTTCCGCTATTTGTATTTGT  
TGAATAATTTAGTATCTATTTCCATTTTCATTATAATTCACGTTTTTAGCAGCCTCTCTT  
CTTCTAGGTAATTTGGAAATCTTCTTCTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG  
ATCTCAATATGTCCCGATAGGCCAATTTTCCACCAGATAGTTTCGATGGCATTTTATTTT  
TAGTCTCTTTTGAAGAGAAATATCATAAAATATATAGTTCTCCATGATGTTTCGGGTCAGT  
CGCTCCGAAGCGTAACCTAGTATAATAAATAGTTTCATTGCAGAAAATAACGAAAGAAATG  
GTGGAATACGATCTGTTATATCTAAACTAAAGCTAACTAACGGAATAAGCAAATACGAAT  
CGACCGCTAATTTAACAAATATGGTTTTAGCAATGGAAGTAGAGTGGCACCGGAAATTC  
CTGGGCTCATTTCAACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATTAT  
TGAATTTCCCAAAACCTACGAAAACATTCCCTGGTTCCCAGCCTGTGTCTTTTCAGCATT  
CTGATGTGGAAGAGAAGCTGCTTGCGCATGATTACTACGTTTGTGAGAAAACAGATGGTC  
TGCGGGTGTGATGTTTATAGTGATAAATCTCTGTGACGGGTGAGCAAGGATGCTTTATGA  
TTGATAGGGAAAATAACTATTATCTGGTTAATGGATTTAGGTTTCCCAGATTACCCCAAA  
AGAAGAAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACCTG  
TCATACAAACTAACCCTAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTTCGATTGTC  
TTGCTATCAATGGTAGATGTCTCACACAATCACCAACAAGTTCTAGACTAGCCCCACCTTG  
GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCTAATCGTTGTACTA  
CTTTTCCGTTCAAATTTCCATGAAACATATGGATTTTCAGTTACCAATTAGTAAAAGTTG  
CTAAAAGTTTATGATAAACTACCACATCTTTCTGATGGTCTGATATTTACTCCTGTGAAGG  
CACCTTACACTGCCGGCGGAAAAGATTTCATTGTTATTTAAAATGGAAGCCAGAACAAAGAAA  
ACACCGTGGACTTCAAATTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTGCCTA  
AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTTCAGCTTATATG  
TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAACATTTTCGACCAGCCTTTCGATA  
GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG  
ATGAGGAATGGCAAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT  
GCGCAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTCAGGGATGATAAGTTAA  
ATGGTAAATCATACATCGGTGGTCCAGAAAGTTTTGGAGAGTATCAACGATTCAGTTTCAT  
TGGAGGACCTCGAGGAAATTTGTTGGTGATATTTAAAGGTGCTGGGACGAGAGAAGAGCAA  
ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAATGCGACATTATCTA  
CCTCTAAGCCAGTCCATTACAGCCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG  
AGGATGATTGGTCCGATTAG

YGL130W, 459 aa (SEQ ID NO 102)

MVLAMESRVAPEIPGLIQPNVTQDLKMMVCKLLNSPKPTKTFPGSQPVSFQHSDVEEKL

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LAHDYYVCEKTDGLRVLMLFIVINPVTGEQGC FMIDRENNYYLVNGFRFPRLPQKKKEELL  
ETLQDGTLLDGLVLIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP  
YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLSDGLIFTVPVKAPYTAGG  
KDSLLLKWKPEQENTVDFKLILDI PMVEDPSLPKDDRNRYWYNYDVKPVFSLYVWQGGAD  
VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET  
GAWEMLRFRDDKLNHNHSTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG  
RPLPSQSQNATLSTSKPVHSQPPSNDKEPKYVDEDDWSD

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)

CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT  
CAAAAAGAAAGGTTTGTA AAAAGAGCATTGGGCAGAGAGTATTTGTCCTGCGTATAGAGGA  
GAAAAAATTGTACTGATGCTAATTTTGGTGTGCTTCTTTTATTTTGTAAGACTGT  
TTTCCAGAAATGTTTGGGTTTATTTTAAATTTTGAACATTTTTCATCCTTTCTC  
ATTTTGTTCATTTTCTGTGGAAAATTTCACTGACGCGAAGAAGCGATGAAATTTT  
CAACATCCTCCCATCATCCCAATATTGGCATACACACACATGCAGCACAGCGGAAGTGC  
GAGGTGAGAGCAATGTGGCAGAGACGCTGGCGCGCTGTATTGTATAATAGTATATTTT  
ACACTCAATTCATTTTGTATTAATAGTGTGTA AAAAGCTTCTGAAATCAAGAAG  
CCCGTACCAGAAGTTCATCATGAAATACATCCAACTGAACAACAAATCGAAGTCCCAG  
AAGGTGCTACTGTGAGCATCAAGTCCAGAACTCGTCAAGGTTGTTGGTCCAAGAGGTACTT  
TGACCAAGAAGCTTGAAGCACATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA  
AGGTTGCTGTTTCAACGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCGTCAAGTCTT  
TGGTTGACAACATGATCACTGGTGTCCAAAGGTTACAAGTACAAGATGAGATACGCTT  
ACGCGCATTTCCCAATCAACGTCAACATTGTGAAAAGGATGGTGCCAAATTCATTGAAG  
TCAGAAACTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTACTA  
TCGAATTTTCCACCAACGTTAAGGACGAAATTTGCTTGTGTCAGGTAACCTGTGCGAAGAC  
TTTCCCAAAACGCTGCTGACTTGCAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTA  
AATTTTGGACGGTATCTACGTTTCTACAAGGGTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)

MKYIQTEQQIEVPEGVTVSIKSRIKVVVGPRGTLTKNLKHIDVTFTKVNNQLIKVAVHNG  
GRKHVAALRTVKSLVDNMITGVTKGYKMKRYVYAHFPINVNIVEKDGAKFIEVRNFLGD  
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVNRKDIRKFLDGIY  
VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)

AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCCTTCAT  
CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT  
CAGGGAAGTCATATGGGATGGTGCTTCTCTACATCTCTCTCCAATCGTGTCTTCAGTTTCC  
AAAACCTCGGAATACCTTTTGTAAGGCGCTTGTGTTGGTGTACTAACACCGTATAAAACAT  
ACTTGGGGTTGATTTTAAACATCGTCCACCTTGATTCTTAACTTTTCACTCATTTTCCCTA  
CAGAATTAGCTGCCATCAATATCAATTAACCCCTTATATGACTTTATTGTTTTTGT  
TTGTTGGCTAATTAATTGATACAAATCTTTAGGCGAAAAATAAAAAAATATAAAGTAAA  
GAAGGAAAAATTAGGCGATATTAAAAACAAATCTAAAAATAAAGACAAGAAACGAAAAAGAG  
GTTAATCAAGTATTGGAAAAATGTCCAAAGTGTTTATTGCCACAGCAAATGCAGGTAAAG  
CTCATGACGCTGATATTTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTCAG  
GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTTAGATAATGAAAATCCAAAAGATA  
AGTCATATTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTGCGATGTCTTGCAAGCTA  
TTGAGAGAGATGCATTTGAATTATGCCTTGTGCTACCACTTCATTTTCTGGCGATTAC  
TCTTCTATCGTATCACTAGAGAAAGATGAGACTAAAAAAGTTATATTTCAGAAATTGGATC  
TTCTAGACTCAGACATGAAAAAGCATTCCTTTTGGGCATTAAAAATGGGGTGCCTCAAATG  
ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA  
AGTTTCAACCGTTTGCAGATGAGTCAAATCTTTAACACTAAATTTGGAGCCCCACGTTAG  
AATTACAAGGCACTGTGCAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA  
TCTCTGAACGAGGACTAATTGCCACAGGTTTAAATAATGGAACAGTACAAATTTCAGAAC  
TATCTACATTACGCCCCGTTGTACAATTTTGAATCTCAGCATTCTATGATTAATAATTGCA  
ATTCCATCAGATCGGTGAAATTTTCTCTCAAGGATCCTTATTAGCCATTGCTCACGATT  
CAAATTCATTTGGTTGCATCACTCTATATGAACTGAATTTGGTGAAAGAATAGGCTCCT  
TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTCTAGCTGGG  
TCATGAGTCTATCGTTTAAATGATTCTGGTGAAACATTATGCAGTGCCGGATGGGATGGTA  
AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

1950

the 1990s, the number of people in the United States who are 65 years of age or older is projected to increase from 20 million to 30 million, and the number of people 75 years of age or older is projected to increase from 10 million to 15 million (U.S. Census Bureau, 1997).

ATGATATTGA

YGL213C, 3  
MCHLPT2TBNMSKVF L A T A N  
H K S G L H H V D V  
H K G E L R L H I G

YGL235W, 1

CTGGTTCCAA  
TGGAGGGACA

YGL235W, 1

MTLWPHPGSY  
ILNCTPARSV

YGL260W, 7

TACCATGGAA  
GTGGTGAAGT

YGL260W, 7

MEMLLFLNES  
KNIRILDLDP

YGR085C, 1

TCCTTACTTT



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TTTTTAATTTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTTCCT  
GTGTAGCCTAATGTTTAAATGCCTAATTTTTTTCTAAAATGCAGCAACATACATATGTTGA  
GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACA  
TTTTTAAACATCCGTACAACGAGAACCCATACATTACTTTTTTTTAAATATCTTTTTTGT  
CACCGCCTTCTTTTTTATTTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA  
GCTAGGATACCAAATTGAAACTTGGACATAACTCATCATTAAGAAGTATACTGTTAAGA  
GAGGCATTCAATTCGTGTATTATAACGTTTAGCATCAGTTACCCCTGAAAGCCCAACATA  
TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCAAAACCCATGCGGTGATTTGAAGA  
TCGAGAAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAAACCAGAGCCT  
CCAAGGTTTTAGAACAAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG  
TCAGAACTTTCCGTATCAGAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC  
CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA  
GAAACTTCTCTGCTACCGGTAACCTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA  
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTCTATGTCGTCATGAACAGAC  
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCCACAAGA  
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA  
AATAA

YGR085C, 174 aa (SEQ ID NO 112)

MSTKAQNPMDLKIIEKLVNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR  
RNEKIAVHVTVRGPKAEIILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI  
GIFGMDFYVVMNRPGARVTRRKRCRKGTVGNSHKTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:  
886-1258 (SEQ ID NO 113)

AGCCATGTCGGTTCGCACTAGACTTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT  
CCTTTTTTTTTTTTGGCATTCTTATACATTTTCTTTCCTTCTGAAATTAAGTGTACACCCA  
TACCCTATATACACCCATACCCCTATTTTTTAAATATAAAAAGTAACTTCATTTTGAAAGA  
CCACTCTGCATCAGCACGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCCT  
TTCAGAAAGGCTCTGCTCTTGTGGCTGGTTTCACTGGGAGACACCCAGCGGAGCTCCTCCCGAG  
AAAGGCCCTTCTCTGCGGATTTGCTGACGGAAAGCAGTAGCGGAGGTTTGAGTTCTC  
TACGCCGAGAGTACACTGCCGTAATATCACAATGTTCGACTAACCGTTACAGTACGTTA  
AATTAGATACTGCCTATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG  
ACAACAGGAAATAAACAAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAACCTCTGCTAGAA  
AGCTACGTGTCCACAGAAGAAACAAGTATGTTGACTATTTCAAATTAACAAAAAAGTATC  
AACCCCTATTTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA  
TTTATCAAGTAACATATCCTGGCGCAAAATCAGTTTGGAGAGGCTTAAATGACACGTCAC  
AGTGATAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT  
GTGGAAAAATAACCTTTTCTTCCCAAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTA  
CAACGGAAATCATTTTTTTTACTAACAGTTTTTTTTTATTATTATAGCCGTTGGGCCGAAAA  
CAACTACAAGAAGAGATTGTTGGGTACTGCCTTCAAGTCTTCTCCATTCGGTGGTTCTTC  
TCATGCCAAGGGTATCGTCTTGGAAAAATTGGGTATCGAATCCAAGCAACCTAAGTCTGC  
TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCAGTCTTTCGT  
TCCAAACGATGGTTGTTTGAACCTTTGTGACGAAAAATGATGAAGTCTTGCTAGCAGGTTT  
CGGTAGAAAGGGTAAAGCTAAGGTGATATCCAGGTGTTAGATTCAAGGTCGTTAAGGT  
CTCTGGTGTCTCCTTGTGCTTTGTGGAAGAAAAAGAAGGAAAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114)

MKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFKSSPFGGSSHAKGIVLEKLGIE  
SKQPNSAIRKCVRVQLIKNGKKVTAFPNDGCLNFVDENDEVLLAGFGRKGKAKGDIPGV  
RFKVVKVSGVSLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)

GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT  
GTATGTACTGTGCATCGTCATGTAGCACTATTTTCAGCCGTATTTTTCTTTTTTCTTTCCG  
CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTTTCTAGAAAGTCCGGAAAAATTGC  
GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTCTTGTTCGGCGATATTCGAACCA  
GGTCCGGTTGGGCTAACAGCCGCCAGGATGGAAGAAATTAAGAATTTTCATAGAAGCCTTC  
AGTTCTTGGCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA  
AGCATTAGAACAATCTTTTCTCATTGACAGGTATTTCTATTGCTCTATATATATTTTTCTT

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CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA  
GACCCCATTAACAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC  
TGCCATCTTTTAGTCAGCCCCACATTCGCGTTATTTTGATTGCAGTTCTCCAGTGAGCT  
ATTATCCAGAATGTAAAAGGAGGAAAGCAATAAAAGCTAACCTAAGAGCTCCAAAAA  
GCGATGCAAAATGTTCAGAACCTTTGAGGTATGCACCTTGCTGAAACACCAATGGTTATA  
CATTAAAGCTTGCTTAAGCGGATTCATATGAACFTTTTTTCAAAGTACGTTAATGAGAAAT  
TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTT  
GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATGTA  
AAGATCTGGATTTTAGAGCCATAGGAAAGAAAATPGCTAAGGATCTTTTCCAAGACTACG  
AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT  
TTAAGGAATTCTCTCTAGACCAAGTGTGTTGAAGATGTTTTTGTATTGGCTGTGGAGTTG  
AAAACATAGATGATGGCTCGAGAGAAAAATATGCACFTTTTAAAGATTTGGTTTAGTTAAGC  
ATGAGGAAGAAATTTCCGAAGGTGGCATCAACGAACCAAGATGCCAATAATTGAATCCA  
AAATAGACGAGTCTCAGATGATGTTAACATGTCTGAATCTTTGAAGGAGGAAGAACCGG  
AGAAAGCGAAAGAACCCTAACCAAGAAGACCAATAAAAAAATGGATAGAGGAAGAAA  
GATTGATGCAGGAGGAAAGCAGAAAATCAGAACAGGAAAAAGCTGCCAAGGAAGATGAAG  
AAAGGCAAAAGAAAGAGAAGGAAGCCAGATTGAAGGCAAGGAAAGAATCTTTGATAAATA  
AGCAAAAAACCAAGAGGTCCCAGCAAAAAAATTCGAAAATTCCAAATCATTCGCTATCT  
CTGAGATTGAGGCCAGCAATAAAAAATAATAGCAATTCTGGTTCAGCAGAAAGTGATA  
ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTTCTCTGTGCTCTGGTAATACAC  
TAAAAAAACACGCTTACCCCTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA  
ACGAGTCCCTAAGCAGATCTCCAAGGGAACCTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)

MFSIFNSPCVFEQLPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKKS DANCSE  
PLRYALAETPNGYTL SLSKRIPYELFSKYVNEKL GELKENHYRPTYHVVDFFGNQYYVE  
DEADEDALLRSALKDLD FRAIGKKIAKDLFDY EIELNHRGDELSILSKKDKIFKEFSLD  
QVFEDV FVIGCGVENID DGSREKYALLKIGLVKHEEEI SEGGINEPKMPIIESKIDESH  
DVMNSES LKEEEAEKAKEPLTKEDQIKK WIEEERLMQEESEKSEQEKAKEDEERQKKEK  
EARLKARKESLINKQKTKRSQQKQLQNSKSLPISEIEASNKNMNSNSGSAESDNESINSD  
SDTTLD FSVSGNTLKKHASPLLEDVEDEEVD RYNESSLRSRSPKGN SIIIEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)

CAAAAAAGTTTTCGGATGAACCGGATTAATACAAGTAAAATCAGCAAAGATATAGAAGAC  
AAAATAAGCGTGAAAACAATCATAAACCACTCACAAACGGGGGTTTTTCAGCTGTTACTCCT  
CCATACATACATTTTGATAAAGATATAATGTTATTTCTTTTCGTAATTTTGTTTTACT  
TCGGTTTGCTCTATAGATTTTCATCAGCCGCACCGAAAAGGGAGATCAATAAGGATACCCTT  
TAAAAGGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTGGATGA  
AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT  
CTTCTTCATATAAATTGAACTGCCAAATCTCTTTCACATTATCCAGGATAGTTTGGAAATG  
TGTGTTACTGAAGGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA  
TTCAAACAAAGTTTACTGAAATGAAGTTAGATTTCAGGAATATACTCAGAGGCACAAAGAG  
TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC  
CGACCGCATACATGAGGAGAGGCTATACGGTTCCGTCACATAGCTTAGACAACATCAACG  
GCGTAGACACAACCTAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG  
GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTTGATGTTCTCTTCA  
ATCATGTAAGGGAATTTGTACTTGTTCCCTGCATTTATGTTCTTTGCATTTTGTTCG  
CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)

MKLDSGIYSEAQRVVRTPKFRYIMLGLVGA AVVPTAYMRRGYTPAHSLDNINGVDTTKA  
SVMGTEQRAAMTKGKSLQEMMDDEV TYLMFLFNHVREFVLGSLHLCSLHFVFAFNHST  
NGEGDCDFT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)

AATCTTTGCGATTGAATTGCTGCACGAACATTAACATTAGTTCTTTTGCTAAAGTTTCTC  
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC  
TGCCATTCTGTTTGTTCAGAGTAAATCCACAACATTTTTACAAATTTATGTTGCGGCCAA  
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCTCTGTAAGTTGTCCATTGTAAAT  
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCAGTTTCTCTCTGAAATTTAA

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TGCTTTCATCCTGTATGGTAGCGGTAGACATGCTGGT'TTGTAGCCTTTTTATTCTTTTT  
AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAATATAATTTTTCAAGAGTACG  
TAATGGAAAAAGATAAAAAATAAGGACCGTCATAAAAAGAGACGTGATTAACCTAAAAAT  
CTAAAGTAAAGAAGTGTAAGATGGTTGAGGAAAAATCCAGAGTTTGTATTGTTCTTCTT  
ATACACCGCCTAGTGCTACTTTGTCAGAGGATTATAGGGCAAACCTATTCGGTCTTAAGAG  
AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAAAACCTCATTCAGTTGG  
ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCCTTTTGGGCTATGGAATGA  
TCAACAGCGGAATCAACATCATA'TTCAACAATATTTCATTTTCGTCGAGAGTAATTTGCAAT  
GGAAAGTGGT'TTTATTGCCACAGGAATCCACTTTTGAAACTTGGAAGCTAGAGTTGGGAC  
AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG  
AAGGTCCCAAAGATGCTAACAAAT'TTCATGTACCGCATTGGGCGGAACGTTTCGACCACA  
TTCACGATGGACATAAAATAT'TGTTGAGCGTCTCTACATTTCATCACGTCACAAAGGTTAA  
TTTGTGGAATTACGTGCGATGAGCTCTTGCAAAACAAGAAATACAAAGAGTTGATTGAAC  
CTTATGATACGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAAACCGGATCTCT  
CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG  
AATGTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA  
TTGAAAAAGGCATGAGCCCATTTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG  
AAGACGGCTGGAGCGAGAAGTTAAGCAGCACGGAAATCAGACGCCTACTTAAGTCCTCTG  
CTTCGCCAACGTGCACTCCACAAAACCTTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)

MVEENSRVLIVLPYTPPSATLQRIIGQTIPFLRECQSQLDIVIVPEFKTSFQLDSALGKM  
YSITRDVLLGYGMINSGINIIFNNIHFVESNLQWKVLLPQESTFETWKLELGGQYHSI  
EHYALHDNIMEEIEGPKDANKFHVLTALGGTFDHIHDGHKILLSVSTFITSQRILICGITCD  
ELLQNKKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPETIECLVVSR  
ETVSGAETVNKTRIEKMSPLAVHVNVNLGGREEDGWSEKLSSTEIRLLKSSASPTCTP  
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)

AGAGAGCCATCCGTAACCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA  
CCACGATTGACGAACAAGTTGGT'TTGATCGTTTGACAGTTTGAATGACGAAGAGTTAGTGT  
CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTGAAGGAATCTG  
CAAAGACTATTGTCGATTCTGGCAAACCTACCATCCAGCTTGTGTCCTACTTCGTGTGAA  
TACCGTAAGAAATGGAATAGAATATATACGAATGTATACGAATATPATAGAGAACGTTCT  
CTTTTATTTCTATAATGAATAGGTTTCGGGTAACGGTTCCCTTTTATAGGTATTTCTAGAAG  
ATGAGAGAAGAGGGAATAATGAGAAAGGCGAAAAATAAAGGACACCTTTAACGAAAGATC  
AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAAGTGAAAAAC  
AAAACCTGAAAGGATAGATCAATGTC'TTACAGAGGACCTATTGGAAATTTTGGCGGTATGC  
CAATGTCATCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAACC  
AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCCTTTTGAAAAGTTTGCCTCCAGAA  
TTGAGGGGGCTCACTGACAATGCAGTTGTTTATAAATTAAGCCTTACATTCGAAGTTTGT  
CAAGATTTTTCATTGTGGCCACCTTTTATGAAGATTTCGTTTAGGATCTTATCACAATGGT  
CAGATCAAAATTTTTTATCTGAATAAGTGGAAGCATTACCCATACTTCTTTGTCTGTGT  
TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTAGTTTAAAGAAAGC  
AAACCAATTATGCCACCGGTGTGTTATGTGCTTGCCTTATTTCTCAAGCATTAGTTTATG  
GGTTGTTTACGGGTTTCATCATTTGTCCTAAGAAAACCTTTAGTGTTATTTGGTGGGTTGTAA  
TTGCATTACAGCGATTCAATTGTTCAAAACAAGACAACATTCGGTATGCTTCCTGAATTAA  
ACAGCAAAAACGCAAGCGAAGGGTTACCTGTTGTTTGTGCTGGTAGAATTTTAAATTGTTT  
TAAGTGTATATCGCTTTTACCTTTCAGTAAATCATGGT'TTACTGTTGTTTGGACCATTATCG  
GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA  
TACTAACTTTTTTACAATATCACGCTAAACAACCTACTGGTTTTATAACAATACTAAGAGAG  
ATTTCTTGAAGTATGAGTTTACCAGAACTTAAGCATCATTTGGTGGGCTTCTATTAGTTA  
CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFGMPMSSSQGPYSGGAQFRSNQNSTSGILKQWKHSFEKFASRIEGLTDN  
AVVYKLPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHYFFVFFVVLVVVTV  
SMLIGASLLVLRKQTNATGVLCACVISQALVYGLFTGSSFVLRNFSVIGLLIAFSDSI  
VQNKTFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI  
GYKTKFASIMLGLILTFYNTLNNYWFYNNTKRDFLKYEFYQNLISIGLLLVNTNGAGE

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LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123)

CATTTAGTTCTGATTACAGCAGAAATCGTAGCGGATGAGACATTTTCATCAAATGGCCTT  
TTTTTTTTTGGGCAATTTTTTTTATATCTTGAAATGATAGTTGCCTTGACTTTTCAACCGTT  
CATTTTCATTAAGAACTTGACTAAATATGAACATTTCTTAAAAAAAAGGTTGACATATAAA  
AATAATCGAATATAAACGATGGAATTTTTTATAAAATTAAACACATATATATATATATT  
AACTATAAATATGTCAAAGAAACCATACAATCATAGATTTATAACTATCTTTTTGGATGAC  
ATTAATGAACATAACGCTCCTAATACAAATGTCCAAAAAATATTACCCGCAAATACGAAT  
CTTTTTTTTTTCTCGATGAAATTTTGCAAAGAGTTTCGAAATTTTTATTTCAAGAGCTGGT  
AGAGAAAATTTTCATAAGGTTTTCCCTACCGATGCTTTTATAAAATCTTCGTTTTGTCTCAC  
ATATACCAACAAGAGTAACGATGTTTTCTTTACCTACCCTAACCTCAGACATCACTGTTG  
AAGTCAACAGTTCCTGCTACCAAAACCCCATTCGTCCTGTCGTCGGTCCAACCGGTTGGTA  
AGTTCTTTTTTGGCAACATGCTCAAAGAAGTTTGAGAAACCACACCTGGTCTGAATTTGAAA  
GAATTGAAGCTGAAAAGAAGCTCAAACCGTTGATGAATCCAATGTCGACCCAGATGAGT  
TGTTATTCGACACTGAATTGGCCGATGAAGATTTACTGACTCATGATGCTAGAGACTGGA  
AAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAGTTGCGTTTCAGAGCTACTGAAA  
GTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAGTACCATCCAGACAAGCAATCTG  
CTGCTGGTGGTAGTTTTGGACCAAGATGGCTTTTTCAAGATTATTCAAAAGGCCTTTGAAA  
CTTTGACTGATTCCAACAAGAGAGCTCAGTACGACTCATGTGATTTTTGTTGCCGATGTTT  
CTCCTCCAAAGAAGGGTACCGATTATGACTTTTTATGAAGCTTGGGGCCCCGTTTTTCGAAG  
CTGAAGCTCGTTTTTCTAAGAAGACTCCTATTCTTCTCTAGGTAACAAAGATTCTTCCA  
AGAAGGAAGTTGAACAATTCTATGCTTTCTGGCACAGATTTGACTCCTGGAGAACCCTTTG  
AGTTCTTGGACGAAGATGTCCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG  
AAAGAAAGAACAAGGCCGCAAGAGACAAGAAGAAGACTGCTGATAACGCTAGATTGGTCA  
AACTTGTTGAAAAGAGCTGTCAGTGAAGATCCCCGTATCAAATGTTCAAAGAAGAAGAGA  
AGAAGGAAAAGGAAAGAAGAAAATGGGAAAGAGAAGCCGGTGCCAGAGCTGAAGCTGAAG  
CTAAGGCCAAGGCCGAAGCTGAAGCGAAGGCTAAAGCTGAATCTGAAGCCAAGGCTAACG  
CCTCCGCAAAAAGCTGACAAAAAGAAGGCTAAGGAAGCTGCTAAGGCCGCAAGAAAAAGA  
ACAAGAGAGCCATCCGTAAGCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGG  
CCACCACGATTGACGAACAAGTTGGTTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAG  
TGTCCACCCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAAT  
CTGCAAAGACTATTGTGCGATTCTGGCAAACCTACCATCCAGCTTGTGTCTTCTACTTCGTGT  
GA

YGR285C, 433 aa (SEQ ID NO 124)

MFSLPTLTSDITVEVNSSATKTPFVRRPVEPVGKFFLQHAQRTLNRNHTWSEFERIEAEKN  
VKTVDENVDPELLEFDTELADEDLTHDARDWKTADLYAAMGLSKLFRATESQIIKAH  
RKQVVVYHPDKQSAAGGSLDQDGFVKIIQKAFETLTDSNKRAQYDSCDFVADVPPPCKGT  
DYDFYEAWGPVFEEAEARFSKKTPIPSLGNKDDSSKEVEQFYAFWHRFDSWRTFEFLDEDV  
PDDSSNRDHKRYIERKNKAARDKKKTADNARLVKLVERAVSEDPRIKMFKEEEKKEKERR  
KWEREAGARAEAEAKAKAEAEAKAKAESEAKANASAKADKKKAKEAKAAKKKNKRAIRN  
SAKEADYFGDADKATTIDEQVGLIVDSLNDDELVSTADKIKANAAGAKEVLKESAKTIVD  
SGKLPSSLLSYFV

YHR010W, 1472 bp, exon1: 501-531, intron1: 532-1092, exon2:  
1093-1472 (SEQ ID NO 125)

GACTCGGACGGAACCGTCTCATATTATACGTTTCACTGAATATTTTTTACGGAAGAATGGA  
AAGGGCCTCGAAAGACGTTAATGCATCCGTACACCTACATCTTTTACATTTTTTGCTGTTG  
CACCTACACTGTTTTTTTTTTTTTTCACCTTATGAGTCCTGTATTTCTTGAAAGAGCCGAT  
AACAATATTCCAGGTGGAGTCCCGAGGCAGAATCAAGGCTGCGGAGAGAAGTTCCCTCTCA  
AACTAATGGGAGTGATCCGCTCAGTTCTCCCATCACGACAGAAGTGTCTGAGACAAAAGTC  
TTTCCAGCAGAGTCCGCCTACGCTCTTGCTGCAGAGATTCGCCCCAAGGCAGGTTTCTCT  
AAATTCTTTTCACTAGTAAAGTGTTCGTTCACTGTAACATACCTGCGTAGTTTTTGAGCT  
AAAATTAAAGATATATTAGATTTTATAGAATTTCTTAGATAGTCTCAACGTGTTAAAACAA  
AAGCATAACCAAAGAAAAAAATGGCTAAGTTCTTGAAAGCTGGTAAAGTTGGTACGTATC  
ATTTTCAGTTTTTGGACATCAACAAAAAACCGTGCAACTGTGGTATTAGAAATCCAAGTT  
ATTAGCAGTTGATGTTGTATAATTTGAGTTGAATTCGAGTATTGTATCTTCATATGGGA  
GTAGGGAGGAAAAAGCGTGAGATGTTAGATCTGGGAAAAAACCTTTAAATTTGAATGAT  
AGCTTATTAATAGAAATATTGGACAAAAAGATGAATGATTTAGGAGCGAAACTAACGATT

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ATTCATATTCATGTAGCTATACGAGGCAGTGAAGGGTTATCAAAAAGTTGTAATTTAAA  
AGAAAAAAGCATCAATAGCCACCAAATAAGATGGTGAAAGTTCCGCGATATATTTGCTAA  
GACCATAGGCACATGTACGCAGGCGACCAGGGCCTTTTATTTACTGTAGTTCTTTCCATG  
CCCTATTAAAAAATTCGTGGGCCTATGATAATTTTCTCTCCCTAGTATTGAAGAACAAAA  
TTGAGAATTCGCCAAACTTTAAGAAGGGTTACATTTACTAACTATTTCTTTTCCTTCCT  
TTTTTTACACAGCTGTCGTTGTCCGTGGTTCGTTACGCCGGTAAGAAGGTTGTTATCGTTA  
AACCACATGATGAAGGTTCCAAGTCTCACCATTGGTTCACGCTTTGGTTGCCGGTATTG  
AAAGATACCCATTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA  
AGATCAAGCCTTTCATCAAGGTCGTCAACTACAACCATTTATTGCCAACCAGATACACTT  
TAGATGTTGAAGCTTTCAAATCCGTGTGTTTCTACTGAAACTTTTGAACAACCTTCCCAAC  
GTGAAGAAGCTAAGAAAGTCGTCAAGAAGGCTTTTGAAGAAGACACCAAGCTGGTAAGA  
ACCAATGGTTCTTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFHALVAGIERYPKVTKKHGA  
KVAKRTKIKPFKVVNHNHLLPTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKKAFEE  
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:  
1054-1299 (SEQ ID NO 127)

TTACTTACGTCTATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGTAT  
TTAGCCCATACATTTTCACCCATGCACCATTGGATTATAAAGAAAAAAATTTAATAAAAA  
TCTGCCGGGGAAATTTTCAAGAAAAAAGGAAGGTGTGTTTCGCATTTAACACGGGGCCACC  
ATAAACTTTTGTGTTGCCACCCATCTAGACGGGATCCGCCCCGCCCAAGGCTCTCTTCCTC  
TAGCTAGGCAATGTGGCTCTCGGAAAGGAAACTCCACCAGGACGTGGTGGGAAATGCAG  
CAATTCCCCCTCTGCTTCCCGCTGACCTTTCTTGGGCCCAGTTTAGTAAGTATGCTCTCAT  
CTTTTCATGTGTGCTGTAACTTGCAAGTCATTAACACTATCTATAATTGATATTAGACGTT  
AAAAGTTCTATATAGCATTTGCTTTTATTTAGAGAATACGAAAACACACCAGATAAATTAG  
TGCATATATATTAGATCAATATGGTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA  
AACAGAAGAGAACAAATATTGAGGAATGAATTCGGATGAAATTCTAGTAGAAGAAAAAAG  
CCTAAAATAAAAAAGAAAGAAAGGAAATTAAGCAGTAATCAACCTCTGACATTTGATAGG  
AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAAACTGGTAACGGAGACTTTAAAG  
ACGTGCAAAAGAAAGCAATTAATTTTATAGATAGGGAATTGAAAGGCTCTGTATAGCAGAAA  
ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTGAGTTATGGGTAATCTAACAATAA  
TAGAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGGTACTGCTGGGTAATGAT  
TTATCCTTCTTTTTTTGGAGCACAAATGCTCACTTTTCTCTCTCTCTAATTTTCTG  
ATGTATCCTACCCAACCCTACAGTTTTCAAATTACTAACATCAATTTTGTGAAACGA  
CTTTTCGTTTTCTGTTTCTATTTATTTTCATTACAGGTTTATAGTTCAAGATTTGTTGCACCCA  
ACTGCTGCTTCTGAAGCCAGAAAGCACAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC  
TACTTCTTGGATGTCAAATGCCAGGTTGTTTGAACATCACCAGTGTCTTCTCATGCT  
CAAACCTGCTGTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG  
GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAASEARKHKLKTLVQGPSYFLDVKCPGCLNITTVFSHAQTAVTCESS  
TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:  
946-1262 (SEQ ID NO 129)

TAAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA  
TGTTGCTACATATTATTTTCCATAGCATTTCTCTGTACAAACTTCAAAATAAAAGACAGT  
GACATCCGAACATCCGATACACCCATACATCATGAAAAATAATCCTGACATTGGAAGAAG  
TCTTGATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCGCTGCATCGTACCA  
ACAGTGCCTATGTTTCAGACGGAGAGACGACCTCTAGAGAGACGTCCGTGCGGTGCGGCAAC  
GCTGACGGTTAGTTGTTTCGACGGGATGATGGGTTCCGCCAGGGGGAGGGAAGGCTTTCC  
ACCAAGAGAGGTAAAATTATTCGTGCAAAATGAACTCAGAGATACATCCATATTGTTGACA  
ATGTATATCTTAATTGATGTGGTATTTTCACTGTTTAAACGTAAATTGAAGGAGATTAAG  
CAAAAAACAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAACCATGTTAT  
TTATCTCCATTAGGGCGTGAGAGTGTAATTAGTACACAGGTACTACTAGAATGCTAAAGA  
ACTTTTTTAAAATATCCTGAATCGTAGGGCAAATCCATGTCAAGCAAGAACTAATAGTTA

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TTAAACTTCATTTACTTTTGTAGCTAGTTAAATATTTTCATCATTTTCCTAAAGTACTGAAC  
ACCTGAATGATACTTTTATTGGCCCTTTTAATAAGAAGTCTGGTTAGAAAATATATTGAG  
GATATCATTTAGTAATACTCATTAGATATTTGTGAATTTAGCCGTTTCCCCATTACAGAAA  
AAAGATACAACATAATTACATGTGCAGTCAAATTACTTTTTTTTAAAGATCAATTACTAAC  
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAGTTAACGTCCCAAAGA  
CCAGAAAGACCTACTGTAAAGGGTAAGACCTGTCTGTAAGCACACTCAACACAAGGTTACTC  
AATACAAAGCTGGTAAGGCTTCCTTGTTCGCTCAAGGTAAGAGACGTTATGACCGTAAAC  
AATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAAGACTACCAAGA  
AGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACTAGAGCCCAATTAACCTTGAAGA  
GATGTAAGCACTTCGAATTGGGTGGTGAAGAAGCAAAAGGGTCAAGCTTTGCAATTCT  
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK  
KAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFEKGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTCGTTTTCAATT  
TCCATGGTGCACAGTATCTTAAGTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGT  
TGCTCAGCCGCTTCGTGGATATTCCTTGGATACCTTTAAACATGGACCTACGTTCCGCTC  
TCGAAAAGACCAATATAATAAAAAGTTATAAATTACATTTCCCTATTAGGTATACGACCT  
CGCGCTTCGAAGTAGAGGAGCCCTTTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA  
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAAACAGACCCATTCACCCACGAC  
GTATCAAGTTACTTCCTTGGTGCAATGTCCCACTATAAAAAAATTTCCTTGACGCTAGATC  
GTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTTTCGTACAA  
GGTTACTTCCTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAAT  
ACAGTGACATATATATACACACACCACACCCACACCCACACCCACACCCACACACACCCA  
CACACACACACCCACACACACCCACACCCACACCCACACCCACACACACCCACACACC  
CACACACACACCCACACCCACACCCACACCCACACCCACACACACCCACACCCACCTATCTA  
ACCTGTCTCTTAACCTACCCCTACATTACCCCTACCTCCCCACTCGTTACCCCTGCCCACT  
CAACCATACCACTCCCAACCACTCCATCTCTCTACTTACTACTACCATCCACCCGCCA  
TCATAACCGTTACCCCTCCAATTACCCATATCCAACCTCCACTACCATTACCCCTGCTATTAC  
CCTACCATCCACCATGTCTACTCACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT  
AA

YHR217C, 153 aa (SEQ ID NO 132)

MSLRPLTPSSMQYSDIYIHTPHPHPHPHPTHTHTPHPTPTPTPHPHPHPTPHPHPTPTP  
TPHHTHTPHTTSLNLSLNLPSHYPTSPLVTLPHSTIPLPTTIHLSTYYHPPPIITVTLQ  
LPISNSTTITLLLPYHPPCPHCTVVLPSILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)

TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA  
CGTGCAAGCCAACAGTTATAGAAAAGTACCGTGTAGAGAGAGAAAAAAGATATAGCA  
TTCAATGAGGCTTTATTGAGGGGCACGATGCTCTTTTTTTTCTTCTGTACTTTATAAAATA  
TTCCGTATTTCTTCGCTTTGTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG  
AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGTCCTTAGAAGAACAAGGTTTGGATT  
TGGTAGGGTTCTTGTAAGGAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC  
TAGTTTATTCCGGGTAACAAGTTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA  
CTATGTAGTAAGTTACACAAAGCAACAAGGATATTATTATATGTGACAGAGAAGAAATTG  
CTGTAGAGATTATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT  
CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAAAGATTTCTA  
AACAAGAAACATCCGAAGAGGAAGATACTGCCGGCAAGCATGAACAAAGGGAAACACTGT  
CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTTCGCTCACAGACTACAA  
GCGTTCATCAAGCCACCCAAAATAACCTGAATGCAAAGGAATCCGAAGACCTGGCCCAT  
AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCGCGACGATGTTT  
CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTTTCGTATCATCATCAT  
CACCCAATGTACGTAATGTTGATATCCAAAACCATCAACCTTTTTTCGAGAGACCAACTTC  
GAGCGATGTTGAAAGAACC AAAAGGAAAACCTGTTGATGATTTTCATAGAAGAAGAGGGTT  
TGGGAGCTGTTGAAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATACAACAGAAC  
CAGAAAATGTGAAAAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG

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GAAGCGATGATCCACGGCACCCAACTCACCAATAAAACTTGGTCGTCGCAAACCTGGTTA  
GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAATAACGAATCAGATTCTGAAT  
TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTTAGAGGCGGT  
CTTCACCTGTGAAAGAGACAAACAACCTTTCAAATATGAATTTCTTCACCAGCACAAA  
ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG  
TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTAGAACAAAGAC  
TACAGATTGCCTGTGACAAGGGCAAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG  
GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGTCATGAAGCGGCGTTGC  
AAGGTCATATTGAGATTGTGGAACGTGTTGATAGAAAATGGTGCAGATGTAAATATCAAGT  
CTATTGAAATGTTCCGGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG  
TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACTATACGTAACGCTAAAGGGTTAA  
CTGCGTTTGAATCTGTGCGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAGATTT  
TGCGTGAAATAAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA  
TTCATAATGACAAATCTAAAAATGGCAATAATGCTCACACAATAGATCAGCCACCTTTTG  
ATAATACCACAAAAGCCAAAAACGAAAAGGCCGCTGACTCACCTTCAATGGCTTCCAATA  
TTGATGAGAAAGCTCCGGAAGAGGAATTTCTATTGGACAGATGTTACTTCTAGAGCGGGAA  
AAGAAAACTGTTTAAAGCTTCGAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG  
AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG  
ATATTACAAGTATCTTTTGGCATTCGGATTTCCTGTAATCAAACCTTCAAGGGATAATA  
AAACATCCGCTTTAATGGTAGCTGTAGGTGCTGGCCATCTTGGAACTGTTAAACTGCTAT  
TAGAGGCAGGTGCAGATCCAACCAAAAGAGATAAAAAGGGTCGTACCGCTTTGTACTATG  
CCAAAAACAGCATAATGGGAATAACAACAGTGAAGAAATTCATTTGATTGAAAATGCTA  
TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATGATA  
ATAATAATGAAACATATAAACATGAAAAAAGAGAGAGAAAAACGCAATCACCCATATTAG  
CAAGCCGAAGAAGTGCCACTCCTAGAAATTGAAGACGAAGAGGACGATACGAGGATGCTCA  
ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACCTTCGGATT  
CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA  
AACGTAAAACAAATGCCTTGCAAGATGAAGAAAAATTAAAAAGTATCTCACCACTCTCTA  
TGGAACCTCATTCTCCAAAGAAGGCAAAATCTGTAGAGATAAGTAAATACATGAAGAAA  
CGGCTGCTGAAAGAGAAGCAAGACTCAAGGAAGAGGAAGAATACAGAAAGAAAAGATTAG  
AAAAGAAAAGAAAAAAGAACAGGAACACTACAAAAAGCTGGCCGAAGATGAGAAAAAAA  
GGATCGAAGAAGACAGGAGAAGCAGAAAGTCTTAGAAATGGAAAGATTGGAAAAAGCTACTT  
TAGAGAAAGCAAGAAAAATGGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGGG  
CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACCTCAACGATAAACCTTGATT  
ACAAAAGATTTTTCGCGCTATATTATTTGTAGACGAAAAAACGATAAAATTTGTGCTCG  
ACTTGCAAGTAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCA  
CTTCTGAGAAGATTCCCGTCGATCCCTCGCACTGACTCCATTGTGGAATATGTGAAAT  
TCATTTTCCTGTATGGAGGTAGTTATGATGATAAAAAGAACAACATGGAAAAATAAAGAT  
ATGTTGTAACTTTGATGGGGTTGATTTGGACACAAAGATTGGGTATGAGCTTTTGGAGT  
ACAAAAAATTTGTTAGTTTGCCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA  
ACCACGCAAAAAGAAAAGAAATGGAAGGAAATATGATTCAAATATCAATAAACGAATTTG  
CACGATGGAGAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAAACAGCGTTCTC  
TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAAACACCGTATGAGCATATCCTCCGTC  
TCCAGCAGACATCCAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEDTAGKHEQRETLSEEVS  
DKFPENVASFRSQTTSVHQATQNNLNAKESEDLAHKNDASSHEGEVNGDSRPDDVPETNE  
KISQAIRAKISSSSSPNVRNVDIQNHQPFSSRDQLRAMLKPKRKTVDDFIIEEGLGAVE  
EEDLSDEVLEKNTTEPENVEKDIEYSDSDKDIDDVGSDDPTAPNSPIKLGRRLVLRG  
DQLDATTSSMFNNESDSELSDIDDSKNIALSSSLFRGGSSPVKETNNNLSNMNSSPAQ  
NPKRGSVSRNSNSNKSSHIAVSKRPKQKGIYRDSGGRTLRQIACDKGKYDVVKMIIEG  
GYDINDQDNAGNTALHEAALQGHIEIVELLIENGADVNIKSIEMFGDTPIDASANGHL  
DVVKYLLKNGADPTIRNAKGLTAFESVDDSEFDDEEDQKILREIKKRLSIAKKWTNR  
AGIHNDKSKNGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDV  
TSRAGKEKLFKASKEGHLPYVGTYVENGKKIDLRSFESVKCGHEDITSIFLAFGFPV  
NQTSRDNKTSAALMVAVGRGHLGTVKLLLEAGADPTKRDKKGRALYYAKNSIMGITN  
SEEIQLIENAINNYLKKHSEDNNDDDDDDNNNETYKHEKKREKTQSPILASRRSATP  
RIEDEEDDTRMLNLADDDFNNDRDVKESTTSDSRKRLDDNENVGTQYSLDWKKRKT  
NALQDEEKLKSI SPLSMEPHSPK KAKSVEISKIHEETAAREARLKEEEYRKKR  
LEKKRKEQELLQKLAEDEKKRIEEQEK

QKVLEMERLEKATLEKARKMEREKEMEEISYRRAVRDLYPLGLKIINFNDKLDYKRFLPL  
YYFVDEKNDKFVLDLQVMILLKDIDLLSKDNQPTSEKIPVDP SHLTPLWNMLKFIFLYGG  
SYDDKKNMNMENKRYVVNFDGVDLDTKIGYELLEYKFVSLPMAWIKWDNVVIENHAKRKE  
IEGNMIQISINEFARWRNDKLNKAQQPTRKQ RSLKIPREL PVKFQHRMSISSVLQOTSKE  
PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAAC TGAAC CAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC  
GCCCTGAGAGATTTTATTTTCTTATAAATTTTACTAAATAAGGATTTGTACTTTTGATAG  
AGTTTTTTTTTTTTTCTGACGTTTGTTTAGTTAATATTATATAATAGTATTTAGGAACTA  
GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTTTTTCAATTGTTT  
GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA  
AAATTGTGTTTGACATCGGCGTTTAGGCTTGTTTGTCTGTACACATACGCTGCTTCAC  
ACCAATTCATATTTCTCAGGTTAATTTGTCTCCTCTCCAAC TCAATAACGATTTTGCGT  
GAAGGTTTAATTTTCAATTATTGCAATTTTAGCAGAGAAACGCACATAAATATATATATATT  
GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG  
AAGACTTCGGTTTTAAGT'TTTTAGGTCAAAAACAAAT'TCTACCTTCTTCAATGAAAAAC  
TGCCATTTGCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTCGTTGCTG  
CCTCTGGTAGTAAGGCGGTGGTCGGCAATTACAAATTACTGAGAGATCATATCACCTCCG  
ACTCTACTCCGTTAACGTTCAAGTGGGAGAAAGAAATCCAGATGTAATATTTGTGTGCT  
TTCATGGTGATCAGGTTTTGGTTTCAACCAGAAATGCATTATATTCGTTAGACTTGGAGG  
AATTGAGTGAATTTTCAACGGTCACTTCTTTTGAGAAGCCAGTTTTTCCAAT'TGAAGAACG  
TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA  
CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTCACAAATTCGCAGT  
TAGCAGTTCTTACTAAAGATAGAAAGTTTTCAAAGTTTTGCATGGCGAAATGGCGAAATGG  
AAAAACAATTTGAGTTCTCTCTACCCTCAGAAATAGAAGAGCTTCCAGTAGAAGAATATT  
CCCCTTTGAGTGTTACCATTCTCTCTCCACAGGATTTTTTTGGCGGTTTTTCGGTAATGTTA  
TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAAATGTACATTATAAAGCACATAG  
ACGGCAGCGCCTCATTTC AAGAAACTTTTTGATATTACACCTCCATTTCGGGCAAATAGTAA  
GGTTCCCATATATGTACAAAGTTACCTTGCTGTTAATTGAACCTGATGCAAACTGAA  
AATGTGCTAGCATCATCATGTTCAAGTGAAGTAAAGTATATGGGACTCGAAACAAGTTAT'TG  
AACCTTCCCAGGATTTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA  
CAAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTTCAGGCAC TATTCTAGAACCTTGTT  
CCGGTGTTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT  
TACAGATAGTCGGGTTGTTTCATGTGGCAGCAATCAAAAAGCGGCCATTATAGCATAAATC  
TGGAATCTTTAGAACATGAGAAATCTCTCTCTCTACATCAGAAAAAATTCCTATTGCTG  
GACAGGAGCAGGAAGAAAAAAGAAAAATAACGTGAATCAAGTAAGGCTTTATCAGAGAAATC  
CTTTCACATCAGCAAAATACATCAGGCTTCACTTTTCTTAAACACAACCAGCCGCTGCCA  
ATAGCCTGCAGTCTCAAAGTTCTTCAACCTTTGGTGCTCCCTCATTGGATCATCCGCAT  
TTAAATTTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAAG  
ACGCAACAGATCCTGCTTCTGCTAAGCCAGTATTCCGGCAAACCCGCGTTCGGAGCTATTG  
CCAAAGAACCCTCAACATCAGAAATATGCCTTTGGCAAGCCATCTTTTGGTGCTCCCTCCT  
TTGGCTCTGGAAAGTCATCTGTTGAATCGCCTGCCTCCGGATCTGCCTTTGGTAAAGCCCT  
CTTTTGGTACTCCTTCCCTTTGGCTCTGGAAATTCATCTGTTGAGCCGCTGCCTCCGGAT  
CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCCCTTTGGCTCTGGAAATTCATCTGCTG  
AGCCGCCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTCGGAA  
CTGCATCAAGTAACGAAACTAACTCTGGATCCATATTTGGAAAGGCTGCATTTGGTTCAT  
CATCTTTTGCACCCGCCAACAAATGAAC TTTTCGGATCAAAC TTTACTATTTCAAACCTA  
CAGTTGACAGCCCAAAGGAGGTAGATTCAACGTACCTTTCCCATCTTCTGGCGATCAAA  
GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTGGTACGAAACCTA  
ACACCTCTACGAAACCAAGACCAATGCCTTTGATTTGGGAGTTCTTCCCTTTGGATCTG  
GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAAC TTTTAAATTCGGTACTCAGG  
CTTACCTTTCTCTTACAGTTAGGAAACAAATCACCATTCAGTTCCTTCAAAAAGATG  
ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG  
AACACGAAAGCAATTGGTCCCAACGTAAGCGGTAATGATTTGACAGATTCTACGGTTGAGC  
AAACATCTTCTACTAGATTACCGGAAACTCCCTCGGATGAAGATGGTGAAGTTGTTCGAGG  
AGGAAGCGCAAAAATCCCCATAGGCAAGCTAACTGAAACTATAAAAAAAGTGCCAATA  
TTGACATGGCTGGTTTAAAAAATCCTGTATTTGGAAATCATGTCAAAGCAAAATCCGAAT  
CGCCGTTTTTCAGCATTTGCAACAAATATTACCAACCAAGCTCTACAACACCTGCTTTTT  
CGTTTGGTAAC TCCACAATGAATAAAAGTAATACATCTACGGTTTCACCAATGGAAGAAG



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CTGATACTAAAGAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT  
 TTCTACCAGCGAAAGAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC  
 CAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAGTGCTTTTG  
 ATACCACAGCAAACGAAGAAATTCAAAAGTCACAGGACGTGAACAATCATGAAAAAGCG  
 AAACAGACCCAAAATATAGTCAACATGCTGTGGTTGATCACGATAACAAGTCTAAAGAAA  
 TGAATGAACTTCGAAGAATAATGAAAGGAGCGGTCAACCAAATCATGGTGTCCAAGGAG  
 ATGGAATAGCATTGAAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA  
 AGCAATTCGAAGACCACCAATCTTCAGAAGAGGACGCGAGCGAAAAAGACAGTAGACAAA  
 GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACCTCAACAGTGACCGGGATGAAAAGTA  
 TATCTGAGTCTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG  
 AAGCTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAAACTTCATTAG  
 AAGACAATTATGCTGAATCTGGCATAACAGACAGACCTTTCAGAAAGTTCCAAGGAAAAATG  
 AAGTTCAAACGGATGCCATACCCGTGAAACACAACAGTACACAAACTGTAAAGAAGGAAG  
 CAGTCGACAATGGTCTGCAAACCTGAGCCTGTTGAAACATGTAATTTTTCTGTTCAAACAT  
 TTGAAGGTGACGAAAAATTATTTAGCAGAGCAATGCAAACCAAAGCAATTGAAAGAATATT  
 ACACAAGTGCAAAAGTATCAAATATTCCTTTTCGTTTCACAAAATTCTACGTTAAGGTGTA  
 TTGAGAGTACATTTTCAGACGGTCGAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA  
 ATATGGATACTTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCGGT  
 CTATCAATAATCTGTATACTTTGGAGAATACCAGAGGCTGAAATTCTATTAAATATTGAGA  
 ATAATATCAAGTGTGAACAAATGCAAATAACAAATGCTAACATTCAGACCTGAAGGAAA  
 AAGTTACAGATTATGTCAGGAAAGATATTGCACAAATAACTGAAGATGTAGCCAATGCAA  
 AAGAGGAGTATCTGTTTTTAATGCATTTTGATGATGCTTCGAGTGGATACGTTAAAGATC  
 TCAGCAGCATCAATTTAGAAATGCAAAAGACATTACGTCAAAAGCTATTTCGATTGATCCG  
 CAAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAAAATTGTTCACTGTAAAGAATA  
 AGAGATTGGACGATAATCCATTAGTGGCAAAACTAGCTAAAGAATCTCTTGCACGTGACG  
 GTTTACTAAAAGAAATCAAATTATTGCGTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA  
 AAGGTAAAAAGGCTTCGTCGTTTCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT  
 TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTCTCTCA  
 AAAATTTGAACATGGCAAAATAG

YIL115C, 1460 aa (SEQ ID NO 136)

MSSLKDEVPTETSEDGFKFLGQKQILPSFNEKLFPASLQNLDISNSKSLFVAASGSKAV  
 VGELQLLRDHITS DSTPLTFKWEKEIPDVI FVCFHGDQVLVSTRNALYSLDLEELSEFRT  
 VTSFEKPVFQLKNVNNTLVILNSVNDLSALDLRTKSTKQLAQNVTSFDVTNSQLAVLLKD  
 RSFQSF AWRNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE  
 VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPPYMYKVTL SGLIEPDANVNVLASSC  
 SSEVSIWDSKQVIEPSQDSERAVLPISEETDKDTPNPIGVAVDVVTSGTILEPCSGVDTIE  
 RLPLVYILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSPITSEKIPIAQEQEEK  
 KKNNESSKALSENPFSTANTSGFTFLKTQPAANSLSQSSSTFGAPSGSSAFKIDLPS  
 VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSGSGKSS  
 VESPASGSFAGKPSFGTPSFGSGNSSVEPPASGSFAGKPSFGTPSFGSGNSSAEPASGS  
 AFGKPSFGTSAGFTASSNETNSGSI FGKAAPGSSSFAPANNELFSGSNFTISKPTVDSPE  
 VDSTSPFPSSGDQSEDESKSDVDSSSTPFGTKPNTSTKPKTNADFSGSSSFGSGFSKALE  
 SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP  
 NVSGNDLTDSTVEQTSSTRLPETPSDEDGEVVEEEAQKSPIGKLTETIKKSANIDMAGLK  
 NPVFGNHVKAKESESPFSAFATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEDTKETS  
 EKGPITLKSVENPFLPAKEERTGESSKKDHNDPKDGYVSGSEISVRTSESASFDTTANEE  
 IPKSQDVNNHEKSETDPKYSQHAVVDHDNKSKEMNKSKNNERSGQPNHGVQGDGIALKK  
 DNEKENFDSNMAIKQFEDHQSSSEEDASEKDSRQSSEVKESDDNMSLNSDRDESISESYDK  
 LEDINTDELPHGGEAFKAREVSASADFDVQTSLEDNYAESGIQTDLSESSKENEVQTDAL  
 PVKHNSTQTVKKEAVDNLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTSKVS  
 NIPFVSQNSTLRLESTFQTVEAEFTVL MENIRNMDTFFTDQSSIPLVKRTVRSINNLTY  
 WRIPEAEILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYLF  
 MHFDDASSGYVKDLSTHQFRMQKTLRQKLFVDVSAKINHTEELNLILKLFVKNKRLDDNP  
 LVAKLAKESLARDGLLKEIKLLREQVSRQLQLEEKGKKASSFDASSSITKDMKGFKVVEVG  
 LAMNTKKQIGDFFKNLMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2:  
 943-1321 (SEQ ID NO 137)

TCGATCAACTCTATCCAACAATCTATAATATCCACTGTTTCATTAAACGAATATTGGTCTT

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TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA  
TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTCTATTT  
TTGTGCTCCGTGTGATATTTTCGTGGAGCAAACCAGAAAAGATGCGGAACCTCTTAGCAC  
TCCGCCTGGACATAGGCGGAGCATATTCTCTCTATGGGATGGGTTTTGTGTACTCTTTT  
CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTCCGGCCTCAGGAC  
GGCCTTCTCCAGTTTCTAGCGAGGCATACATTCCAACCAAAGGTGTATCAAGAATATCTG  
AAATTAAAGGTAGTTGAATCTCTATTTGTTGTTGTTATTACCGCTTATTATCCCATAGTT  
GAGACGACCAAGATTCAAACATGCAAATGTATGCACCATATCCATTCTAAACATAGTTTT  
TCGAACGTTTCAGAGCTTAAAGGGACAATTTATTTTAGAACTGAATTTTTTACCCAGTGGAA  
TAACATCGTATCTGTAAAGTCTACAAAATTTTTTATCCATCAAAAATTAAACAAAGAAA  
ACTGCCAAACTGAATATGAGGAACCTTCTCTCTAGGAATGACTTAGTGAATGTACAGTG  
ACTTGTGGAATAATGATTAGATTTTGGAGCGGTGATGCGACTTAACAGTCTCATTGCCT  
AAGAAATATCCAAATTTGTGGTTCATGCTCTCCCCAAGATATGACGATGAGAGCTCGTT  
TAAATTTTGTCTTCTTCCGAACAGTTATGAAAAAACTATTACGTGTTTTATGATATCC  
TTACTAACTTGTCAATTTTTTATAAAATTTATTTTTTAAACAGTTTTGTCAAGACTTTGAC  
TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA  
GATTCAGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA  
ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACCT  
AGTCTTGTAGATTGAGAGGTGGTATCATTTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA  
CAACTGTGACAAATCTGTTTGGCGTAAGTGTTATGCTAGATTGCCACCAAGAGCTACCAA  
CTGTAGAAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTAAATG  
A

YIL148W, 128 aa (SEQ ID NO 138)

MQIFVKLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN  
IQKESTLHLVLRRLRGGIIEPSLKALASKYNCDSVCRKCYARLPPRATNCRKRKCGHTNQ  
LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)

AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA  
ACTAACAATAGCACCGGATGGAGCAAAAATAACAGAAATTTGGAAGTACATCTAAACGGCCA  
ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTAAAGAGAGTCCAGCAAAT  
GATCAAGCTTCCAACGAGTGATGTAATATTAAACAATGTAATTATATAAATATGAAACAT  
CTACATATTTTAAATGTCACTAATGTCAATTACAGAGGACATAAAGTGATTTATGACACAT  
CCGTACTAGTAGTTAAGTATGAACAAATTTTGGGTTTATTTGCCATTTTTTTTTCACGCGG  
GTTTCTTGGATGCGCAAACCCACCTTTTCTAACACCACTAAGAAATATCAACTTTATAGG  
CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTTCAACCTCACATTTTCAACGCGCATTA  
AGCACTTGGTTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTTGATCCGTACA  
ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAACTTGAATTTATGG  
AACGAAAGAGGCAGGCCTTAGTGGAACGATTAAAAAGAAAGCAAGAATTTAAGAAACCCC  
AGGATCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCTTACCAAAAACCGTGTGAAAG  
TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTTGAATATTATGAAG  
TAAGGTTATCTCAATTACAGCAGCAACCAAAACCACAGCTAGTACAACCACATACCTTTA  
TGGAGAAATTTCAAAACGCAAGAAGAAGCAAGATAAACAATTTGCCAAGTTTGAAGCA  
TGATGAATGCAAGAGTACATACGTTTCACTACCGATGAGAAGAAATATGTGCCGATAATCA  
CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG  
ACTTAAACCGGGCTTTGCATGAGATCAAAATCCTTCGGTTGGGCAAACTTTTTGCTAAAA  
TTCGCCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGCCACCGTAGGCCCATTA  
GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTTCTCATGTTCA  
CCATAACGGACTTTTCAGCATACACTAGATGTTTATATCTTCGGGAAAAAGGGTGTAGAAA  
GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATATTAAACCCAGAAGTACTACCAT  
GGAGACCCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCGAATTAGTCATGACT  
TCAAATGTATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA  
AAAAGACTCACAAAAAATGTGGCTCTCCCATTAACATATCTCTTCATAAGTGTGTGGCATT  
ACCAGTAGAGAAGTGCAATTTTCGTGGAACAAGTGCTAAAAGAATTGAATTAAATGGTGGGT  
ACGCCTTGGGCGCGCCTACGAAAGTGGACTCTCAACCAAGCCTATATAAGGCCAAAGGGG  
AAAACGGGTTTAAATATAATCAAAGGTACTCGTAAGCGCCTGTCAGAAGAGGAGGAAAGAC  
TAAAAAGAGCTCTCACAATTTTACGAATAGTAATTCCTGCCAAAGCATTTTTTCGACGAGA  
AATTTTCAAGATCCAGATATGCTGGCAAACCTTAGACAATAAAGAAGGAAAAATAAGAAA  
CTAAGAAATCGACAGCACTGAGCCGCGAAGTGGCAAAATTTATGAGAAGGAGGGAATCCA

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GCGGATTAGAAGATAAGAGCGTCGGAGAGCGACAGAAAATGAAACGAACCACAGAAAGTG  
CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTCGATCCCACATCATGGAAAAATTTCCC  
AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACCTTACTCGGTAAAAAAA  
AAACTGTTATAAACGATCTCTTGCATTACAAGAAGGAAAAAGTCATTCTCGCACCTTCAA  
AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAAACATTTCCGAT  
CCAAGGAAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140)

MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA  
IEVPQSPTKNRVKVGSNATQOGTKFEFSNINEVRLSQLQQPKPPASTTTYFMEKFQNA  
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFNLWVKRYIPEDDLKRALH  
EIKILRLGKLFKIRPPKFQEPEYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH  
TLDVYIFGKKGVERYNLRGLDVIAILNPEVLPWRPSGRGNFIKSFNLRISHDFKCILEI  
GSSRDLGWCPIVNKTHKKCGSPINISLHKCCDYHREVQFRGTSAKRIELNGGYALGAPT  
KVDSQPSLYKAKGENGFNIIKGRKRLSEEEERLKKSSHNFNSNSAKAFFDEKFQNPDM  
LANLDNKRRIIETKKSTALSRELKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI  
QRLGFDPTHGKISQVLKSSVSGSEPKNNLLGKKKTVINDDLHYKKEKVILAPSKNEWFKK  
RSHREEVWQKHFGSKETKETSDGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)

GACATTTTGAAAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG  
GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG  
AAATGACTTACTATGAAAAGACACCTTTGATTTCGTCAATTTTGAACAATGGTAAGACAA  
ATTCGTGGTTTTACGTTAAGCATGAGATGTTACAACCAGGTGGAAGTTTCAAATCGAGAG  
GAATCGGGCATTTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC  
TTGCTGTATTTTCTAGCTCTGGGGGAAATGCTGGTTTAGCAGCAGCAACTGCCTGCAGAT  
CGATGGCACTTAATTGCAGTGTAGTGGTTCCCTAAAACCTACAAAACCTAGAATGGTAAAGA  
AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG  
AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTTCAAGACACTATATG  
TGACCCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA  
TAGAACAATTGAAGGAAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG  
TTGGTGGTGGTGGGCTATTTAGTGGCATAATTAAAGGCCTAGATAGGAATCAGCTTGCTG  
AAAAAATTCGGGTCGTTGCTGTAGAACTGCCGGTTGTGACGTATTGAATAAGTCTCTCA  
AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTGCAACTTCTTTGGCCTCCC  
CATACATAGCATCATTCGCGTTTGAGAGTTTAAACAAGTATGGATGTAAGTCTGTAGTTT  
TATCAGATCAAGACGTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG  
TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA  
TTCTGGAACAAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCGGTGGATCAT  
GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHGSKTLVHPFDNETIWEHSTIVDEIIIEQLKENDISLPRVKALVCSVGGGGLF  
SGIIKGLDRNQLAEKIPVAVETAGCDVLNKSLLKGSPTLEKLTSVATSLASPYIASFA  
FESFNKYGCKSVVLSQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY  
EDDIVIIIACGGSCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACCTCAGCATGTGCTACTCCAGTTAATGACTTGTTCGTATCGTTTCATGCCATAAG  
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT  
CAAGAGCGTATCTAGCCAAACGGACAGCTGTCCTCATATGTTTAATATGCTGCATAGTGT  
GAGTCCTCTAGTTTTTACCGCAGCCACCAGCCGCTTCTCGAGCAAAGTGATAGATCCCATT  
AGGACTCATCATTATCTAATTTTGCTATGTTAGCTGCAACTTCTATTTTAATAGAACC  
TTCTGGAAATTTACCCGGCGCGGCACCCGAGGAACCTGGACAGCGTGTGAAAAAGTTGC  
TTTTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT  
CTAAAGATTAACGTGTTACTGTTTTTACTTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA  
AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC  
CACTCTCCGTGGTCTGTACGCCCTTTTTCGTGGTAATATTACCTTTACAGAAATCTTTCC  
ACTCCTCCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACCTACGGAACGTGTTATCG  
GTATTGACTTAGGTACTACTTATTCCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA  
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTACCGGATGATG

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AAAGATTGATTGGTGATGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT  
TCGACATTAAGAGATTGATCGGTTTGAATATAACGACAGATCTGTTTCAGAAGGATATCA  
AGCACTTGCCATTTAATGTGGTTAATAAAGATGGGAAGCCCGCTGTAGAAGTAAGTGTCA  
AAGGAGAAAAGAAGGTTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAGATGA  
AACAAATTGCCGAAGATTATTTAGGCACATAAGGTTACCCATGCTGTCTGTTACTGTTCTCTG  
CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTTGA  
ACGTTTTTGAGAATTGTTAATGAACCAACCGCAGCCGCCATTGCC'TACGGTTTTGGATAAAT  
CTGATAAGGAACATCAAATTATTGTTTTATGATTTGGGTGGTGGTACTTTCGATGTCTCTC  
TATTGTCTATTGAAAACGGTGTTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG  
GTGGTGAAGATTTTGACTATAAGATCGTTTCGTCAATTGATAAAAAGCTTTCAAGAAGAAGC  
ATGGTATTGATGTGTCTGACAACAACAAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA  
AGGCTAAACGTCCTTGTCCAGCCAAATGTCCACCCGTATTGAAATTGACTCC'TTCGTTG  
ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAAACCTAGATC  
TATTCAAGAAGACCTTGAAGCCTGTCGAGAAGGTTTTGCAAGATTCTGGTTTGGAAAAGA  
AGGATGTTGATGATATCGTTTTTGGTTGGTGGTTCTACTAGAATTCCAAAGGTCCAACAAT  
TGTTAGAATCATACTTTGATGGTAAGAAGGCCTCCAAGGGTATTAACCCAGATGAAGCTG  
TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTCGAAGATA  
TTGTTTTATTGGATGTCAACGCTTTGACTCTTTGGTATTGAAAACCACTGGTGGTGTCTATGA  
CTCCATTAATTGAAGAGAAATACTGCTATTTCTACAAAGAAATCCCAAATTTTCTCTACTG  
CCGTTGACAACCAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA  
AGGACAACAATCTATTAGGTAAGTTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG  
TACCTCAAATTTGAAGTCACATTTGCACCTTGACGCTAATGGTATTTCTGAAGGTGTCTGCCA  
CAGATAAGGGAAGTGGTAAATCCGAATCTATCACCATCATAACGATAAAGGTATTA  
CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT  
CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAAC'TACGCTCACTCTTTGAAAA  
ACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGACAAGGAAACCTTATTAG  
ATGCTGCTAACGATGTTTTAGAAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG  
ACTTTGATGAAAAGTTCGAATCTTTGTCCAAGGTCGCTTATCCAATTACTTCTAAGTTGT  
ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG  
GTGATTATTTCGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSNNVLVRGADDVENYGT'VIGIDLGTT  
YSCVAVMKNGKTEILANEQGNRI'PSYVAFDDERLIGDAAKNQVAANPQNTIFDIKRLI  
GLKYNDRSVQKDIKHLFPNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY  
LGT'KVTHAVVTVPAYFNDAQRQATKDAGTIAGLNVLRIVNEPTAAAIAYGLDKSDKEHQI  
IVYDLGGGTFDVSLLSIENGVEVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD  
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETL'RAKFEELNLDLFKKTLK  
PVEKVLQDSGLEKKDVEDIVLVGGSTRIPKVQQLLESYFDGKKASKGINPDEAVAYGAAV  
QAGVLSGEEGVEDIVLLDVNALT'LG'IETTTGGVMTPLIKRNTAIP'PKKSQIFSTAVDNQPT  
VMIKVYEGERAMSKDNNLLGKFELTGIPAPRGVPQIEVTFALDANGILKVSATDKGTGK  
SESI'ITNDKGRILTQEEIDRMVEEAKEFASDASIKAKVESRNKLENYAHS'LNQVNGDL  
GEKLEEDKETLLDAANDVLEWLDNDFETAIAEDFDEKFESLSKVAYPITSKLYGGADGS  
GAADYDDEDEDDDDGDYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCCGTTAGTTTTCTACATCATCGGCACCTCTAACTA  
AAACATTTGGAGGAGTGGAAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA  
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT  
GTTTGATACGCTTTTTTCCCTTGAGACTACTCTTGGGGACTTTAAAAAAGTAAAACAGTAA  
CACGTTAATCTTTAGAAATTACATAGCCATATTTATATCTTCCAGAGAACCC'TTTTCGTGT  
CCTTTATATAAAAAAGCAACTTTTTTCGACACGCTGTCCAGTTCCCTCGGGTGCCGCGCCGG  
GTGAAATTTCCAGAAGGTTCTAT'TAAAAATAGAAAGTTGCAGCTAACATAGCAAAATTAGA  
TGAATGATGAGTCC'TAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCGGTA  
AAAATAGAGGACTACACTATGCAGCATATTTAAACATATGAGGACAGCTGTCCGTTTGG  
CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA  
CTGGCCAGGTGATGGCTTATGGCATGAACGATACGAACAAGTCATTA'ACTGGAGTAGCAC  
ATGCTGAGTTCATGGGGATCGATCAGATCAAGGCGATGTTGGGCTCCCGAGGAGTTGTTG  
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACC'GTGTATAATGTGTGCATCTG  
CTCTCAAGCAATTAGACATTGGAAGGTGGTGTTCGGTGTGGCAACGAGAGATTTGGAG

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GCAACGGTACTGTCTTGTTCAGTAAATCATGATACGTGTACATTTAGTGCCCCAAGAACAATA  
GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAAGAAGCAATAATGCTGCTGA  
GATACTTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG  
TGTTGGATAAAAACACGTTTCCGCCATATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT  
TCATTTGAGACTTTTGGTGATGATTACAGGACTTGTCTTTCGGAATAAAGTTGACTTGTCCA  
GTAATAGCGTCGATTGGGATTTGATTGACTCCACCAAGATAATATAATCCAAGAAGTGG  
AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAAHAEFMGI  
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFGCGNERFGGNGTVLS  
VNHDCTLVPKNNSAAGYESIPGILRKEAIMLLRYFYVRQNERAPKPRSKSDRVLDKNTF  
PPMEWSKYLNEEAFIETFGDDYRTCFANKVDLSSNSVDWDLIDSHQDNIIQELEEQCKMF  
KFNVHKKSKV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCCTGATGGTCAAATACTGTGCATGGCATCCCCGTGCAGTCAAGGATGCTTTGAGACTA  
GTTTCATCTGCCTTCTTGTAGCGTGTTTCAGCAACTGGCCTACCAGCGGGACGCCCTTTGGGT  
AAAGTTACCAGTGTGCGCATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAACGAACAA  
GGTAAAGTGAGGCTCTGGAAATTAAACCACTACTAAATTTCCATTTATAGACAAACTTAG  
ATATTAAAAGCAATGTACAAATACATACACAAAATATCACTGTAAAAAAATTCGGAAGAA  
ACTTGAAATTGAATATGATTCTGCCCACTTTTTTCTTGCTGTCATTTATAGTCAGAAATG  
AAAAATTGTCCGAGAAATTAATAATATATATGGAAGGACATTTGAGTTTAAAG  
AATTTGATTAAAATGTCTCTCAATATCCTCTGTAAAGAGTTATCTAAATCTCACTTTACT  
TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG  
AATATCAAAATTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAAGCCAGGGTCTTGT  
CAGAGAATGACGGTGATGTCTCCCCATCTGTTTGAACAGAAAGGAAATATCAGTCGATG  
ATATGGATATGATTTCTTTGCCACGGAATTTGACAGGCAAATGGTTTTAGGTTACCTA  
TGTTTTTCGATCTTGAAGACGAAGAAAACAAAATTTGATCCACTTCCTTCAGTTTCCCATC  
ATTTTGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAATCTGAAAA  
CGGGTGAAGAACTAAAGATCTTTTCATTAATCCGTTTGAATTTGGTTTTCTCAAATGAGAA  
AAAGATACATTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA  
AGTGGTTTTTATACCCAAAACCACTGCCAAAGTTTTTGGAGATTTGAAGACGATAAACGAT  
TCCAAGATCCCTCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG  
CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT  
ACACAAAATCTGGTTTGAAAGGAAAAGGAAATATAAAAGTACCATAACCGGTGAATATT  
TCGATTTAGAGGATTACAAAAACAATACATTTACCATTTAAGTAATCAGGAAAATACGC  
AAAACCCACTTTTCACTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTAAACAG  
ATGTGCCTACGTTTCAAGAATTTAGGGATGATTTTGCATACATAATAGAGTTAATCCAAT  
CTCATAAATTCAACGAGGTTTTCAGAAAGCGATTTATCTTATTTATTAGATAAATTTGAAT  
TGTTTTCAGTACCTAACTCTAAGAAAGAAATTTAGCTAATAAAAATGTTCCCTACAGAG  
ATTTTATAAATTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC  
GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCTGAAAGGATAGTTTATC  
AAGACCCGGAACGTCAAGGAAACTCAGTTTGAGAGACATTTTTTCAGTTTGGTTGTTCTT  
CTAATGACCAACCCATTGCGATTGGGTTGAAATTGATTGATGATGAATTCCTGGATTGGT  
ATAGAAATATTTACC'TAATAGATTACCATCTAATCCTAACAAAGTAGCAAAGTTGGTCG  
GCAAAGAAATGAGGTTTTTACCTATTAGCCAAAGTGTCTTGAGTTTGATAATTTCAATTG  
AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTTCATATCCTCGAAAAATCAA  
AGTACCAATTGGCCCAAGTATCAGTTAATTTTCAATTCTATTCAGTGGTGAAGACTGGT  
ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA  
ATATACAAATTGCCAGGATTTTTCCTCAAACTATTCAAGGAAAATGTCGTGTCAAATTTCC  
AGGAGTTTTTGGATCTTATCTTCAATCCTTTTATTCACTCTGGAAGAGGAGCAGTTACCAA  
TAGATTCATCTGTAAATACTGATATCATTGGTCTGCAGTTTTTTTTTATCAAATGTGTGTT  
CTATGGATCTGGTCATTAAAGAGTCGGAATGAATATTACTGGAAGAATTTACTGATATGA  
ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAAC'TGTTGCGCATTACATGT  
ATTATATTTATAAAAGTTTAGCGAAAGTTAATTTTCTGCGGTCACAAAATCTTCAAAAATA  
CAATCACCCCTAAGAAATTTATTGTTCTCCACTATCCAGCAGAACTTCCCAATTTGGAGTGG  
ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG  
GTCTGCTACAGGTAGAACCCTTTGGGATACTGCAACAATGATTCAATATTTATTTTATC  
TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGTTTCATTACTGAATTCGCAAA

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AATCGACCTTTTTGAAGAATAAAAAACGTGCTTCTAGAACATGATTATTTGAAAGACCAGG  
AAACAGCCAAAATCAATCCTTCTAGAGATATCACTGTGGGCGAACAAAGATCATATGAGA  
CAAATCCTTTTCATGAAAATGTTTAAGATGGGACTAAAAATTTCTTTATCATCAAAATCGA  
TTCTTTACAATAGTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA  
GTATTTACTTTGCTGAACCCAACAGATTTGTGCGAGTTGTCTGAGAACAAGTGTGCTATCTA  
GTGGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT  
ACTTTGAGGAGAACGTGGGTGGGATAGATAATTGGTACGATACAGCGAAAGATACCTCGA  
TAAAGCACACGTTCCGATGATTAGAAGAAGATATAGAAAGGAGACATTGGATCAAGAGT  
GGAACCTCGTTCCGGATCACTTTGGAGTAATTAACCTCCATTTGGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRPSLLFDEYQNSVTKPNETKNKEARVLSENDGDVSPSVLKQKEISVDDMDMISL  
PTEFDRQMVLGSPMFFDLEDEENKIDPLPSVSHHYNGESDSFVSSYTPSNLKTGEETKD  
LFINPFELVSQMRKRYIAASKQDGISNIKNDEKWFLYPKPLPKFWRFEDDKRFQDPSDS  
DLNDDGDSTGTGAATPHRHGYYPYFTDHYYYTKSGLKGKGNIKVPYTG EYFDLEDYK  
KQYIYHLSNQENTQNPLSPYSSKEESLEEEFLTDVPTFQEFRDDFAYIIELIQSHKFNEV  
SRKRLSYLLDKFELFQYLNNSKEILANKNPYRDFYNSRKVDRLSLSGCISQRQLSEYI  
WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFDLDWYRNIIYLI  
DYHLTPNKVAKLVGKEMRFYLLAKVFLEFDNFIEGEYLAEIFIKYVIHILEKSKYQLAQV  
SVNFQFYSSGEDWYKKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSNFQEFDLDI  
FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW  
TAQGDNPVTAHYMYIYKSLAKVNFRLSQNLQNTITLRNYCSPSSRTSQFGVDLYFTDQ  
VESLVCNLLLNCNGLLQVEPLWDATMIQYLFYLFQIPILAAPLSSVSLNSQKSTFLKN  
KNVLEHDYLDQETAKINPSRDITVGEQRSYETNPFMKMFKMGLKISLSSKSILYNSSY  
TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGKAPYFEENVG  
GIDNWYDTAKDTSIKHNVPMI RRRYRKETLDQEWNFVRDHFVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTCTGCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT  
GCAGGTGCTTCGTTTACTTTTCTCTGCGTGCTCGAGAACTGATAAAATACTGGTTTAGGA  
AAACCGTCCACTTATGGATTTAACAAGGAGGTGAAAGGTAGGTACCATGGCAATATAGCT  
AGCAACGCTACGCACTAGCTGTGTGTGCTTGCTCTCTGTGTTCGTCTTTCGTATATTGC  
GGTTCCTCCGCGGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA  
GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTGGAAGAA  
TTCTCTAAAACATATTCTATACTTCAAAGTTTTAGCTTCTTGCTTTTCGGTAGTTGCCA  
AACCAATATCGGCATATAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACTTAAAC  
AACTTAAAACGAAAACGCTTATGCTGGAGTTTCCAATATCAGTTCTGCTAGGATGCC TAG  
TAGCCGTCAAGGCACAAACCACGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA  
ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA  
CCTATGCGCAGAACTACGCCGACCAATATGATTGTTCCGGGTGTCTTAACGCATTCCGATG  
GCCCATATGGTGAGAACCTTGCCCTTGTTTACACAGACACGGGAGCGGTGGACCGCTGGT  
ACGGGGAGATAAGCAAGTATAATTATTCAAATCCCGGATTTTCTGAATCCACGGGTCACT  
TCACACAGGTGGTTTGAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA  
CGACATGGAACAATTATATTGTGTGCTCCTACAACCTCCTGGAACTACCTGGGTGAGT  
TTGCAGAGGAAGTGGAACCACTTATAAGCACTGTTTCCTCGTCCTCATCCTCGTCTCTT  
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCGCTGTAG  
CGCAAGGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAAATCGACGA  
CCATAAACCTTGCCAAGACCGCTACCCCTCACTGCGTCTCTTCTACCGTAATTACTAGTA  
GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT  
CCTATGCTACCTCCTCGAGTACCGTCTGCTCTAGTGATGCTACTTCATCCACTACCACCA  
CCTCATCGGTGCTACATCGTCCAGTACCCTTCTTCCGACCCTACCTCGAGCACTGCTG  
CTGCTTCTTCTTCTGATCCTGCCTCAAGTTCCGCTGCCGCTTCTCTCCAGCGGAGTACCG  
AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGCTCCTT  
TGAGTAGTACTTTACTACTTCCACCGCAAGCTCCAGAAGGTAACTTCCAATTCAAGTTA  
ATTCTGTTAAGTTTGGCAAACACAACCTGTGTTTCTGCTCAAACAACCTTCTGTAAGCG  
CCTCATTATCATCATCTGTAGCTGCTGACGATATTCAGGGTAGCACTTCCAAGGAGGCCA  
CAAGCTCAGTTTCCGAACATACTAGTATAGTAACTAGTGCAACTAATGCTGCCCAATATG  
CAACGAGACTTGGGTCACTTCCAGAAGTCTTCCGGGGCCGCTCTTCTCCTCAGCTGTGT  
CGCAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACCTCAGTTA  
GTAGCACAGCCCATAACCACAAAGGACACCGCCACCCTTCAGTAACCGCCTCAGAAAGTA

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TCAC TTCGGA AACTGCTCAGGCTTCAAGTTC AACAGAGAAGAATATTAGTAACAGTGCCG  
CCACATCGAGTAGCATT TACTCCAACAGTGCTTCTGTGTCAGGACACGGTGTAACATACG  
CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA  
CAAATTGCTCTAGTATCGTGAAGACCACAACCTTTAGAAAATTCGAGTACCACAACCATCA  
CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACCTCCACAAGGCAG  
CTACCGCAGTAACCATAGATCCCACATTGGACCCCTACCGACAACCTCAGCTAGTCCAACCG  
ACAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT  
TACGCACAACCACCAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA  
CTTCCGAGAGCGATTATTCCGATAGTCC TAGCTTCGCCATCTCCACTGCCACCACCCTG  
AAAGCAATCTGATCACAAACACCATCACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA  
CCTCCGCTGCTTCTTCTACAGATGAGACGGCCTTCACTAGAACAAATCTCGACATCTTGTA  
GCACCTTTGAACGGCGCCTCAACCCAAACAGTGAGCTAACCACATCGCCTATGAAAACCA  
ACACGGTGGTTCCAGCTTCTTCTTCCCTTCAACTACAACCACTTGTCTAGAAAATGATG  
ACACTGCCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAAACCCGGAG  
AAACATCTTCTCTCGCTAGCGATTTCGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG  
TCAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACAACCTACCAACAGACTGTTG  
CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACCTACTGGTAGCA  
ACGGTCGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACCTCCTCGA  
TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAAACTTCTGCATACGAAGGTG  
CTGCAACACCTCTTCCATTTTCCAGTGAATAGTCTAGCTGGAACGATTGCCGCTTTTG  
TCGTAGCTGTTCTGTTTCGCCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEFPISVLLGLVAVKAQTTFPNFESDVLNEHNKFRALHVD TAPLTWSDTLATYAQNYA  
DQYDCSGVLTHSDGPYGENLALGYTDGTAVDAWYGEISKYNSNPGFSESTGHFTQV VWK  
STAIEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTSD  
TVSTISSIMPAVAQGYTTTVSSAASSSSSLKSTTINPAKTATLTASSSTVITSSTESVGS  
STVSSASSSSSVTTSYATSSSTVVSSDATSSTTTTSSVATSSSTTSSDPTSSSTAASSSDP  
ASSSAAASSSASTENAASSSSAISSSSSSMVSAPLSSTLTSTASSRSVTSNSVNSVKFAN  
TTVFSAQTSSVSASLSSSVAAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS  
SRSSSGAVSSSAVSQSVLNSVIAVNTDVSVTSVSSTAHTTKD TATTSVTASESITSETAQ  
ASSSTEKNISNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPATNCSSIV  
KTTTLENSSTTTITAITKSTTTLATTANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS  
TYGSSSTGASLDSLRTTTSISVSSNTTQLVSTCTSESDYSDSPSFAISTATTTESNLITN  
TITAS CSTDSNFPTSAASSTDETAFTRTISTSCSTLNGASTQTSELTTSPMKNTVVPAS  
SFPSTTTTCLENDDTAFSSIIYEVNAATIINPGETSSLASDFATSEKPNPTSVKST SNE  
GTSSTTTTYQQTVATLYAKPSS TSLGARTTGTSGNGRSTTSQQDGSAMHQPTSSIIYTQLKE  
GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATTCCATTTCTCTAGAGGAGTTTTTATAGTCCTGCCATCTAATT  
GTAGAGCAATCTTTCCTTTCTCAACATCCCTATT TAGTGACACCTTTTCCCAAAACTTCT  
GTGAAGTTTGTCTCAATCTATTTGTTTCCGTAGGAGTGTTATTCTCAATCGTGTGTCTG  
TCCCCAGTGGCTGGGCATTTAATGAGTAGAATCGGGGCAGTTTCAATCTTATGGAATTCA  
CAATGAAGCATCCCTTCCTTAATGATGGCAGCATTC CGTATTCTCTTTTGTAGGGTTTCG  
TTTGCCTTCAAGTGTTTTGTCTTATTTAGCCTTTTCCCTTTACCTTAATTTTTTCTTTT  
CTCTGAAGAAAAATGAATGAGTTTAAAGATATAGCAATTA AAAAGTAACAGTGAAGAAAT  
TCTCAGATGAGCAGATGGGAATTAAAGAACTATCTACAGAGCTCTTTACTAAATTGAATC  
AATAATACATACTTACAAACATGTCACAGATAGCACAAAGAAATGACAGTGAGCTTAAGAA  
ACGCCAGGACACAATTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA  
AGCTTGCTGAATTGACAAAGAAAGAACTAGAGTCTTATCCAACGGACAAAGTATGGAGAT  
CTTGCGGTAAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCACATG  
CCGAAACTGTTCTTCTGGATCAAAGAAAAACATTAAAGATAAAGAAAGAACTATTTAGAAA  
CTACTGTTGAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTAA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNQQ LAYLDRQEKLAELTKKELESYPTDKVWRSCGK SFI  
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)



AAATAGTTCTTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG  
ATAAATCATTAACGTATTTGGATTTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC  
ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT  
GTCTGTCCAAATATGCTAGCTGCTGATTTGACCATATCCAATTTGTGTCCTGGCGTTTCTTA  
AGCTCACTGTCATTTCTTTGTGCTATCTGTGACATGTTTGTAAAGTATGTATTATTGATTCA  
ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTTCCCATCTGCTCATCTGAGAAATTTT  
TTCACGTGTACTTTTTTAATTGCTATATCTTTAAACTCATTCAATTTTCTTCAGAGAAAAGA  
AAAAAATTAAGGTAAAGGAAAAGGCTAAATAAGAACAAAACACTTGAAGGCAAACGAAAC  
CCTACAAAAGAGAATACGGAATGCTGCCATCATTAAGGAAGGGATGCTTCATTGTGAATT  
CCATAAGATTGAAACTGCCCCGATTCTACTCATTAATGCCAGCCACTGGGGACAGACA  
ACACGATTGAGAATAACACTCCTACGGAAACAAATAGATTGAGCAAAACTTCACAGAAGT  
TTTGGGAAAAGGTGTCACATAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG  
ATGGCAGGACTATAAAAACCTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAAGTCTC  
TCTTAGCATACCTATTAAAACCTGGAGTGGTCGTCCTATCCAGTCTTTCCATCAAAACTC  
ACTCTTTGCCACTAACTTCATTAGTGGCAAGATGCATAGATTTACAAATGACAAATGAGC  
CTGGCTGTGACCCTCAATTAGTTGCAAAGATTGGAGGCAACAGTGATGTTATAAAAAATC  
AGTTGTTAAGATATTTAGATACCGATACTTTATTTGGTCTTTTCCCCCTATGAATGAGTTTG  
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG  
AGTTTTTACGCACTTTTTCATCCGAGTCTAATATTTCGACTACAAATTTTAGATGCCGACA  
TCCATGGGTTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAAATATA  
TGAGCAGCTTATCACCATGGGATCTTGCAATTCCTTGAAAAAAGTGTATTAACCACAAAGT  
CCTTCATTTGCGGCGTGCTATTATTAGAAAAATAAAAAAGATACTGCGAACTTAATTCCCCG  
CCTTGAAAAGTGAATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG  
TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA  
AAATTCATACTGCTGCGATTGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)

MLPSLRKGC FIVNSIRLKLPRFYSLNAQPLGTDNTIENNTPTETNRLSKTSQKFWEKVSL  
NRDVEKGKIALQLDGRITIKTPLNGIIVDNAKSLLAYLLKLEWSSLSLSIKTHSLPLTS  
LVARCIDLQMTNEPGCDPQLVAKIGGNSDVIKNQLLRYLDTD'LLVFS PMNEFEGRRLRNA  
QNELYIPIIKGMEEFLRNFSSSNIRLQILDADIHGLRGNQQSDIVKNAKKYMSLSPW  
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTDMDNIVRAATLETIFQVEKWGEV  
EDTHDVKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)

GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAACGGTGCTTCTAAT  
GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA  
AGAGGTACGTGTGCTAGTGAAATAGGTACATGTACCAGAAAATCAAGAAATCTTAGATG  
TGTGTAATCTTGCAATTTAGTTTCAAACAAGATCCTTGTATTTATATAAACAAGATATA  
ATTTT'ATAAAAAAATTAGAAAAAGCAAATATAATTCAGGTCCCACTTGAATAATGGCA  
CTGTATTGATGCATTTTCTTATGCTTAGTGACGCGTTTTCGCGCGTCAGTTTCAAGTTT  
TTCTTGGCTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAAGGATTAAAAATGCAGTA  
TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCTTCCAG  
GACAGTACGCGCAAACATATTATGGAGATATTCAAGGAAGAAGAAGAAGCTTTTTTCGG  
CGATAGAAGGTATAATATATGCCGTGTGAGGTGTATGACCCTGTACCCCGTCATTTACATA  
AAAGCAAAACAAGATCATCAATGCTGCTAAATTAATTATAGAAACGCATCTTTCATATT  
ATACAATACTCAATAACATTTACAGATATACAAGCCTATCTTTCTACTTGGCTTAGGGATC  
TTGGAACGACAGGTCCATACCAAACAATTCCTTTCAGAAAGTATTTCTCTCATGTTTGACC  
GCATCTGATCTATCTTTCAGGAAATGTACGATAGAGGGAGGTTTTCCACATTTGATCGCAC  
GCTTTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT  
TTTTTTCAAGCTACGATTATGCTTTTCGGGGTTGCATACAACCTTGTAATTTGCTCTGAAT  
ACAGGTATGACGAAGTTCATTACATATCGAACGGCACTTACTCATTAGTTGCATCGATGA  
AGATAGATCCTGCTGAAGTCATTAAAAGGGAACATTTTAGGCTTACAATTCGAAAATTTA  
ACATATCTAATATATTAATTGAAATTTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG  
TGAACCCTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTCGCAGTATCT  
CCGAAGGTAATCATCAGGTCCTAGAATTGGGGAGAAAGTTAATGTTTCCATTGTTGAGGA  
CTGGAGATTTTGAAATCTGTCGTATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG  
CGAAGGATGTAAACTAGAAATAATCAGTCTGGATGAAGTTTCTTGGGTAATGCAGTGGA  
AATCTTGTCTTCAAATTTATGAGAGAAGGGCAGCAATGACAGTTCATTTATCAAAACAC  
ACCTACAATTTAAGAAGGCCAACAAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG



TAGACAGAAATATTTCCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAAGTCCCC  
CGCCTTCAAATACTGGTTGTTTCATTACACAGGTCTAAACCCTTGCATATCCCTTTATCAT  
CTGTTATTCGTGAAGACTTTTATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG  
ATAGCAGTTGTGAATCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTCATG  
ATAATGAATTTTTTAACAACCAAGTCACCTCATTATTTTTTCAGAACACATAGACAATAACT  
CGAGAGAGGTGGTAATAACAGATGAAAATACGATAATATCTTTGGAAAATACCCAAGTAA  
GTCGGTGGTCAAATTACTCATGGCAAAAAATTTACCCGCATCAATTACAGGTCTCTATTA  
TCCAACTGCGCATGGGAAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT  
TCAAAATTCGTTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA  
TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA  
AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG  
TATCGCACTCAAACAATCAAGATGCTACTGCAAGTCCACTTTTCGTCACTTTTCATCAGCAA  
TGGATCTCAAGCATTCATTACAGAAATGTTCTCTACAATAATGCCCAAGAGTTGACGC  
AGGACGTCATCGGTTCAAAATCAGACCTAATCAGTAATATTCGTCAAAAAATATAA

YJL181W, 611 aa (SEQ ID NO 156)

MEIFKEEEEEAFSAIEGIIYACEVYDVPVRHLHKSCTKIINAAKLIIETHLSYYTILNNI  
SDIQAYLSTWLRDLGTTGPYQILSESIISLMFDRTVSIFRKCTIEGGFPHLIARLYLRLK  
SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV  
IKREHFRLTIPKFNISNILIEIFHLLDGLAFKVNPDLSISISTASAETIFRSISEGNHGV  
LELGRSLMFPLLRGTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY  
ERRAANDSSFIKTHLQFKKANNFNEDNNGLLGLIVDRNIPTDDFTLASTNRQSPPPSNTGC  
SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHDNEFFNN  
QSPHYFSEHIDNNSREVITDENTIIISLENTQVSRWSNYSWKIISPHQLQVSIILQRMGN  
FIVAYDSYDNLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL  
RVLSFYTTDHTAVSHSNNQDATASPLSSVSSAMDLKHSLOKCSSTIMPQELTQDVIGSK  
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)

TCTTGCAACCATCGTCCCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA  
CAGATGCCAACATGTGGGAGATAGGGGGCTATTCGCAATTTATTAACGTCTCTAGTACTG  
GTAAGCCTTTCTAACATTCTTGTGGTCACGTGATGTGTATGTTTCTTTTTTTTATTCTC  
CGGGTGATAACGACGCGAAAAATATTTTTTCATTTTTCTTTTAACCATCACAATTTGCGA  
CGCGACGCGAAAAAATGCAGAGAAGTAAAAGAATGCTGGATAAGAAATCAACAACACAG  
TTGAACATTGGCGTGCCCTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTTGTA  
TGTATGCGTGTGTTAACTATCCTGCACATCATCTTGCGCAGTTAGTCCAATAAAAAAGGA  
TTACTACTGAACAGGTCTTACTATTTTTTGATTGCGTAGTGCTGGGGAAAAGTAAACACAC  
ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC  
TGGACACGGAGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAAACAGGCCGGCGAAG  
ACGAGAGTGATGATTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC  
CATATTCGAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCTATTAAGTAATA  
CAGCTTTGTTCAGAGGCTAACTCCAAATTTCTTGGGAAAATTGAAGAAGAGGAAGAAGG  
AGGAAGAAGGCAAGGATGAGGAAAGCGTGGATTCTCGTATTAAAAGGTGGTC'TCCGTTCC  
ATGAAAATGAAAGTGTTACTACTCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC  
CTATTTCTCTCAAACAATGGAACCAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA  
ATACATCCTCATCTCTTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT  
CGGGCCTCGTATCTAAATGTCTATGGACACTTCGTTATACCCTGCGAAATTGAGGATAC  
CAGAAACACCAAGTGAAAAAATCACCTTAGTGAGGGAAGAGACCATAAGCATGTCCAC  
TTTCGAGTTCGAAAAATGCATCGTCTTCTCTAAGTGTTTCCCCCTTTAAATTTTGTTGAAG  
ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT  
CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATGCACATG  
ATCGTCAACAATAACCAGACAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT  
CTCCACAAACATTGCATTCTAACAAGTTCAAAAAAATCAAAAGAGCAAGGAATTCGGTTA  
TTTTGAAAAATAGAGAGCTAACAACAGTTTACAACAATTCAAAGATGATTATACGGCA  
CGGACGAGAATTTCCACCTCCAATCATAATCAAGTCATCATTTCAACTAGAAAGAACCC  
CTCAACCTTATCAATTTTCGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC  
CAACAAGACGAAAATCTATTATTGGGGCAACATCTCAAACACATAGAGAAAGCAGACCAT  
TGTCACTCTCTCTGCCATCGTGACAAACACAACAAGTGCAGAGACGCATTCCATATCTT  
CCACCGATTCTTCGCCGTTAAATTCAAAAGGCGTCTAATCTCTTCAAATAAGTTATCAG  
CAAATCCAGATTTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC

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AGTTTTCCACGGTCTACCAGGTTACGTTGCCCAAACAAACAAAAAGTATGCAATCAAAG  
CCATTAACCAAACAAATATAATTCCTTGAAACGCATATTACTGGAAATTAAAATACTAA  
ACGAGGTAACAAACCAAATTACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA  
TCAGTTCCTGGAAGTTTCAAATTCATACTATATTATGACAGAATTGTGCGAAAATGGTA  
ATTTGGATGGATTTTACAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGAAGATTGGA  
GAATTTGGAATAATCATCGTGGAAATTAAGCCTGGCTTTACGATTTCATCCATGATTCTTGTC  
ACATTGTGCATCTGGACTTGAAACCCGCAAACGTCATGATCACATTTGAAGGTAACCTAA  
AACTAGGTGACTTTGGAATGGCTACTCATTACCGTTGGAGGATAAAAGTTTTGAAAATG  
AAGGTGACAGAGAATATATTCACCAGAAATCATTTCTGATTGTACGTACGATTACAAGG  
CAGATATTTTTCCCTGGGTCTGATGATTGTGAAATTGCAGCGAACGTTGTGTTACCTG  
ACAATGGCAACGCATGGCATAAGTTGAGATCGGGTGATTATCGGATGCAGGAAGATTAA  
GTTCCACAGATATTCATTCTGAATCATTATTTTCAGACATTACGAAAAGTAGATACAAATG  
ATTTATTTGATTTTGAAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA  
CTGTTTCATAACAATAGTAATATCAACAACCTAATATGAATAATGGCAACGATAATAATA  
ATGTCAATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATTTCCCG  
CATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACGATGGATGA  
TAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGAGGAATGCC  
TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA  
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSSLDEDEEDFEMLDTENLQFMGKKMFGKQAGEDESDDFAIGGSTPTNKLKFPYPSNNKL  
TRSTGTLNLSLNTALSEANSKFLGKIEEEEEEEGKDEESVDSRIKRWSPFHENESVT  
TPITKRSAEKTNISPISLKQWNQRFKNDARTENTSSSSYSVAKPNQSAFTSSGLVSKM  
SMDTSLYPAKLRIPETPVKKSPLEGRDHKHVHLSSSKNASSLSVSPNLFVEDNNLQED  
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHDRHNNQTNILSPTNSLVTNSSPQTLHS  
NKFKKIKRARNSVILKNRELTNLQQFKDDLYGTDENFPPPIIISSHHSTRKNPQPYQFR  
GRYDNDTDEEISTPTRRKSIIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL  
NSKRRLLISSNKL SANPD SHLFEKFTNVHSIGKQFSTVYQVTF AQTNKKYAIKAIKPNKY  
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFNQSYIIMTELCENGLDGLFQ  
EQVIAKKRLEDWRIWKIIVELSLALRFIHDSCHIVHLDLKPANVMITFEGNLKLGDFGM  
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLDPDNGNAWH  
KLRSGLSDAGRLSSTDHSESLFSDITKVDTNLDFDFERDNI SGNSNNAGTSTVHNNSN  
INNPNMNNGNDDNNVNNTAATKNRLILHKSSKIPAWVPKFLIDGESLERIVRWMIEPNYER  
RPTANQILQTEECLYVEMTRNAGAI IQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCCCGCATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACG  
ATGGATGATAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGA  
GGAATGCCGTGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTT  
TGGACCTAAGCCAAAATTTTTATATGATAAATGGAACAAAAAACCTTGTTTTATTATACA  
TACTTTTTTCCCAACAGCTGCTTATGGCCGCAATTTGTATATAAATAATCCAATAACGAAAAAG  
AGTGTAATTGCAGTCCGGTAGTAATACCATGTAAAACCTTAGATGAGTTTATTTTAAGTA  
CAGCCGCTTCAAGCATTTTTATTTTTATTTTACAGATGTAGCAGATAACAACCGTTAAAT  
TATATTATATATATATATATATATATATCAAAATACGACGTATTACATATATATTGAGAAT  
AAGGGAAGGATGGAAGACAAATGACAAAAAGTTTGAAGCATAAATATGTTCTTCGCTTAG  
ATGTTTCATCTTGGTTCTTCTCCAGTTTCTTCTCTTAGCGTTGTAACGGATAGTGTGTGTTG  
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTCTTAGCCTTAGCCATTTTT  
TGCTTGATTCTGAAAGACTTTTGAGCCTAATTAAAAGGGAACATATCGTGCACATACGA  
AGTGTAACAATTGTAATAAATGTTAGTAACAATGTTCAAACCTCATCAATATGATGCATTCA  
CGGATCCAAGGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHKYVLRDLVHLGSSPVSSLSVVTDSVVGVSQSDPLWQWSVLLLLSLSHFLLD SERL  
LSLIKRETYRAHTKCTIVKNVSNNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:  
893-1042 (SEQ ID NO 161)

TATTCAAGAATTATTTACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC  
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

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AGTATGTGATGTATGGGCGCACAGTACCAATTTAACTTTTTTTTTTTTCATTTTTTTAGC  
TTGATTTTTCAAAAACTTATGGGCGTTTTAGGCTCCGGCTCAAACCTACCACCACCACGCG  
GCAGGCCGAGGCAAACAGTACGCCCTTGGCGGGGACGCCGAAGCGACTCCTTCTGTTCCAA  
GCTCAATGGTCTTTCGCTTTACGCTCGCGCGTGGGCTAACTAACGCAATTCGGCTTTTGG  
GCTGTCGAGAACCGAGAATTATCTTCGCCTTGATAGATACTTTAAAACCTTCTACTTAAT  
ATACTTTCTACAA'TTTTTGGTACATTCATATTATACTGAAAATTCGAAAAAGACAAGCAA  
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCCAGTTAGA  
TGCTGAACCTGATCAATAGCAAATTATAAACCACATCCATCTAAATGACCTTACCACCTAC  
AATTTGGATTTGAAATAGAAGCAATGTGTAAAAATATAGGGAAAGGATTAGGAGTGTAAAC  
CATACTAAAAATTTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAATA  
TATGGTCATAAACTGCTTATTCTGAGAACTTTTGGTGGTCCAGCGTGGT'TTATGTCAGGT  
GGTATTGCCTTGGATCCGTGAA'TGCATCATATTGATGAGTTTGAACATTGTTACTAACAT  
TTTTTACAATTGTACACTTCGTATGTGCACGATATGTTTCCCTTTTAATTAGGCTCAAAA  
GTC'TTTCAGAAATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTGCCACA  
ATGGATCAGATTGAGAACCAACAACACTATCCGT'TACAACGCTAAGAGAAGAAACTGGAG  
AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)  
MAAQKSFRIKQKMAKAKKQNRPLQWIRLRTNNTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)  
TCTCGACAGCCCAAAGCCGAATTGCGTTAGTTAGCCCACGCGCGAGCGTAAACGCAAGG  
ACCATTTAGCTTTGGAACAGAAGGAGTCGCTTCGGCGTCCCCGCCAAGGCGTACTGTTTGC  
CTCGGCCTGCCGCGTGGTGGTGGTAGTTT'GAGCCGGAGCCTAAAACGCCCATAAAGT'TTTT  
TGAAAATCAAGCTAAAAAATGAAAAAAAAAAAAAGTTAAAT'TGGTACTGTGCGCCCATAC  
ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAAACT  
CAAATATTGAGGACGCGCGGATTACCAGCGGCATGTTTACTCGCTGGAAGATGTGAAATAA  
TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTC  
AATCTTAAATTTGTAAGGTTTTTTAATGGCCTTTCAGTTCTAGTATTTTTTATAAAACAA  
GACCAACATACATATCCAAGATGACCAGATCTCCGTTTTAGCTGATGCTTTGAATGCCA  
TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTT'TAATCAGACCATCCTCCAAGGTCA  
TTATCAAGTTT'TTGCAAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG  
ATGACCACAGATCTGGTAAGATTGTTGTTCAAT'TGAACGGTAGATTGAACAAGTGTGGTG  
TTATTTTCCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAACTTGT  
TGCCAGCCAGACAATTCGGTTACGTCTATCTTGACCACCTCTGCTGGTATCATGGACCATG  
AAGAAGCCAGAAGAAAGCACGTTTCTGGTAAGATTTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)  
MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLQVMQKHGYIGEFYIDDHRSKG  
IVVQLNGLRNKCGVISPRFNVKIGDIEKW'TANLLPARQFGYVILTTSAGIMDHEEARRH  
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)  
CTTCTTCGGGGTTCCCCAATGTCACTGCCATCTCTAAAGTAGATAGAAAGGGCGATCGCT  
ATTTAAGT'GTCATGACTTTCTTAACGAGAGGTGTTCCAGCTTCTATTTTGGCTTTTCCTAT  
GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG  
CGTAAGAGATACGTCTACGATAGCATGTAACAGCGTATATATAATCTATATGTATTCGAT  
TAATCCAACACTTCTGTTGTGTAGTCTAATGTTTCGAAAAAAGGTACGCTTCCCTGTTAT  
AATCAGGTATA'TTTCGTTATTCTTATAAGCTAAAAGATTAAAAATTTT'TCCACTTTCCTT  
GAAATTTGGTCGGTTTCGTGGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA  
AGATGGGATTACTGGAAAAATAAAGGGAGGAAAATCCTGCAGAACGTTGTTGTTTCAATC  
GAAGGTTTCTTCAATTCGAAAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTCAATTGG  
TTTATAATGAAGATCCCGATTTACCCGATGGCACAACACCATGTGATCGGTTGGGAGTGG  
ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCCAGTCTCAG  
ATCTGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCAATTTGCTAGCGCTA  
ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAACTAATCTTGGAACATAATGGTCAAG  
ATGGAAGAAATGTCTTAGAACAACAAGAGACGTGGTTGCTAGACTAATAGAAGAAAACA  
AGGAAACGCAAAAGAGGGTGATAAAGTCTGTATTGTCCCCAAGGTTTGGTACGATAAAT  
TTTTTCGACCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT  
GCAGAGACTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGTATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG  
TGGTAACCTAATTTGGTTATCAACCAAACACAGGGGAGTTAGAGACAGAATACAATAAAAT  
GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC  
AGGACGATTCAATAATGTACCTCTCGATGTCTGCGTTGAATTTAGTACGTGATTTGGTTG  
AAAAGAGTATGAATCTGTTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGCGGTGGATT  
TAAAAATTTGGTTTGTGTGTCAGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT  
TTTTGAATTTCTTCATATGAAATAACTCCGCTTCAATTTCTCGAACTACCGATAAAGAAAC  
TACTAATACCAGACATGTTTTGAAAACCGTTTAGACAAGATAACTTCAAATCCGAGTGACC  
TTGTTCATAGAAATTAACCTATAGAAGGGAATCACCATTGGCCTTCAAACATATTTTGCTT  
ATAATAAACTCGAACCCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT  
ACATGAATTTCTGCGTTGCAATGCCTGGTACACATTTCCGCAGTTGCGTGATTATTTCCCTT  
ATGATGGTTATGAAGACGAAATCAATGAAGAAAAATCCTCTTGGGTACCACGGCTATGTGG  
CTAGGGCATTTAGTGACTTGGTTCAGAAGTTGTTTCAAAAACAGGATGAGCATAATGCAAA  
GAAATGCTGCTTTCCCCCTTCAATGTTCAAATCCACTATCGGGCACTTTAATTCGATGT  
TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTTAGCCTTCTGTTAGACAGTTTAC  
ATGAAGATTTGAACAGGATAATAAAGAAAGATACACAGAAAAACCATCATTTATCTCCTG  
GTGATGACGTGAATGAATTTGGAATGTAGTCAAGAACTGGCAGACGATACTTGGGAGATGC  
ATTTAAAGAGAAATTTGTTCCGTTATAACGGATTTATTTGTGCGGATGTACAAATCAACGC  
TATATTGTCCCGAATGTCAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT  
TGCCGCTTCCGGTTGATACAGTGTGGGATAAAATATAAAAAATTTTTCCCATGAACTCTC  
CACCACCTTCTTCTTGAAGTTGAGTTAAGCAAATCGTCCACTTATATGGACTTGAAGAATT  
ATGTTGGTAAAAATGTCGGGCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA  
ATCAAATCTATGTTAACTATGAGTCAACAGAGTCGAATGCTCAATTTTTAACCTTGCAGG  
AATTGATCAAACCTGCTGATGACGTTATTTTTTATGAATTACCAGTAACAAATGACAATG  
AAGTAATTTGTTCCCGTATTTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT  
TTGGAGTCCCTTTCTTTATTACGTTAAAAGAAGATGAATTGAATAATCCAGGTGCAATAA  
GAATGAAATTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCCCTGAAC  
CTGTAGGAAATCGAACCGATTTTGTGCTGCTTTTCCATTATTAGTAGAAAAATATCCAG  
ATGTTGAATTTGAACAAATATAAGATATACTACAGTATACGCTATTAAGGTGACTGACA  
AGGATAAATCCTTTTTTTTCCATCAAGATTTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA  
GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCAGTTAAACCTTGACAAAG  
CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCATCCT  
TAGTAGATTGTGCTGAAGGGGTCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA  
GTGAAGCAAAGAATTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAAATAAGAAA  
CTGTAACAAATAATGAAAATGTAAATAATACTAATGATCGGGATGAAGATATGGAACATAA  
CAGATGATGTTGAAGAAGATGCAAGTACAGGCCAGAATTAACAGATAAGCCAGAGGCGT  
TAGATAAAATTAAGGATAGCTTTGACTTCCACTCCGTTTGGCGATTCTTTCTATGAATGATA  
TTATTGTTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT  
ATAACTGGGAAAATCCAGCTACTTTGCCTAACAAAGAGTTGGGAGAACGCTAAGTTGGAAA  
GATCTAACGCTAAGGAAAGAACCATAACCTTTGGACGATTTGTCTCCAATTATTTTCCAAC  
CAGAAATACTAGGATTAACCGATTCTGTTGACTGCCCTACATGCAAGGAACATCGTCAGG  
CTACCAACAAATAACAACCTTTGGAATACACCGATATTCTGTCTAATTCACCTTCAAAGGT  
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTGATGCCACGGTTAATTTCCCCATTTACAG  
ATTTGGATCTGTGAGGTACGTTGTCTATAAAGATGATCCCAGAGGTTAATCTATGACC  
TGTATGCAGTAGATAACCACTATGGTGGTTTGGGTGGTGGGCACTATACCGCGTACGTAA  
AGAATTTTGCCGACAATAAATGGTACTATTTTGATGATTCTCGAGTAACCTGAAACTGCGC  
CAGAAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTCGCCGTCATAAAGATG  
GCAATGGATTAGGCAGCTCTAAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG  
ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG  
ACGAGGAGGAAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGCAGGCCCTG  
AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG  
ATGACAAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAAGTTAAGATTGTTGAAAA  
AAGTCTACAAGAATAATTCAGGCTTGGGTTTCATCGAGTACGTCTGAAATATCTGAGGGAT  
GCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG  
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)

MGSSDVSSRECSLVYNEDPDFDGTTPCDRLGVLDLMNVLDDKDEIKQESVPVSDREIEDT  
ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG  
DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFNF

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LSEIYGMTSGSYPVVTLVINQTTGELETEYKWFRLHYLTEKQDGRKRRHGQDDSIMY  
 LSMSALNLVRDLVEKSMNLFFEKADHLDVNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE  
 ITPLQFLELPIKKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHWPSNYFAYNKLEPA  
 SGTTLGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL  
 VQKLFQNRMSIMQRNAAFPPSMFKSTIGHFNSMFSGYMQQDSQEFALFLDLSLHEDLNRI  
 IKKEYTEKPSLSPGDDVNDWNVVKKLADDTWEMHLKRNC SVITDLFVGMKSTLYCPECQ  
 NVSITFDPYNDVTLPLPVDTVWDKTIKIFPMNSPPLLLEVELSKSSTYMDLKNYVGKMSG  
 LDPNTLFGCEIFSNQIYVNYESTESNAQFLTQLQELIKPADDVIFYELPVTNDNEVIVPVL  
 NTRIEKGYKNAMLFVGPFFITLKEDELNNPGAIRMKLQNRVHLSGGYIPFPEPVGNRTD  
 FADAFPLLVEKYPDVEFEQYKDILQYTSIKYVTDKDKSFFSIKILSVEKEQOFASNNRTGP  
 NFWTPISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAGVLMQVDDDEGTGSEAKNFS  
 KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS  
 LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER  
 TITLDDCLQLFSKPEILGLTDSWYCPTCKEHRQATKQIQLWNTPDILLIHLKRFESQRSF  
 SDKIDATVNFPIITDLDLSRYVVKDDPRGLIYDLYAVDNHYGGLGGGHYTAIVKNFADNK  
 WYFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSKLQEI IQKSRHGYDERIKKI  
 YDEQMKLYEFNKTDDEEDVSDDMI ECNEDVQAPEYSNRSLEVGHIE TDQCNDEDDNDGDGE  
 RTNSGRRKLRLLLKKVYKNNSGLGSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3146 bp, CDS: 501-3149 (SEQ ID NO 167)  
 TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGCTAGATTGTGAATAAATCATT  
 TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG  
 GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCCACACTCCTTGTATGACTGC  
 ATACGCATAAAGAGGTGCTTGTCTGTAGGCGTATATGATCCTAAGCAACAGAGAAACCAC  
 GGTCTCTTCTCTTCTTATTTTCGTTATTGTCTTCCCTTTTTTACTATGGGTAAAGTCGCCC  
 TAAAGCGGGGCGCTCACAAATATCGCCGCAGCTACAGCCGTTTTTTTTTTTTTGTTTTTT  
 TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTTCATCGATATAAA  
 GAACACTGTTCACTTCGATGTCATCCGGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA  
 GTGGTAGCTGGTACAGGATCATGAGATTTTCACTTCTTGAAGTACAATGCTGTCCCAG  
 AATGGCAAAAACATTATATGGACTACAGCGACTGAAAAATCTTATTACACGCTACAAA  
 CAGATGAACCTCAGGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAGAGCTCTAACA  
 TTACAGATAGGTTCAAAAACAAGTTTCTTTTAAAAATGCGAAGGAAGATACGTCTTCCG  
 GTATGAACAAAGATGCAGGCATCGTTGAGGAACCATCGAGTTGCGAGAGTTGCCTACTG  
 CTCAGACGGTGCCTGCCAAACCTTCTCCTTTTCAAGAAGATGAAGGAAAAGATATTTTACA  
 AAAGAAGGTGCTCTTCCGCATCGTCCGTCTCCTCCACGGCCAACGAAAAATCTGCAATTAG  
 ACACCTTATGATACGTTTGTGGTGATTAAACAGCTGAAAAACAGAAAGTAGATGATTTTT  
 ATAAGAGGACAGAAGCGAAGTTCTACGACAAATTTGACGCGCTGGTGAAGGACCTGAAGA  
 AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAAACGAACCGATTGCCA  
 GCACAAATGACGAAGTTCCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT  
 ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTTCGCAGTATAACA  
 TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT  
 GCCAGTTGAAGTCGTTTCACTGAATTGAACCGCATTGGGTTTGCAAAAATTACAAAGAAAT  
 CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACCTGATCGGAATCGGACAGTTTTC  
 AAGACACATATGCATTCCAGGCAGAAACGATCGAATTGCTAAATTTCCAAAATTTCCAGC  
 TAGTCACATTTTATGCGCGCATCACTGACCGGCCTCATAATATCTCGCATAGCAAGCAAG  
 AGTTGAAATCCTACCTGCATGACCACATTGTTTGGGAAAGAAGTAACACTTGGAAAGACA  
 TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAATATAATGCAA  
 ATAAGCTGGTAGGCAAGTTAGATTTGGAATACTACAGATGGCCACTACCCAGACCGATAA  
 ACTTAAAATTCAGTAGTATAAACAACGTTGCACTACCGAAATTATTTTACCAAGAAAG  
 CATAAAGATTTACTTTATTATTCTAGTCACTGGACTCTTGTAGGAATAAAGACCTTCA  
 ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTGAGTGTGTGCGCCTTTTTGTGGGCTA  
 GTGAGGCCATCCCATACACATTACAGCATTCCTTGTACCACTACTTGTAGTCCTTTTCA  
 AAGTCTTAAAAACCTCCGACGGGGCTATAATGAGTGCTGCAAGCGCTTCATCAGAAATTT  
 TGGCCGCCATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG  
 TACTTGCAACAATAACATCGCCAAAGTCTTGCTCGTGGTGTGGCCTTCGCTGGTT  
 GTAAACCCAGAAACGTTCTTTTAAATGGCAATGTGTGTCGTGTTCTTCCATCAATGTGGA  
 TTTCCAATGTGCGCAGCACCTGTTCTAACAATATCGTTGTTATCTCCCTATTGGATGCCA  
 TGGATGCAGATAGCCCATTTGCGCAAGCATTGGTGTAGGTGTAGCGTTGGCTGCAATA  
 TCGGTGGTATGTCTTACCAATCTCTTCACTCAAAACATCATTTCATGTCGTACTTGA  
 AACCTATGGTATTGGCTGGGGCCAATTCTTTGCTGTTGCATTGCCATCTGGTATCCTGG

CCATGCTTTTGGTTTGGATTATTATTGTTCACTACTTTCAAGATGAATAAGACCAAATTGG  
 AAAAATTTAAGCCTATTAAGACGAAATTCACAGTTAAGCAGTATTATATCATTACTGTCA  
 CTGTGGCCACTATTTTGTGTGTGGTGTGTGGAAAGCCAGATTGAAGGTGCTTTTGGGTCAT  
 CAGGTCAAATTGCAATCATTCCCATCGTTTTGTTTTTGGTACCGGATTACTATCAACAC  
 AAGATTTAAATGCCTTTCCGTGGTCAATCGTTATTTTGGCAATGGGAGGTATTGCTTTGG  
 GGAAGGCCGTCTCATCCTCGGGTTTGCTATCAACCATTGCAAAAGCATTACAAAAGAAAA  
 TTGAGAATGATGGTGTTTTTGCCATTCTATGTATTTTCCGTATCCTGATGTTGGTTGTGG  
 GTACTTTCGTCTCGCATACAGTATCCGCTATTATCATCATTCCTTGGTGCAAGAAGTTG  
 GTGACAAGCTTGGCAACCCCAAAGCTGCTCCTATCCTTGTTTTCCGTTGTGCATTATTGT  
 CATCCTGTGGTATGGGACTAGCTTCTTCCGGGTTCCCAATGTCACTGCCATCTCTAAAG  
 TAGATAGAAAAGGGCGATCGCTATTTAAGTGTCACTGACTTTCTTAACGAGAGGTGTTCCAG  
 CTTCTATTTTGGCTTTTCTATGTGTCACTACTCTAGGTTATGGTATCATGGCATCTGTTG  
 TCAAGGGTAACGCAACCTCTGCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAVPEWQNHMYMDYSELKNLIYTLQTDDELQVGDNEEGFGAGKSSNITDRFKN  
 KFSFKNKEDTSSGMNKDAGIVEETIELRELPTAQTVAAKPSPFRRMKEKIFYKRRSSSA  
 SSVSSTANENLQLDITYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY  
 DIDDDTLFNEPIASTNDEVPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS  
 LLKKSIVNLYIDLQCLKSFIELNRIGFAKITKKSQKVLHLNTRTELIESEQFFKDTYAFQ  
 AETIELLSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ  
 ADELTPKETEYNANKLVGKLDLEYRWRPLRPINLKFTSINNVALPKLFFTKKAYKIYFI  
 ILVTGLLLGIKTFNDAAQHRCMALVECVAFWLWASEAIPHLHTAFLVPLLVLVFKVLTSD  
 GAIMSAASASSEILAAMWSSTIMILLAGFTLGEVLAQYNIKVLASWLLAFAGCKPRNVL  
 LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP  
 ISSPQNIISMSYLPYIGIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK  
 TKFTVKQYIITVTVATILLWCVESQIEGAFGSSGQIAIIPIVLFFGTGLLSTQDLNAFP  
 WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFVVSHT  
 VSAIIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVTAIKVDKRGDR  
 YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATTCTTTGAAAAGATTATTAAGTTCGTTCGTTAAGTTCGCAATCT  
 GCATTTTCATTTAAAGACGGATCATATATTCTTGTGCTTTTTTGTTTTATCTCTTTACTTA  
 CTTGTCGCTTCCATTTCGTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCTCGGCC  
 TCTGGTAACGTGAATAATCCTTGTATCCACCTGCCGACTCTGCTTGCTGCTCTTGAAATC  
 GTACCAGAAGTGAAGTGGCCTTATCTACATTTCTACTCATTTTGAATGCACAGGTATCTG  
 ATTACTGATGTGGTGGCCTTGGCATATAACGGTGTGTCACTTTTATTTGCTCTTTTCATG  
 CATCCTGAAATATTTACCCGCACTACGCAAGAGAACGGAGAAAAAGGTATAATAGGGC  
 AAATGATCATTGACATCGTGATCGTAAGCAAAAAAAAAATAACAATAGGCTCCCTAAATAA  
 GTAGAGTAAAAGCTCTTGAGATGAAGGAGATGACATGAATAATGGCGTAGATAAATGGG  
 TAAATGAGGAAGATGGTCAAGATGATCATATAACAACAATAATAACTTGATGAAGAAGG  
 CCATGATGAACAATGAGCAAAATGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT  
 TGAGGAAAAATATCAAGTGAAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTTCAT  
 CTCTCGTGAACGGCAATGCAACAGTGGCGGTGGTACGAGCA'TTAACGGAACAAGAGGAA  
 GTTCTAAGAGTAGTAATACACACTTTCAGTATGCCTCCACGGCGTATGGTGTGAAGAATGT  
 TGAGTAAAGATATATCTAATAACCAAAGTGGAATGGATGTGGAATAATTGATGATTGTTA  
 CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTGG  
 TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG  
 CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA  
 AGGATTTTCATCAGGGAACATGATGTTTTCTTCGATTTGGTAGTGACTTTGGGTGGCGACG  
 GTACTGTTCTTTTTGTAAAGTTCCATTTTTTCAGAGACATGTACCACCCGTTATGTGCTTTT  
 CATTAGGGTCTCTAGGATTTTTTAACAAATTTAAGTTTGAACATTTTCAGGGAGGATTTAC  
 CTCGGATTATGATCATAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGCACAAATTT  
 ATCGTAGACACCGCCCTGAAGTAGACCCAAACACGGGGAAGAAAATATGTGTGGTGGAAA  
 AACTAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGGTCCAAGTCTTTTC  
 TATCCATGTTAGAATTGTATGGTGACGGCTCATTAATGACCGTTGCGCAGGCGGACGGAC  
 TGATTGCTGCTACTCCGACTGGGTCCACGGCCTATTCTTTGAGTGCAGGTGGGTGATTGG  
 TATGCCCAACCGTCAATGCAATCGCTTTAACACCCATTTGTCCACATGCATTGAGTTTCA  
 GACCCATCATCTTACCAGAAAGTATAAATTTAAAAGTGAAAGTCTCGATGAAGTCAAGGG

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CTCCAGCATGGGCGGCTTTTGATGGGAAAGATAGAATTGAATTGCAAAAAGGTGATTTTA  
TAACCATATGCGCCAGCCCATATGCTTTTCCAACCGTGGAAGCCTCGCCCGATGAGTTTA  
TTAACAGTATCAGTCGACAACCTAAACTGGAATGTGAGGGAACAACAAAAGTCCTTTACGC  
ATATTTTGTCCCAAAAGAACCAAGAAAAATATGCACATGAGGCGAACAAAGTCAGAAATC  
AAGCAGAACCTTTAGAGGTAATAAGAGATAAATACTCTCTGGAAGCAGACGCTACTAAGG  
AAAACAACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAAGTGCAGAGCTTGCA  
AATTAAGCCTTCGAGCGTCCCAAAACCTTCTCAAGCAAGGTTTTTCAGTATAA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNNGVDKWVNEEDGRNDHHNNNNNLMKKAMMNNEQIDRTQDIDNAKEMLRKISSE  
SSSRSSLLNKDSSLVNGNANSGGGTSINGTRGSSKSSNTHFYASTAYGVRMLSKDISN  
TKVELDVENLMIVTKLNDVSLYFLTRELVEWVLVHFPRVTVYVDSSELKNSKKFAAGELCE  
DSKRESRIKYWTKDFIREHVVFFDLVVTGGDGTVLVSSIFQRHVPPVMSFSLGSLGF  
LTNFKFEHFREDLPRIMNHKIKTNLRLRLECTIYRRHRPEVDPNTGKKICVVEKLSTHHI  
LNEVTIDRGPSFPLSMLELYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA  
IALTPICPHALSFRPIILPESINLKVKVSMSKSRAPAWAAFDGKDRIELQKGFITICASP  
YAFPTVEASPDFINSISRQLNWNVREQQKSFTHLSQKNQEKYAHEANKVRNQAEPLV  
IRDKYSLEADATKENNNGSDDESDESVCNCEACKLKPSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2:  
877-1255 (SEQ ID NO 171)

AGGTTGTGTTCTTCAATGATGGGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT  
AACAGCGAAATTTATGACATATTATTTCAACCTTTTACAACTAGTAGATTTAGTGATT  
TATTACCTATTGGCATTCATTTGTGTTCTATATGTGGATGAGGATAGCCGCCTTTCTTCT  
CATCGGAGGCCATATCATCTTTTCGACAATCCTTTTTAAATACTATTTCCATCCGTGCCTC  
TAATAGATTTGTGTAGTTGTCTGGGTGCAATCTTTCCATTTTGTGCTGAACTTTTTTTTT  
TTTTTCATGTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT  
GATCCGCCTCATACTAGCCATTACCCATCTATCCCAGGCATTTATGGGTATGCAACTCATA  
ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTTCCCGTTTCAGCAAGAGGT  
AAAGCCACCAAAGGTTCAAATGCAATGTATGTACGGCGAATACAGAATACTATGTTC  
GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGGAAA  
ATGATTGACAAGCTCACAATTTATTAAACAAGTAGCAATTGAGAAAACTATTACTCGCG  
GCAAGCTTCTGAGTTTACATTAAATCTGTAGAGCAAATTGAAAATGTTCGCATATGTGCTG  
AAGGGTTTGTGTTGTTCCATCTTATTTTGCATAACATAGTTATATTTACTTGGTCGCATAA  
AAAATATTTTTTACTAACGTGAAGTTTCTTTCTTTATGATGTACGCACGCACGTCTGTGC  
TTACTCCATAAATGAACCTTATTTCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA  
GACCATCACTTTGGAAGTTGAATCTTCTGACACCATTGACAATGTCAAGTCCAAGATCCA  
AGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA  
AGACGGTAGAACTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT  
GAGATTAAGAGGTGGTATCATTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACCTG  
TGACAAATCTGTTTGTCTGTAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG  
AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN  
IQKESTLHLVLRRLRGIIIEPSLKALASKYNCDSVCRKCYARLP PRATNCRKRKCGHTNQ  
LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAACAACATAACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTCAAGTC  
AAGCCATGTCTTTACTTCGTTTAAATGTTAGAAACAATCGCTTATTTGTTTTCTTAAACA  
AATATATTAGGTTCAAGGTCTTCGCAGGTGTAAGAAAACCCGTGGTCTCCATATTCTTAA  
GTATGATAAATAAAAAAACTTAATAAATTATTAATTGCTTCAAACCTTTTTCTTTTTT  
TAGTTTTTAATATTCAAACGTTATCTTATGAACGCCCAAATAGGGAAAAATCCTGGC  
AAATTTTTTATTGCTGTCATCCAAGGCTATGCTAGAAAAATTCAAGAGCTTGGATGATTTA  
AAAAGACACTCTCAATCGAGAAAGTTTATTCTTTGTTATTCTGCTTTACCTGATCATATT  
CCGGCGTATTGTTTCTAATCAAGTGATTTTCGATATCCAGTTACGAACCATTTACAACATT  
CCTGAAAATATTGCGTATCAATGATATTTGCTCCTTCTTTCTCCCTCATTAATAAATATTC  
TCCTGGTAAGCTTTCTAATCAGCCACAGTTTGTGCTGCCAAAACCTTAAACGTCTAGTTCCA  
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATTCTTCATGGAGT

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TTTTAAACGATTTTCGACACCGCTTTTCCACAGTATACCTCATAACATGATGCAAAACCATT  
TAACCCCTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAG  
CAGATTTACAATCTGATATTGCTCAGAGTTTCCGTTCACTCAATTCCAAACATTCATTA  
CGGCCTTTCCATGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTC  
CCCAACACTTCATAACAGGTGAGACAGAAGCTACCATGACTAACTCATCTTATGCCAGCC  
AAAAAACTCCGTTTCCAATTCTGTTCTTCTCGACAGCGAACGCAGGCCAGTCCATGA  
TTTCCATGGCTAATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACCTCTTCTT  
CAACATCCAGAACTAGTCAATCACAGAATGGTGCCCATGCCAAAAGCTTATATTTCCCCA  
TGGCGTTGTTTCGGAATCTTTGCAGTTGCCCTTTAA

YLR040C, 224 aa (SEQ ID NO 174)

MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDLARSAAADADMAFFMEFLNDFDT  
AFPQYTSYMMQNHLTLPQPVADYYHMYDLASTADLQSDIAQSFPFTQFQTFITAFPWYT  
SLLNKASATTIYLPQHFITGETEATMTNSSYASQKNSVSNVFPSTANAGQSMISMANEE  
NSTTALISASNSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:  
950-1618 (SEQ ID NO 175)

GCACCCTTTTTCTTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTTCAACACTTTT  
AATATTTCCCTTTTACATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT  
TACCTATTTCTTAAAGGCCTTTGTCACTTCTTTATGGGAATGGCGCTACTTTAATTTTCC  
GCCTACTTTGAAAAATTTACCAAGGCGAAATGAGTGCGCTAGGCGGAAGTTCCAGGGCA  
CGGTACCCGAACCTTTGTGCTGTTTCGAACGAGGGTCCCGCTGGAGGTTGACGGACGCGG  
GAGGAGCTGGAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTTCGTGGTAGG  
GAACATCACCTTCTCTAGTTTCTGTAAAAATAATATGATCAAGTTTGAATCCTCGTATTG  
AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAAGAAGAGATAA  
GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTTGACTCCAGAGGATG  
CCCAACTTTTGTGTCGCGCTAACACCCATTAGGTGCTAGAAACGTTCAAGTATGTACAC  
ATATCCCATACGATTATGTTCTATAGATGATAAATAGGTCTCGAAAAGAAATATGTCCCCGA  
TTTAATCATATTTGGAGGTCAGAGGACCAAAGGTAATTTGAGAGGAATTTTGAACACGCC  
GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAACTCAATAAG  
AATATACATCCTCGACTGTGTCAAAGATTATGAACTCCGATGAAACAGTAAAACGTCAAA  
AAATTCACGGGATATAATTCGGTACTTTTATGGATATGGAAGAAAACATTATATATGCA  
CAAATGAACGCTCTTACTAACATAATTTATCTTTCTCTCTTTTGTAGGTCCACCAAGA  
ACCATACGTTTTCAATGCTAGACCAGATGGTGTTCACGTTATCAATGTTGGTAAGACCTG  
GGAAAAGTTGGTTTTGGCTGCTAGAATTATGCTGCCATTCCAAACCCAGAAGATGTTGT  
TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG  
TGCTACTCCAATCGCCGGTAGATTCACTCCAGGTTCTTTTCACTAATTACATCACCCGTTT  
TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA  
GGAAGCTTCTTACGTTAACATTCCAGTCATTGCTTTGACTGATTTGGACTCCCCATCTGA  
ATTGTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTTAATCTG  
GTACTTGTGTTGGCTAGAGAAGTTTGTAGACTAAGAGGTGCTTTGGTTCGACAGAAGTCAACC  
ATGGTCCATCATGCCAGATTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC  
TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGTTAAGGAAGAAGTCACTGA  
AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)

MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA  
ARIIAAIPNPEDVVAISSRTYGQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL  
VIVTDPRLDAQAIKEASYVNIPIVIALTDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE  
VLRLRGALVDRTPQWSIMPDLYFYRNPEEVEQVAEEAAAAEEGEEEEVKEEVTEGQAEAT  
EWAENADNVEW

YLR088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)

CTTCCCATGTAGAATATCATTGTCAAACATACTACTACCGTGAGAATCCAATCTACTAA  
AAGACCCAGCTAAAGTCCTTTTGGTGTGTCAATGGAACACCACGTAATTGTGAAATAGCT  
TCCATGCTTGCTAACTTATTACCGTCAATAGAAGACTTGAGTCAGGTGGCTTTAATGAGT  
ACTATTCCTTTTTTTTTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTTTTG  
AGTATCCTGTAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCCAACAGCTTTATAGTGG



GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG  
CATCGTGAACCTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACAATACACGC  
CGGCTACACTTAGAAAAGAAATGACATTTGCTGTCTTATAAAAGGACTTGACAGACCAAAG  
ACGCGTATAATAACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA  
TGGGGCTTGTCCCGGTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT  
TTGGGTTTATTTCTATAGCTATTCTGCCTATGGATGGACAGTACAGAAGAACATACATTT  
CTGAGAATGCATTGATGCCCTTCACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA  
TTTTGAGGGGCTATCGATCTCAAATTAAGAAATGGTAAACATGACTTCTATGGAAAAGAA  
ACAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG  
AACAAATATGGAGAAACATTGTACGGTGTAAATGCACGCTCCTAGGGGTGATGGAACGAAG  
CGATGGTGCCTTCCCGTTCATGGTTTAATTCAGATGATGAATTCAATATTGGCGGCGCAG  
CTTTGGGTGTATCTTTAGCAAGATTTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA  
TTGTTGTCTTCAGCGAAAATCCTCGTGCAGCATTAAGATCATGGGTTGAGGCATACCATA  
CTTCCTTAGATTTGACTGGTGGTTCCATTGAAGCTGCTGTTGTGTTGGATTATTTCGAGTA  
CGGAAGATTTCTTCGAGTATGTAGAAATCTCATACGACGGTCTGAATGGTGAGCTGCCCCA  
ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT  
TGCACGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAATAATAT  
TATGCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTAAAAAGCCCCATGGTAACGAGG  
CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAACAGTGGTCATG  
ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG  
AAAAATTTACCAATCGTCTCTCTTTATTTGTTATTAGCACACGTCAGTTCGTATCCA  
TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTCGCCATAAGTTTCAATTA  
ATGCATTTATAAACAATGCTTATGCAAAATATATCCTTATTTTCCGAGTATAAATTGGTAG  
CGTTGTTGGTTTGGTTCGTGTCAATTGGTGATATCATTTGTTGTTTTCACAAGCGTTTCTTC  
TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA  
TACTTTCCAGAAAAATTCACATCTCAGAACCCTATCATACAGGTTGAAAAATGTTGCTTT  
TTTTATATTTTCAGTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC  
TGATCGGCACATTTGGCATTTCCTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG  
AACATGAGGTGACAACTCAATCCTCTAACCCAAATAAAAACTGAGCCGAAAGATGAGATAG  
AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAACAAAAAC  
TAAAAAATTTAGTACTATTAATTTTGACAAATCCATTTATTTCAATAACCTTATTTCGGAC  
TATTTTTTGTATGATGAATTTTCATGGATTTGATATAATAAACAACTGGTTTCAGCATGGT  
TGGATTTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT  
TGATATTAGCGTCATCGTTTGAATCTAAATCTGTCTAGTAAGGTCGAAAGAAAAGCAAA  
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIIALLPVISMLCALFGFISIAILPMDGQYRRTYISENALMP  
SQAYSYFRESEWNILRGYRSQIKEMVNMTSMERNNLMSGWLQEFGKTAIYENEQYGETL  
YGMHAPRGDGEAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIIVFSEN  
PRAALRSWEYAYHTSLDLTGGSIEAAVVDLYSSTEDFFEYVEISYDGLNGELPNLIDLVI  
AISITEHEGMKVSLHGLPSDQLTNNNFW SRLKILCLGIRDWALSGVKKPHGNEAFSGWRI  
QSVTLKAHGN SGHDITTFGRIP EAMFRSINN LLEKFHQSF FFYLLLAPRQFVS ISSY LPS  
AVALSIAFAISSLNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFLLIPSSGL  
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFSLVSTSLLMINFAMALLIGTLAF  
PMTFVKTIVESSSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLKNLVLL  
ILTNPFISITLFLGLFFDEFHGFDIINKLVS AWL DLK CWSW FVLCIGWLP C WLLILASSF  
ESKSVVVR SKEKQS

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAAGATAGCTTGATCATCCTAAGCGGGTCGCATTTTACTATCCCCAGTTCCG  
AAGAATAACAAGGCTCAATGCATATGCTGTTTATCGTGCTCACAAGGCGGTATGACGTTT  
TTAGCAATGTAATTATATTA AAAAGATCTTCAGTCACTATGAGTGGTTGATTGCCCCATA  
GAGAGCTATAAGCCGACGTGAAAGCTGCTGGTTCCAGCTTGGCTCATGTGCTCACCAGTC  
ACTAGTCACCTGGTCGCATTCAATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA  
CTTGCCAAGGGATTAGAATCACGTAAGACTCTTGATCCTTAGAAGATATTTCTGACAAAG  
AACCACCTAAGCCATGCAAGTTTTTTTTTTTCATTTGGTGGCGAAACAAAGGTGATGAAAG  
TTTCTTCTTGTACAAACGCCAAGCCCGATAGGTGAGACAATTCCTGAAGTAATGGACCTC  
TGAGTAAGCATATCAGTCGAATGAAGTTCCAATATGCGTTGGCCAAGGAACAGCTAGGCA  
GCAACTCGCGCAGTGGCGTCAAAAACTAATAAGTAAACACCCTGGCTTCCGGAATACT

10/030019

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ATTTCTCTGATCTCTCATTTTCTGTGTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAAA  
CTACAATCATATCTTGTATGCGGCCCGCAAACCAAGAGATTTATCCTTTGAGACATTGTG  
AGACCCTCCGTTTCGCAACCGTGCTCTCTGTTTTTCATCACTATATGCACGCTCTTTCCAAA  
GCTCCTGCACTTTGCACGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA  
CCTAA

YLR159W, 114 aa (SEQ ID NO 180)

MKFQYALAKEQLGSNSRSGVKKLISKHHLPEYYFSDLFSVQWDSRAIEKTTIISCM  
RPNQEIYPLRHCEFLRSQPCSLFSSLYARSFQSSCTLHVAEPPGFHMYGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181)

ATCAAAAAGAGTGTTCAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA  
GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT  
ATCGATAATAAATATTCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGATCT  
ACCTGGGGTTAATGAACGAGAAGTTCCTTGAGATATCTTTCTGTTTACCTCCGTGCATCC  
TGTAAGGAATTGGGTTTATCATTTATCATTTATTTTAGTACAACTTTTTTTTTTTGGCCC  
GGGCGCACTTTTTCAAGCGGTGGGAACCTCATCAAAATGAAAACTAGATACTTTTAGACT  
TATTAAATGGTTTAAATATTTTGAGATGTTCTGTTATATCAGAACTTCCTTACTTCTATC  
TTTTATTCCAATACAAAGAAGTCACAAGATTACTTGGTAAGAAAGAAGCAGTTAATTTTT  
AATTTTGCCGACAAGCCAAGATGCAAATTTTCGTCAAGACTTTAACCGGTAAGACTATTA  
CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG  
AAGGTATTCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGAAGATGGTA  
GAACCTTTGTCGACTACAACATCCAAAAGGAATCTACTCTACACTTGGTCTTGAGATTGA  
GAGGTGGTGGTAAGAAGAGAAAGAAGAAGGTCTACACCACCCCAAGAAGATCAAGCACA  
AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCTACTACAAGGTGCGATGCTGAAGGTAAGG  
TTACCAAATTGAGAAGAGAATGTAGCAACCCAACCTTGTGGTGTCTGGTGT'TTCTTGCTA  
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCAATTCGCTCTACAAGGTAAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN  
IQKESTLHLVLRRLRGGGKKRKKKVYTPKKIKHKHKVKLAVLSYYKVDAEGKVTKLRRE  
CSNPTCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)

AGCCACCAATTCCACCAGGCCCGGCATTCAAGTACTTGTAAGAACACCAACAGGCAAAGT  
CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC  
CAACCAATATGTCGGGGAATTGGTGGGCAAATGAGGTGATTCGGCCAATATCGAAATATT  
GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTTACCT  
CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT  
GAATAAAAACATTCTCAGGTTCCGAAATTCATGAATTTGCACTGGTTGTAGAAAGCAT  
AATAGTCTGATGGAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGTAGGTT  
TATAAAACGTAATTAAACAATGAATTCAAATTTGCAAGTGAGACTATTCATTACTGCAACTT  
CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGGAAGAATAGGTAAGTCAATGCTGA  
CCCAAGGCACCTTTCTCTGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAAT  
CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA  
AAGAATTCCCGCATAAGTACGTACAGGCTTATCGTCGGACGATAGTCCCATGGATTTAA  
ATGTAGGGATGTTGAATTTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG  
CTTTCTCCATAATTACCAGTTTGT'TTCTTTTCCACAGAATATTTAGGCTTAATATGTA  
CGTATTGA

YLR232W, 115 aa (SEQ ID NO 184)

MGASSGRIGKSMILTQGTFLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFPHKY  
VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIIITSLFLFSTEYLGICTY

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)

GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTAGGTGCCCTGCA  
ACACTAGTCATGGTAACCTTCGCAGTAGCCCCATTTCTGGCAAACGGGAACCCACTAAAC  
ATGAAATCATAGTTCTTTACATACATGTAGCCGGAATCCCTTGAAGTTGATCTGCCTCCT  
CCTAGGATCTGTGAAACTGCCTTCGCTATAGAATTTTCTCTGCGACACATAGCACTTTC  
ATTATTGTCTATAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAGGTGCTTTC

AAAAGCGATGCCCTCTTTATTGACAGTTACTAATTCGCCAAACTGCTTTT'TTTTATCAAT  
GTGATTTTCGCGTTACAGCCAT'TATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG  
CCTGTATGATCCGACCGTTTTTAGCAAAC'TATCAGGGGAAAAAGTATAT'TCCATTAAAT  
GACACATGCCACCATAGATAAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT  
TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCGATG  
AAAATGCATATATCACGTTTCAGATGCTTCTCGGATGGAATACATCGCAAATCTACTAGGT  
TTCTCGAAGAGCTACTTTT'GAAACAAGAAAATATGTACCATAATAACAAT'TACGAACGCA  
TAAATGATTCCGTGATACCATTGGTTC'TGAAACTTTTATGGCT'TCAAATTCACGAACCTA  
CACTCCAATGGTTT'GAGCACTGGTTCATGATATCATGCGACTAAGTAACAGAAGAAAGT  
TCAGAGTTTTTAGAATTTTTCAAAAAAAATGATTCAATTTTTTCAAAATTACACACAGGT  
ATTACTATGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCCGTTATT'TCAA  
ATGCTCTCTTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA  
AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT  
GCGTGATTAATCTAGGTTCCACACATTTTTATAAAACACTACTAAACAAGCCGTCTAACA  
AACCCAAGAGTGTGGAAGGTTTTGAGAAGTCTATTAGGTACTTGAATATTGCCTCACTCT  
ATCTCCCAGCCGTTGGAGATACTTATTTTCAACGAGCGAAAATTTACTTGATCACTGGGA  
AATTCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTGGTAAGGATTCCGTTCTAAAT  
GTGCGTTAAACAATTTGAAAGATTTCATTTTGACTCCTGATTTTCCGGAAAGAAGACGTC  
TGATGAAAAAATTTGGCAATTCTTGTGTCAAAAGATCTCAAAGGTGAGAAATCATTCTTTG  
AAGGTCAAATTTGTTT'GCAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCA  
GGAACGCATCACGTGCTTCTAATTGT'TGGT'TAATTGAAAGAGCATTTACAAATGGCTGCAT  
TAAAGTATCATTACAGTAATATTAATGTTTACTTTGAAAAC'TGGCTGCCACAATGGGAA  
GTTTCGATCTTATGTTTACAACTCGAAAAAGTAAGGAACAAAAGAACAACAACTCAAATATG  
CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTAGACTTGAGCTTTGATTTTATTGCTAATA  
TCATAGACGTCGTCATCAAACCCCTCTGGCAAAAAACATGGAAGACTTTCGATATCTAG  
CCATTATTCGTTT'GCTTATGTGCTGGATTAAGTCATATAGATCTATTTTGCAGTACACTC  
ACAGACACAGGAAGTTT'GCACTTCATTTCGCCCTTGTTGCTGAACGACTTGATAAATAGTC  
CACTGAATTGTTTCAGGAAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTTAGAG  
AAGATATTATTTTTCAGGGAATTTTCTTGCTTAAC'TTGCAC'TAACAGATTTTATATGAGC  
ATTATGTGTATGATTCTCCCGACATGATTAATAATATAATTGGATGCCCTACATTGACTA  
AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTGGCA  
TGAAATTTTTTAGAGAAAAATGACACCGGCGTCATATGGAATGCCAGCAAATATAAGTTTG  
ATTTAATAAGCCCAAATAT'TAAAAATAAACGCCAAATAGCATTATCGGAAATTTCTCTCCA  
AAATAAATGTAAAAACACAACAGGAAAGAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA  
GAGATGAACAACACGCGCAAAAGAGCCGGGAAAAATAGCTGTGACAGAACTGGAAAAACAAT  
TTGCAAAATGTCCGGAGAACAAAAAATTGTCTCCGCTCCAGAAAAAGATGGCGTTTCTT  
CTGAGTTGGTAAACATGCTGCTTCACGAGGGAGAAAAACTATCACTGGCCCACTATCCT  
CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG  
TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)

MDNEEVNEECMRLLFFKNARALDKHLTSRLTCDENAYITFRCLDGIHRKSTRFLEELL  
KQENMYHNNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF  
QKKMIQFFKITHRYYYDIIIEHLCAKYDMNSVISNALFAKLNLMQYTDGLSTHEKIIILNTS  
NPLTFSIVISLQRCVINLGSTHFYKTLNKPSPKPKSVEGFEXSIRYLNIAISLYLPAVGD  
TYFQRAKIYILITGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDFPERRRLMKKLAI  
LVSKDLKGEKSFFEGQIVLQFLSIVEHTLVLPQSWNASRASNCWLLKEHLQMAALKYHSGN  
INVILENLAATMGSDLMFTTRKSKEQKNKLKYADLSERQVFFLDLSFDFIANIIDVV  
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILQYTHRHRKFCTSFALLLNDLINSPLNCSGN  
IYSHRPKRSYLFREDIIFREFSCINFALTDENDDYVYDSPDMINNIIGCPTLT'KVLSPE  
ECVLRIRSIIFSGMKFLEKNDTGVWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ  
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA  
ASRGRKTITGPLSSDFLSYPDIDADEDITVQVPDPT

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCACGGAATCATTTATGCGTTTCGTAATTGTTATTATGGTACATATTTTCTTGT  
TTCAAAAGTAGCTCTTCGAGAAACCTAGTAGATTTGCGATGTATTCCATCCAGGAAGCAT  
CTGAACGTGATATATGCATTTTCATCGCATGTCAACCTTGATGTTAGATGTTTATCCAGA  
TGCGCACGAGCGTTCTTGAAAAATAATCTCATACATTCTTCGTTAACTTCTTCATTATCC  
ATTATCTATGGTGGCATGTGTCATTTAATGGAATATACTTTTTCCCTGATAAGTTTGTCT

AAAAACGGTTCGGATCATACAGGCATGTAAACATTTCCATTATCCTTTTTTGACATTGGATA  
ATGGCGTGAACGCGAAAAATCACATTGATAAAAAAAGCAGTTTGGCGAATTAGTAACTGT  
CAATAAAGAGGGCATCGCTTTTGAAAGCACCTTCGTCTGTGCGCTCGCTTCAGCTACGTA  
AAGGTGTATTATAGACAATAATGAAAGTGTATGTGTGTCGAGAGAAAAATCTATAGCGA  
AGGCAGTTTCACAGATCCTAGGAGGAGGCAGATCAACTTCAAGGGATTCCGGCTACATGT  
ATGTAAAGAACTATGATTTTCATGTTTAGTGGGTTCCTGTTGCCAGAAATGGGGCTAACT  
GCGAAGTTACCATTGACTAGTGTGTCAGGGCACCTAACAGGCATTGATTTTCAGCCATGATT  
CGCATGGGTGGGGAAAAATGCGCCATCCAAGAGTTATTTGATGCGCCACTGAACGAGATTA  
TGAATAACAACCAAAAAAAGATAGCAAGCAACATCAAGCGAGAAGCGAGGAATGCAGACT  
ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGGTTGGGAGATAGGC  
AGGAGGCCAAGAGAGGCAACAGGCTCATACAAAATGATCAAGTATACCGGGCAGTCTTTT  
CGCATCTCGAAAGACAACACATATTAATGCAGCACGAAACCCAAGTCGATTGGATATGA  
AGAGTGTGCACGCTGTAGGCACGCGGATTGAAATCGATCTTCGAGCAGGTGTTACATTCA  
CCAGACTCTTAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCATTGACCAAGG  
ATGGTGCAAAACACCGCGGTGGTAACAAGAACGACTCACAAGTCGTATCGTATGGTACAT  
GCCAGTTTCCAACGCTCGGCTTTGTAGTAGACAGGTTTGAAAGAATACGAAATTTTGTTT  
CCGAAGAGTTCTGGTATATCCAATTGGTAGTCGAAAAACAAAGACAACCGCGGAACAACAA  
CGTTCCAGTGGGACAGGGGCCACTTGTTCGACCGGCTGAGCGTGTAAACGTTTTTACGAGA  
CATGCATCGAAACCGCCGGCAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA  
CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAACTGCGCCCGGTACC  
TGCGTCTGAACGCCAAACAATCACTAGACGCAGCAGAAAAAGCTATACCAAAAGGGGTCA  
TATCGTATCCAAGAACAGAGACTGATACTTTCCACACGCAATGGACCTAAAATCCTTGG  
TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGCAGGCGGCAGAACCGCCTGGGCACTCGT  
ACGCGGCATCGCTGCTCCAACCCGAAAACACAAGTAACAATAACAAGTTCAAGTTTCCAC  
GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC  
CTGAAGCAAATGTTTCGCCAGTGGAAAGAAGAGTATACGAGTACGTGGCCAGGCACCTTT  
TGGCATGCTGCTCAGAGGACGCCAAGGGCCAATCGATGACCCCTTGTGTTGGACTGGGCG  
TTGAACGTTTTCTCAGCTTCAGGTCTCGTAGTCTTAGAGAGAAATTTCTTCGATGTTTACC  
CTTGGGCCCGATGGGAAACCACCAAGCAGTTTACCGCGGCTTGAAATGAATGCCCTCGTAG  
ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCCGCCCAAGCCGATGACTGAGA  
GTGAACTCATTCTCCTCATGGATACAAACGGCATTGGCACAGACGCCACCATTGCGGAGC  
ACATAGACAAGATCCAAGTACGTAATTACGTTAGGAGCGAGAAAGTAGGCAAGGAAACCT  
ACTTACAACCCACGACCCTGGGTGTCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG  
AAGACTCCTTTGCAAAGCCCTTCCAGCGCAGAGAAATGGAGCAAGACCTCAAGAAATCT  
GCGAAGGTATGCCTCCAAGACTGATGTTGTAAAGGACATAGTCGAGAAGTATAGGAAGT  
ACTGGCACAAGACGAATGCCTGCAAGAATACTCTCTTGCAAGTTTATGACCGTGTCAAGG  
CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188)

MKVLCAEKNLSIAKAVSQILGGGRSTSRDSGYMYVKNYDFMFSGFPPFARNGANCEVTMTS  
VAGHLEIGIDFSDSHGWGKCAIQELFDAPLNEIMNNQKKIASNIKREARNADYLMIWTD  
CDREHYIGWEIWQEAQRNRLIQNDQVYRAVFSHLERQHILNAARNPSRLDMKSVHAVG  
TRIEIDLRAVTFTRLLTETLRNKLNRQATMTKDGAKHRGGNKNDSQVVSYGTCQFPTLG  
FVVDRFERIRNFVPEEFWYIQLVVENKDNNGTTTTFQWDRGHLFDRLSVLTFYETCIETAG  
NVAQVVDLKSPTTKYRPLPLTTVELQKNCARYLRLNAKQSLDAAEKLYQKGFISYPRTE  
TDTFPHAMDLKSLVEKQAQLDQLAAGGRTAWASYAASLLQPENTSNNNKFKFPRSGSHDD  
KAHPPIHPIVSLGPEANVSPVERRVYEVVARHFLACCCSEDAKGQSM TLVLVDWAVERFSAS  
GLVVLERNFLDVYPWARWETPKQLPRLEMNALVDIAKAEMKAGTTAPPKPMTSESELILLM  
DTNGIGTDATIAEHIDKIQVRNYVRSEKVGKETYLQPTTLGVSLVHGFEAIGLEDSFAKP  
FQRREMEQDLKKICEGHASKTDVVKDIVEKYRKYWHKTNACKNTLLQVYDRVKASM

YLR238W, 1937 bp, CDS: 501-1937 (SEQ ID NO 189)

CTTCGTTACACTTAATATTAATAACAGCTCTTTCTTAATAATAACATATACACTAGAT  
ATATAATACCAATAAATTAATAAAGAAAAACAAAAATAACGTAGCTTTGTACAG  
TCGTAAAAAAGAACAATAAACCAATCTTATGTCAGCGTCTAACTAGTCCTATTATAT  
TCCAATATATTAAGGGGTAAGGACTACTATTATTCGCCCTGAATTGAAATCTTTTAGAAA  
GCACCTGTTCTCTCTCTGGTGTCTTTTTTCTCATCTATTATCTAATTTCTTCAACCTT  
CGTTATTTGTTGTTATTCGGTAATCGTGGTGTCTCAACTTTTGAAATTTCACTTGTTTACC  
ATAACGGAACATAATTAATAATTTGTTCTTGAAAGTCACAAGCACTACGTGAACACAAAA  
TTAAGGCAAGAGTGACAAAGTAACCCTCACAAGGAGCCTGTCTGTTGGTTATATTGGAAGC

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TATAGATATAATCGAATCCAATGACTGGTCTGGACCTGAAATAAATAAGGAGGAGCACC  
CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA  
TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG  
ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAAATATACTT  
ACATTCTAGTCCTCACATCACTAAATGGAACTTT'TGAGAGCAAACATGTGGTGATACCAT  
TTAAACCAGATGGTTTGAATTTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT  
CATCGCTCAGGGGCGGTAAAAGAGTGGATTACACACTTTTCCCAAGTAAGGTCCGATA  
ATGGTAATTTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTTGTTAAGTTGCGACCCGC  
TCACGGGTAAGGTATATATACGAGACTTAAATCCAGTAATGGTACGTTTATTAACGGTC  
AAAGAATTGGCTCAAATGACGTAGAAATCAAGTTGGCGATGTGATAGACTTGGGACAG  
ATATAGATACGAAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAAC'TATTTGTAC  
AACCTTTATTAGAATCACCGATTTT'TGAAAATGAAGATAGTGATGATTGCCATACAATTA  
CAGAAAAAGAGGAGGCTGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG  
AATTGGAAGAAGTTATCCTGGGCTCTGATACAGAAATACTGAGTGGAATTTT'TATTAATA  
ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATGGAAATTC  
CATTTTCCAAATGCGATAATTTTAAATTACAGTCGATGGAGAATTTCTTAATTAATTATA  
CGACACATCTAGAATACACGAACAAACTTTTAGTGGAAAAAAATGATCAGCAACTGGTAA  
AGCTGCAAAATGGATTAAGAAGGAACTGTCTGGGGAAATACGAAAAGATTATCGAACAAA  
ACAGAAATCAAGTAAAACAGTTGGAAGGGGACCATATGTTTTTCAAAAAGTCATTTGAAG  
TGAAGAAAAGAAGAAATAATGAAAAGCAAAAAGCATGGAAAGGGGAAATAGAAGACTTGA  
AAACTAGGTTAGAAGTGAACGATATAAGAATTCACAAATGATGAAGAAGAACAAACAGA  
AAGAACAAGAATCTCAACTGCATCTAAAAAAAGACTACCGAACATGACACTAGAGGCG  
TCCCGGCATGAATCCTTAAGGGTACTGCACAAATTTAGCATCAAGAACACGCTATGTAATC  
ATTTACACTATTAACATTTGGAAC'TATTTCCATCGGGATTATAGCTATTGTCTTCAAGA  
TCCTTTCCCCCAACTAG

YLR238W, 478 aa (SEQ ID NO 190)

MTGPGPEINKEEHPSSPGKKQITYNSIPKNANLIDGSTNSSKRPIEKYDKRIADPTKSYF  
PHSISRTPRRKYTYYILVLTSLNGTFESKHVVIPFKPDGLKLGRPVANSNSSSSSLRGGK  
RVDSTHFSQVRSDNGNFDNRVLSRNHALLSCDPLTGKVIYIRDLKSSNGTFINGQRIGSND  
VEIKVGDVIDLGTDIDTKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA  
AITSHIYGDSNNLEEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN  
FKLQSMENFLINYTTTHLEYTNKLLVEKNDQQQLVKLQNLRRKLSGKYEKIIEQNRNQVKQ  
LERDHMFFKKSFEVKKRRNNEKQKSMEREIEDLKTRLEVERYKNSQMMKKNKQKEQELST  
ASKKKTTEHDTRGVPGMNPKGTDKFSIKNTLCNHFTLLTFGTISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191)

CGAACATACCTGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGAT  
TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCATTTTTCAGAATCTAATCAATGATA  
GTGTAATGCTTTTGCTGCCTATCGTGATTGATCATTACATAATCTGGCACAATACTGGC  
GGACCTGATTTGGTGATAATTGGTGCTTCAAAATTTAAATTTTCGTCACTCTAATTATACT  
TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT  
AATTTGCACTTTT'TTATTTAAAAATAAAAAATCACAGTTAATTTTTCATGATCTTGCAAA  
GACACGCCTCCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAAACTCAACACTT  
TAACATAATGGCGGGCACGAAGGCTAAACAAACAAGATTAGCATTGAATGCCTTTTTTGG  
GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT  
ATCTTGATACAGATTCCAGATGAGCATCATGATTTTCAGAAAACCCACCGCCAAGGTTGTAA  
CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTTGCTTTGCTTTCTCAATTC  
TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC  
GCTTACCGTCTCGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTGTGATAAGATAC  
GGGACGAACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTGTGTTTTTCA  
AAATGTGCATCAAAATTAATTTCTATTTTTTGTCTTCTCTGTGTGCGTTATATCTCCAG  
TAAGATATCATTTTACTGGAAAAATTGATGACGGCAACGATGATGATGACAGTGAAGTT  
CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG  
CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTTCTCACATATTTCTTCACCT  
TCATAGCAATTAATAATGGCAGTTGCGGAAACAAAGCACGTCGTAAGTACTAGGCAAGCTT  
ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCGATAG  
AGCTTCGTGATTCGGAAGCCTTAAAGACCAGAATTGAACAATTAATAATCGGCACCGTTT  
CATCAATCACTATTTGTGAGAGTGGGGTCTTTGAACAAGCTATTTCAITGTGCGGAAGA  
AAATACTCAAAAACCTGGAATTAATAATTCAGAATGTCCAAGGGAGCTCCGTACTCGAC

AACCATATTTCGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG  
GAGAAAAATGTTCCATCAAGCAATAATAATGACGAGGATACTATACTATATTCTCAAATTT  
CTCTTGGAGAGAGACCAAAAAATGAAAATTGGATATCGTGGTATCTTTGGGAAGGAAGTAG  
ATGCCATAGAGTACCTGGAGCAGCAATTAATAATTTATTGATGCTGAAATTTATTGAAGCGA  
GGAAACAACACTACTCCGCAACACCTACGGCATTCGTTACGATGGATTCTGTTGCTAATG  
CGCAAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG  
CTCCTGCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTAA  
CAAAAGTTTATTCTACTACCGTATTTATAGGCCTTTCAAGTTTGTTTTTAGTCATTCTTG  
TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTCGAAATTCGGCCAAGCGTAG  
GGCAGCTACTAAAAGATCACCAGTGGGCGGCTAACATTGTAACGGGGCTATTACCAACCT  
ATCTCTTACATTTGCTTAACTTTGGAATCCCTTATTTTACGAGTATTGACTTCTTATC  
AAGGATTGGTATCATAACGGAAGAGGAAATCTCACTTGTTCAAAAAATTTCTTTTATA  
TTTTTGTCAACCTTTTCTTAGTTTTCACATTGGCAGGTACAGCATCTAATTACTGGGCGT  
ACCTCAGCGATACCACCAAAATTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT  
TATTCTATGTCGATTTGATTATATGCAAGGTATTGGTATGTTCCCGTTTAAGTTGTTAT  
TAGTTGGTAGTTTGATCGGCTTTCTCTAGTGAAAATCAAGGCTAAGACACCTAGGCAAC  
GGAATGAACTTTACAATCCACCGATATTTAACTTTGGACTACAATTACCACAGCCAATTC  
TGATTTTGAATTATAACGTTGATCTACAGTGTAATGAGCACGAAAATTTTGACTTCAGGGC  
TGGCGTACTTTATTATTGGGTTTTACGTCTATAAATATCAATTGATTTTTGCCACAGATC  
ATTTGCCCATTTCTACAGGAAAAGTATGGCCATTAATTTTGAAGAATCATCGTTGGAT  
TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTGCAAGGAGGATGGGTTT  
TGTCATCTTGCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCTTATATGATTTGAGA  
AGAACTATTTGCCGTTGTCAAAATATATCGCATTTGAGTTCAATTCGCGAGTACGAAAAG  
ACAATTCACGGTGAATTCTGCCAATGAGGAAGAGTCGTATGCATACCCTTACGCTGTGA  
GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAAASYLDTVPDEHHDFRKPTAKVVTQTSLTIATSLGIFALLSFSILLKKWPR  
LYASRRYKDDGNLRLPSWNQSSFLGWLTVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL  
SIFCFVSVCVISPVRYHFTGKIDDDGNDSSSLIHLVKRIVEGSGDGDNHSAPERTNV  
YLWMYVLFYFFTFIAIKMAVAETKHVVSTRQAYLGKQNTITDRTIRLSGPIELRDSEA  
LKTRIEQLKIGTVSSITICREWGPLNKLHFCRKKILKNLELKYSECPRELRTQPYSENY  
HLLGNEQSGAVTHGENVPSSNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE  
QQLKFIDAEIIEARKQHYSATPTAFVTMDSVANAQMAAQAVALDPRVHYFITRLAPAPHDI  
KWDHVCLSRKDRLTQVYSTTVFVIGLSSFLVIVPSYLATLLNLKTLKFWPSVGLLKD  
QWAANIVTGLLPTYLFTLLNFGIPYFYEYLTSYQGLVSYSEEEISLVSKNFFYIFVNLFL  
VFTLAGTASNYWAYLSDTTKIAYQLATSVKEFSLFYVDLIILQIGMFPFKLLLVGSLIG  
FPLVKIKAKTQRNELYNPPIFNFLQLPQILILITLIYSVMSTKILTSGLAYFIIG  
FYVYKYLIFATDHLPHSTGKVVPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSSCLFP  
LPVVTLCFLYDFEKNYLPLSKYIALSSIREYERDNSTVNSANEESYAYPYAVSELEGPM  
LD

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)

TTCAAGTGCACCTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAACTGTGGCCAT  
TATTTTGTGGATCGTGTTTTGCCAAAGATATGAAAAGGGCACCAATGCTTTATATGC  
CACAAGGAGACCCACGGCAGTGCAAAAGTAGCATCTGACTTACAGAAGATGCTAAATAAA  
AGGAAAAGTTGATGGAGAATGCCATATCACCCCAAAATTACACGCACCCGATGCTAATG  
TACAGGAATTATAGAGCACATGACCCATAGATTTATCGAGCATTTGTGCAATTTGAAAG  
ACTCTTTCACATAATAAAGTATGTAACTATATAGATAGAAGATGTCCCGTGTCTTTTG  
TCTACTAAATGATGATCTGCTCATTTAAAGTCGCCGCGACTACTTTGACAAAAA  
ACTTAGAAAATACGACAAATAGAGATTATTGAATGAAGTACATTGAAAAAAGAAAGA  
AAGGCACATAGCAGCACACAATGTCGCACCAAAACCAGCTTATTCACAAGCTTATATTT  
CTAATTTTCATAACAGATTGACAAACGAAGATGATGGTATCCCATCTTTACAAATGGCTC  
AACAAACAAGGCAGCATAAAAGGGCTAAAGGTGTCAACTATGCGGAATATGACAACGATC  
TCTTTGATGAATTCAATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG  
ATAATGCAGTGTCTCATGAAAATACTCCGGCACTTACAAATGGTGTACCATGGACGGTT  
CCGAATACAATGTCTAGAGAACATGAATGGAGCTGATAGTATTATCTTAACAACAAAT  
ACGATGCGGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG  
CCAGCAATGGTCCGAGCAACAAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG  
ATCTGCAAGACCAACACCACAACCCCTTCAACATATTGAGATACCCTAAAATAAGAGATA

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CTTTCATTAACGGAAAAGTGGTGTCTCCATATAGACTCAACACTGATCAAGAAACGAAGG  
CAAACGCCAATTCTGGAGAGGCAATCATGATACCAATTACTTTGGATATAGAACATATGG  
GTCATACCATAAAAGACCAGTTTCTCTGGAACACAAATGACGACTCCATATCTCCGGAGG  
AATTTGCCTCTATATACTGTAAAGATCTTGATATGACTTCCGCTACCTTACAAACTCAA  
TTGCGAATATAATAAAAGAGCAGTTGAAAGACCTCGAAAATATTGCAGCCACTGAGATAA  
TGTCTGACCTCCACGTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTTTGAAG  
ATAACTTCCAGTGGAACTTGAACGACAAATCACTTACTCCAGAAAGATTTGCTACATCCA  
TTGTACAGGACCTTGGCTTAAACAAGAGAGTTTCATCCCCTTAATATCTCAATCGCTTCATG  
AAACTATCTTGAAGATAAAGAAGGACTGGGTAGATGGCCACTTGATTTCAGGACCATGTCC  
CAAACGATGCCGCATTTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACTGGGCT  
CCAAATGGTGGCCCAAGGTGGAATATTAAACAAAAGAAGAAATACAAAAGAGAGAAATTG  
AAAAAGAAAGAAACTTAAGAAGATTGAAAAGAGAAACTGATAGATTATCTAGAAGGGGCA  
GGAGAAGATTAGATGACTTAGAAACCACAATGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)

MSHQNLIPQAYISNFHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNYAEYDNDLFDEFNM  
NGSNFNADTHYKDNAVSHENTPALTNVMTDGSSEYNVLENMNGADSII SNKYDAGSNM  
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHHNPFNILRYPKIRDTFINGKV  
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNYNDDISPEEFASIYC  
KDLDMTSATLQTOIANIIKEQLKDLENIAATEIMSDLHVIINLTCNLQDRFFEDNFQWNL  
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHE'TILKIKKDWVDGHLIQDHVPNDAAF  
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRLRKRETDRLSRRGRRLDDL  
ETTMRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)

GTCATATCAAGATCTTTACAGTATATAGAGGCAAATTCCTCCGGAGATATGGAGTCGTCA  
TTGTAGTTCAGAGAAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA  
ATTGGTATCATGATTGCCTCTCCAGAATTGGCGTTTGCCTTCGTTTCTTGATCAGTGTG  
AGTCTATATGGAGACACCACTTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC  
AATATGTTGAAGGGGTTGTGGTGTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCAATA  
TCCTGTGCCTGCGCTTTGTTGCTCGGACCATTGCTGGCGTTGTTATTGCTATTCAAACCG  
GATAAAGATTCCACAACCATGTTTGAACCCGCATCGTATTTGTTGTTAGAGATAATACTA  
TCAGCTCCATTTCATGTTCTCTAGGACATTGTATTCGGAACCGTCCATGGTAACACCATTT  
GTAAGTGCCGGAGTATTTTCATGAGACACTGCATTTATCTTTATAGTGTGTATCAGCATTG  
TTGAAATTAGAACCGTTCATATTGAATTCATAAAGAGATCGTTGTCTATTTCCGCATAG  
TTGACCACTTTAGCCCTTTTATGCTGCCTTGTGTTGTTGAGCCATTGTAAAGATGGGGATA  
CCATCATCTTCGTTTGTCATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC  
TGGTTTTGGTGGCAGATTGTGTGCTGCTATGTGCCTTTCTTCTTTCTTTTCAATGTAC  
TTCATTCAATAATCTCTATTTGTCGTATTTTCTAA

YLR322W, 104 aa (SEQ ID NO 196)

MRHCIIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDIIIFVCQ  
SVMKVRNISLWNKLVLVRHCVLLCAFLLSFFNVLHSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)

CCACATGTCACAACTACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAAACATCATA  
GCCTTGCCAAATAAACTCGCTTCCCAGAAAAGACGCCAAATTAAGTCCGCTGTTATGTG  
ACAAAACAGGGCATCTCACATATTTCGCTACTGGTGTCTTTTAGCTCATTTCCGATATTA  
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAACCCACACA  
ATTAAAATGCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAATAGACGGA  
GCATCATACGTTTCGAGTGGAAAATTATGGAGAGTTTCCAAGCTCTATGGCATGTAGAGT  
CGTGATTGCTGCTGTACGCTTTTGCACAATATTGAATCTTCAATCTAAAGAATTAAATTT  
TCTAATTTCAATGTAGAAATATTTCAACTGTTAGTTTTTTATTTACAGGTTGAATATAGTA  
CGACAAAATATCAAGGAAAAATGGCTAGAGAAATCACCAGCATCAAACAATTTTGGAAAT  
TGACCAGAAGAGCTGACGTTAAGACCCGCACTGTTAAGATTAAACAAAAAATTGAACAAGG  
CCGGTAAGCCATTCAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTTGTACACTT  
TGGTTATCAACGATGCTGGTAAGGCTAAGAAATTGATCCAATCTTGGCCACCAACTTTGA  
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)

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MAREITDIKQFLELTRRADVKATATVKINKKLNKAGKPFRTKFKVRGSSSLYTLVINDAG  
KAKKLIQSLPPTLKVNR

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:  
967-1331 (SEQ ID NO 199)

TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG  
ATTATTAGTTATTTGTTTGTTCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA  
TCGATTACTTATGCTATTCTATTGTATTTGAGCCGGCGGCTAGTAAACAAGACAGCATAC  
CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAATGTATGGGTT  
AATAATCCTTTCTCTTCTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTT  
GTGAAAGATATGGAATATTCCGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG  
GATGGAATCTTGCCCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCGAAGTACAAGAT  
ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCGATTCTATATTATTGACGTA  
ACCAACAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT  
CACTGAAACCCCTGTAGAGCTGGAATTGAAAAATATAGTTTGTACCTTTTGCCTGAGGGCAG  
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA  
CTTGTAACCTATTTAGGTGATGTCTCATAACTGCAACCCTGGAATAATGACGCAAAATATC  
AAAAATAATAGGGAGATAAAGTCTCACGACATGAAAAAATCATAGAATTATTGTTCAATTT  
ATCTAGCCGTATCTTACCTTATGGAATAAGTGTGAATATGTTTTTCTAAATCGAGCTTCC  
CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTCTCCAAGG  
TCCTGCTTACTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTTCATTA  
TTTTAGACGTTTCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTACCCGCCCCATCCCT  
CCCAACGTCGTGTTTTTGCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA  
TCAAGGCCCTTGCCAATCAGAAGAGATGATGAAGTTTGGTTGTTTCGTGGTTCCAAGAAGG  
GTCAAGAAGGTAAGATTTTCATCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG  
TTACCAAGGAAAAGGTCAACGGTGCTTCCGTCCAATTAACCTTGACCCCATCCAAGCTTG  
TCATTACTAAATTACATTTTGACAAGGACAGAAAAGCTTTGATCCAAAGAAAGGGCGGTA  
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)

MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR  
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVNGASVPINLHPSKLVITKLHLDKDRKALIQ  
RKGGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:  
1117-1376 (SEQ ID NO 201)

ACTTTTTGTCTGCTGCTGGTTCGTTTGTCTTTTCGTTTTTAAAATTGCGCTAGACAAGTAAAC  
AGGGATTGCTTAAGAATCAAAGTAGCTTAACTCTAAAGTATTATTTTCCTCAGTTGTGGG  
CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCGGTTGAAC  
TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTACGCAATTACAACCGCATT  
ATTTACCTTTTCATCTTCAGTTTACGGTTCAGTTTATTCTGTTACGAAAGAATCATGGT  
GATTCAAAGGCGAAGTGCGTAGGATTGTAACCTCCTATATCTTTAGGATACTTACAATTTT  
GTACTGTTTTCAAGACCACTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA  
TTTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAA  
ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA  
TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA  
TCATCAAGTTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAACATTTTTTCAATATTT  
TCACATGTGTTTCAATTTCTGCTTATTTTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA  
ATGTTGCGCAACTCTAACGAAGAAATAATTATGCCATTGTTTTTTTACTCCGGGCTGATA  
ACTAGATGGTGTGATCGGGCAGTATACTAATTTATACTGGACAAAGACTCGTAAAAGATG  
TTCTTTGTGCTTAGTCCCATACTGTTTTTTAAGTGTCCGGGATATTTAATCCCATGTGGA  
AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT  
TACTTTTCTCAAATCTCACTCTTAAATTTTCAATGGCAAAATTTCTCCGCAACAAT  
AGACAACATTTTCTGTTTTTTATGAAGTAAGCAAAAATTTTGAATCAACAACGCTCCAT  
GAGATTCCTCAATACTAACATTTTACTCCTTATTTAGGTTACATTGGCGAATTGCAATACA  
TTGACGACCACAGATCTGGTAAGATTGTGCTCCAACCTGAACGGTAGATTGAACAAATGTG  
GTGTTATTTCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCCAAC  
TATTGCCAGCCAGACAATTCGGTTACGTTATTTTGACTACTTCTGCGGGTATTATGGACC  
ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAAATCTTGGGTTTTGTCTATTAA



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YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIKFLQVMQKHGYIGEFYIDDHRSGK  
IVVQLNGRLNKGCVISPRFNVKIGDIEKWTANLLPARQFGYVILTTTSAGIMDHEEARRKH  
VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCGCATTTTGTGAGAAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC  
CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAATAAAATATCATGTATC  
TCACCCCTCTTCTTGGTATTAGTAAAGAGACGCCTGATCTTGTAACAGTGGTGAAGATTGT  
ACTAGACGAGAATCAAGAATTTAAAAAGTGTAAGGCAAGGCAGAGGCGATGTACATAAA  
ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAAAC  
TACTATAAACGTTTGT'TTTGT'TCC'TTACGCACAATATCCTTGCCTAGAAATCGTTTTTGA  
AATTTAAATTTTTTATTACCATTATTTGATTTCGCCTTCAGAAAAATATGGAAGAGTGCAT  
ATTTAAAAAGGACTATTTTCAGCATATAGTAAAAGTCAGGTTATTTGTTTATTTGCGATAT  
CAGAGTAACTTAACTAACTATGCAGGGCACTTTTAAAAAGT'TTTTACCATCCCACGCTTA  
CGCGGATGTCCTTCTTGGATAAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG  
AATACCAGATCAAACAACCTGGTCAAGCCAATAGGCTTAACACAAGCACCAAGGAAAAAGCA  
CCAAATACTCCCAGGGGAACCTCTTTGAGGGATATGTTTGATTTCGAAAAAGACAAACCACA  
GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAATCTGGACTTTATGACGTGCAAGTCT'TCC  
AAAAGACAAAGGGGAAATTTGTTTATAGCTCCAGTTTCATATTGGAAAGAAGATAAAGCTT  
TGTTTTTTTCTCATTTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG  
ATATGTTAAGGGGTAAAACCAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT  
TGAGTAGTTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAACTGACTACTTGACTG  
AAGCTGATGCGCGTTTAAAGTTTAAATGACAGTAACGTCCAAATCATCGAGGTCAATCTTG  
TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTC  
CATCTTGGCGCCAGCCATTTTATTTTCAATGTTCTAGAGGCCAATGGCCATTTTCCGTCA  
GGGAAGAGCTCTTTTGCAATAATGTCTTTTCTGGATACGTC'TTTCTTGTGGACCAGCAGT  
TAAAAATTAGGTGGGCAGCTTGCGGGGAGGCTACTCCATCTGAAAAGGAAGCATTGTGGA  
AGTTTGCCAAACGTCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MQGTFRFYHPTLTRMSFLDKFLKPMMATASPKYQIKQLVKPIGLTQAPRKSTKYSQGN  
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVFQKTKGKLFIAPVSYWKEDKALFFPHLI  
GTAMDGTKQONIEDMLRGKTSIVRLFSTASGDKLSSSYFQGI VDDNKKTDYLTEADARLS  
LNDNSNVQIIIEVNLVENAVKSALVKTLARWANRVP SWRQPFYFECSRGQWPFSVREELFCN  
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)

TTCTATTGGTGTAAGTTATACCAGAACCATCC'TTCCCAAGGCCCTTTTCCCGCAACATATCC  
CATACTCGAAAGTAACTTCGCACCAATACCATATGTCT'TCGTTAATTTTGAGATCGT'TGG  
GGCATTGCCGCTACTAGTTTTCAGGCATCATTAGTGATGTCATGTCATTCATTCATGCT  
TGAATTATTATTCTTCCATCGCTATAAATTATAGGAATCGATTCTTCTTTTTTTGAAAAA  
GAACTTTT'TATCTGTGTTGGAGTCCGAATCCTCCATGTTTGGCGTACTGAAGGCTTAAG  
TTCTTCGACCTCTCTCGGTTGTACTATTTTCGAAATTTTGGATTTT'TGT'TATTGTTTGTGAC  
ATAATGTAAATACTAGATGCGCGCTCTAAGGCCCTCAGTATTAATAAATTGCAAGATATCCC  
TAACTTGATAATTATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCGAGGATAT  
TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA  
GGAAAACGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA  
TTAAGAAAAAATTGTCATCTTGGCAGTTGAGTATTTCAAACTCAATTTTCTAATAGTTG  
GCTTGAGACAGCAAGGAAAGTTTCTTTTACACTATTTTAAAGGAAGGCATTGGGACAAAGC  
TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT  
GGCAATATGAAATCAC'TTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA  
TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAACG  
TTAACTTATTGAATGACAAACTGAAAGAAAGTGCCAGTAATTGAGCGTCAAATTTGAAAAACA  
TTAAGCTTCAATACGAAAAATATGGTCAGAAAAAGTTAACAAAGAACTGATTGATACCAAGT  
TGACGGACGTAACCTCAAAAATTCCAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA  
ATGTTGCAGAGCAGTTTAGCAGGGAACTAACGGACCTTGAAAAAGATTTAGCAGAGATAA  
TGAATTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA  
ACGATGAACGTGAGGAGCTGTTTAAGGTGGTACAAGGCGACGACAAAGAACTATACAACA  
TTTTCAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATTCTTAACTTGGGTC

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AATTTTTCGAGGCCAAAAATAAAGGAAAAGACAGAAGTACACAGCGAAGTTTCTGAAATAA  
TAAACGATTTCAATAGAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA  
TTGATAGCTTCAAAAAATTCCTGTACACAAGATATTCAAACAACCTAAGGAACCTTTGTGAAT  
TTTATGATAATTTTGAAGAAAGCTACGGTAACTTAGTTCTAGAAGCAAAGAGGAGAAAGG  
ATGTGGCAAACAGAATGAAAACCTATATTGAAAAGATTGTGAAAAGCAGTTGCAGAATTTAG  
ATGCTCAGGACCAGGAAGAACGTCAGAATTTTATAGCGGAAAAATGGAACCTATCTTCCTG  
AGACAATCTGGCCCGGTAAAATTGACGATTTTCTTCCTGTACACTTTAAATTACAACG  
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)

MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQOGK  
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKEYWQYEITSKVQRLDGIVNELSISEKDDT  
DPSKLGDIYISRDNVNLLNDKLKEVPVIERQIENIKLOYENMVRKVNKELIDTKLTDVTQK  
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTLQLQDKKIDNDEREEL  
FKVVQGGDDKELYNIFKTLHEVIDDVDKTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN  
LEYLLIFKDISNLDISFKNSCTQDIQTTELCEFYDNFEESYGNLVLEAKRRKDVANRMK  
TILKDCEKQLQNLDAQDQEERQNFIAENGTYLPETIWPBKIDDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:  
949-1342 (SEQ ID NO 207)

ATCTGTAAATAATAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTCAG  
AATGATTTGACGTAAAAGCAAGTCTCATTCAAGAACTGTAAAATCCGTACACACTACTG  
AATTTTACATCCATACATTTTGTGAAATTTTCATGTTTGTGAAAAATTGGAAAAGGGC  
TAAATTATCCGTCGGGGTGTCTCTAGCTCGGCTCAACCTAGGCAAAATGCGTTTACTGG  
GGCCATCCAAGCTCATCCTTCCAGAGATTTCGCCTTTCAGAGGCAAAGAACTCGTCTCCGC  
AGGCCCTCTTGTTCGGGAGGAGGAGAATTCTTGCGCGGAAACTGGTTGATGCCTGGGCTA  
TGGTAATTTCTGACACCTTTGCTATCCTAACTGGAAAAGGTCCTTAGTAATAACAATATCA  
GGTACTTTAACATTTGTTAAAGATATACTATTAGTGAAAAACCGATCTTACGAAAAGCCAA  
TAGAGCAGAAAGTGCTAAAGATGTCTTTAGTTGTACAAGAACAAGGTTCCCTTCCAACACA  
TTTTACGGTATGTTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTCACATTACATGG  
GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCCTCCGATGGAATAATAAACG  
TCACGGGTTACCAAATACGAGGCCGAATTAACCTCTACGCTACTATAAAAATTATCACTAG  
ATTTTAAAGTAATACACAGTTTATTGGAAAATACAATATATGACTCAATGCGAATTTAAA  
AATTTTCACTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTTCGTACGCCA  
TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCCTAGCAGTGGTGTGAATAA  
ATTACTAACAATAAGATGTACAATTTTTTGTGCGCCCATTAACAATCAGTTTGTGTAACAC  
CAATGTTCGATGGTAACATTAATAAATTTGTTTACGCTTTGACCACTATTAAGGGTGTGTCG  
TCGTTACTCCAACTTGGTCTGTAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA  
ATTGACCCAAGAAGAATTGGAAAAGATTGTCCAAATCATGCAAAACCCAACTCATTACAA  
GATCCCAGCCTGGTTCTTAAACCGTCAAAACGACATTACTGATGGTAAGGACTACCACAC  
TTTGCTTAACAACGTCGAATCCAAGTTGAGAGATGACTTGGAAGATTAAAGAAGATCAG  
AGCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC  
CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208)

MSLVVQEQGSFQHILRLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE  
LTQEELERIVQIMQNPHTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR  
AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)

TATATTATTTTTCCTTCTGGGTTCTTTTCTTCCTTTTCTTGTTTACCTTTTTTGCTTT  
TTCATAAAATAATTTCTCTAGATTTGAAGACAGCATTTTGTACATCCATACACCATACA  
CCATACACCATAGCACCAGTACACTATATTTTATGAATTTTACTAAGAATTATTCCTGC  
AGGAGCTCCACTGAAAAAAGAGCAGCATGGATGTCGGGTAGAAGTGCTACTGAGTAA  
ATGGGAAGGACGCGGTAGATCCAGTGTGGAATCAAGGTGGTGCCGGTGTGAAGCCGCCCTC  
GGCCGGCTGGACTCTCCAGGCCGGAGTGATGATTGCCACGCTGAACGTAACACAGTTTCA  
CAATACCAGTGTCTCATTAGTGAGTTCCAATGTATAGTTAGTAGTGGTATTTTGATATA  
TGTGAGTGGTAGCAGATTTGAACCTAGTTAGTTGTATTTCGCCTTTGAGGAAACCAAGCAA  
AAAACCGATCTAGACTAATCATGGCTGTGTTGTAAGAATAAGAGACTATCCAGAGGTAAGA  
AGGGTTTGAAGAAGAAGGTCGTTGACCCATTTACCAGAAAGGAATGCTTCGATATTAAAG

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CCCCATCCACTTTTGGAAAACAGAAATGTTGGTAAGACTTTAGTTAACAAGTCCACTGGTT  
TGAAGAATGCTTCCGATGCTTTGAAGGGTAGAGTTGTGCGAAGTTTGTGTTGGCTGACTTGC  
AAGGTTCTGAAGACCATTTCTTTCAGAAAGGTCAAGTTTGAGAGTCGATGAAGTTCAAGGTA  
AGAAGTTGTTGACCAACTTCCACGGTATGGACTTCACTACCGACAAAATTGAGATCAATGG  
TCGAAAAATCGCAAACCTTTGATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG  
TTTTGAGAATCTTTGCTATTGCCTTCACCAGAAAGCAAGCTAACCAAGTTAAGAGACACT  
CTTACGCTCAATCTTCCCACATCAGAGCTATCAGAAAAGTTATTTCTGAAATCTTGACCA  
GAGAAGTTCAAACTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAGTTATCA  
ACAAGGAAATCGAAAAATGCTACCAAGGACATCTTCCCCTACAAAACATCCACGTTAGAA  
AGGTTAAGTTATTGAAACAACCAAGTTTCGACGTTGGTGCTTTGATGGCTTTGCATGGTG  
AAGGTTCCGGTGAAGAAAAGGGTAAGAAGGTTCTGGTTTCAAGGATGAAGTCTTGAAAA  
CTGTGTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKNKRLSRGKKGLKKKVDPFTRKEWFDIKAPSTFENRNVGKTLVKNSTGLKNASDA  
LKGRVVEVCLADLQGSSEHDSFRKVKLRVDEVQGNLLTNFHGMDFTTDKLRSMVRKWQTL  
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVISEILTREVQNST  
LAQLTSKLIPEVINKEIENATKDIFPLQNIHVVRKVKLLKQPKFDVGALMALHGECSGEEK  
KKKVSQFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATTGTCTCGAACATGTTTCACAGGCTCGGAGCTTGTGGCGGGT  
GCCTCGCTTACTGGAGTACCATTAGCGGTGTGTTTGAAGCTAACGAGTTCATCTTCAAT  
CTTTATTTCCACTTCTTTACAAGCTTTCTGCCTTTCTCTATGACGTCTTTCCCCAAAACAC  
TACCTCTTGACACGACTTGTGTTTTTCGTTTTTCTCTAAGAATATCACTATTTTCACTTT  
TTTCACTTTTTCCACCATTACGTCGGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG  
GGGAAGAATAAGGGATCTTTGGAACGAAGGAAAATAAGGGAGAGGGAGGAAACAAGGAG  
GCGGTGAAAGGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCCTAGCATG  
ATTAGATTACCGGAGTTTAGAAGAGGATCTGCAATAGAAGAGGAGACAACACAAAAGAA  
CTGTTAATTAAAGAGAAGAAGATGAAGCAATTCAGTTGGTTAATGCGGTTTCCGCATCAT  
TTGTGCTTATTGGCTTAGTGTTGGCCAATTCAGATTCAAGTGTTCGACAAGTGGACGCAGG  
AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT  
CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAAC  
CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT  
TTGGTTATACTGGTTCTTTCGGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA  
CAGACAGTCTAGCTAAGCTTTTGAAGAAAAACGGCGTGGATGTTGACGACGCTAAGGCTT  
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA  
AGTCGTCGGGATACATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAAGATTTGTC  
AAAAGTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC  
TAGTTCAAGAAAGTCAAGGAAAAACATCTACCGAACTTCAGAAAAGGCAGAACAGCAGCGTC  
TGGGTTTGCTAGAAAGCTTGGATTTGGCTCACCAACAAATATTAGACACATCGGGACAAA  
TAAAAGACACTGTATTTGACAAGTGGTCTAGTGATCAGTTAACCAATTGGTTGGAGAGCC  
ACAAGGTCAATATTGACAAGAACATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA  
AAGAAAATTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG  
AGTCTTCTCCATTTTTGACCAAGACCCAGAAATACGTTGGTTCCGTTTGGGACTCTTCTA  
AAAATTTCTCTACAAATTTGTACTCCAAGTTCAGAGGTAAGACTGACAATGTGATCAATG  
ATACTTTTTTGGTTGGCCTAGACTCTTGGCCAAAGGACAAATTGAAAATGTTTTTAGATG  
CTCGTGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA  
AATCCAGAAAACGAAAACTCAAGATCCTGCCAAAAGACTACCAAAAAATCTTTGACAACA  
GTAACCTGGTCTTTGGATGACATAAAGGGTGGTTTGTGACAAAAAGGACGACTTCCAAG  
ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGAACAAGGTTTCCAAAAACACAAATG  
ATGCTAAGGACCAATCGCTAAGACCTGGTCAAATACCTTTCAGAGCTGGTCTCAAGAAG  
ACCTATTCAGTACCTAAAATCATTCGGTGTTCGGTTAAACAGACTTCTACGAAGGACG  
ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTTCGGCACTGTTAAGGAGCCTG  
CTTACAAGAGGTACCTACATAACGTTAAAAACTGGTTCGAAAAGCATATTAGGGTTCAACT  
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT  
EASQVWDKHAQPKPWWQVWSSDSSSVSNPNPGWFGYTGSSDHPVSDWLFDTWSTDLSLRNF

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LKKNQVDVDDAKASKDSLVTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNLNDN  
GIDYDKAVQSKDELVQKVKENIYRTSEKAEQQRLGLLESLLDLAHQQILDTSGQIKDTPVD  
KWSSDQLTNWLESHKVNIDKNMAKKHDYLVMAKENSANLKDDIYWYLDYMKRESSPFLT  
KTPEYVGSVWDSSKNFLTNLYSKFRGKTNDVINDTFLVLGLDSWPKDKLKMFLDARGIKYS  
MLSTEHQLRELKSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST  
IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFQVVPVKQTSTKDDLINLAK  
QNTQWLFGTVKEPAYKRYLHNVKNWSKSLGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTCCTTATCTATCTATTGAGTAATGCTTACTTTTCATATTTTCAATGAAC  
AATAGATATGTAGGAGAATTGATATATTTCACTGCGTATCAGAGAAAAGGTCTACTGACA  
TTTTATGGCAAATGTATTCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA  
CACAAAGAGAAGACTGTTCTAATTAACAAATAATATTGAGCTACCTGCTAAGTATGTCC  
TTTTCCCTTTGTCTTTGGTTCTCTTATAGAAGACCCTGGAAATTTTTCGCATTTTTC  
GGCTTTGGGCGTTAGTAAGAACAAAAAGAAAAGAAGAGAACAAAAAGAAACGATACGGA  
GTACGTGTCATAAAAACTTGTTCAATCATCCTTGAAGCTAAGTATAAAGAGCTTGAAAAG  
GTTTACCACCTTAACTGGTTATCTATTTCAAGAGTGTAACATTTTATTGCATATACCA  
CAGTAACGTGCAGGTAAACATGAGATTAAGAACCGCCATTGCCACACTGTGCCTCACGG  
CTTTTACATCTGCAACTTCAAACAATAGCTACATCGCCACCGACCAACACAAAATGCCT  
TTAATGACACTCACTTTTGTAAAGGTGACAGGAATGATCACGTTAGTCCCAGTTGTAACG  
TAACATTCATGAATTAATGCCATAAATGAAAACATTAGAGATGATCTTTCGGCGTTAT  
TAAAACTGATTTCTTCAAATACTTTTCGGCTGGATTTATACAAGCAATGTTTCATTTGGG  
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGCACTGGG  
ATACACTGCCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACATGA  
AGGAAGCGGATGATAGCGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACCAGTA  
AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAAATGACTTTAACGGTA  
AAAACGCCGTTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTTATGGTGGTA  
AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACGTGTTTACAATTGGCGAAA  
CTGGTGAATCAATTGGCCAAAGATGCATTTTATAGACTTGATCCGGTTTCCATGCCCTCTA  
TCGGTACTCACTTATCAAAGGAATATTGTAACACGAAAACGTGTAATGGGAGCCCCATC  
TGGATTTGTTTATGGCAAGAATCGGGAACCTTCCTGATAGAGTGACAAACATGTATTTCA  
ATTATGCTGTTGTAGCTAAGGCTCTCTGGAAAATTCAACCATATTTACCAGAATTTTCAT  
TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAAATGGATAACGTTATTTCCAGCTGG  
ACACAAAAATTTTAAACGAAGACTTAGTTTTTGCCAACGACCTAAGTTTGACTTTGAAGG  
ACGAATTCAGATCTCGCTTCAAGAATGTCACGAAGATTATGGATTGTGTGCAATGTGATA  
GATGTAGATTGTGGGGCAAATTCAAACTACCGGTTACGCAACTGCCTTGAAAATTTGT  
TTGAAATCAACGACGCTGATGAATTCACCAACAACATATTGTTGGTAAGTTAACCAAT  
ATGAGTTGATTGCACTATTACAGACTTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA  
ACATGTTCGAAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT  
TCTTCCAAAATAACTTCTTCAACATTTTGAAGGAGGCAGGCAAATCGATTTCGTTACACCA  
TAGAAGACATCAATTCCACTAAAGAAGGAAAGAAAAAGACTAACAAATCTCAATCACATG  
TATTGTGATGATTTAAAAATGCCCAAAGCAGAAATAGTTCCAAGGCCCTTAACGGTACAG  
TAAATAAATGGAAGAAAGCTTGAATACTGAAGTTAACAACGTTTGAAGCATTCAGAT  
TTATTTATAGAAGCTATTTGGATTTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG  
TATACAAATTTTGAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG  
AGCCTATTTCTCTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIATLCLTAFTSATSNNSYIATDQTQNAFNDTHFCKVDRNDHVSPSCNVTFNELN  
AINENIRDDLALLKSDFFKYFRDLKYQCSFWDANDGLCLNRACSVDDVEDWDTLPEYW  
QPEILGSFNNDMTMKEADSDDECKFLDQLCQTSKKPVDIEDTINYCDVNDNFNGKNAVLID  
LTANPERFTGYGGKQAGQIWSTIYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK  
EYLNKTGKWEPNLDFMARIGNFPDRVTNMYFNYAVVAKALWKIQPYLPEFSFCDLVNK  
EIKNMKNVISQLDTKIFNEDLVFANDLSLTLKDEFRRFKNVTKIMDCVQCDCRRLWGK  
IQTTGYATALKILFEINDADEFTKQHIVGKLTKEYELIALLQTFGRLSIESVNMFEKMY  
GKRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNNSQSHVFDDLKM  
PKAEIVPRPSNGTVNKKWKKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK  
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

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AACAGTATTGGCTGTTGATTTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATT  
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAAATAGCGTCTCTGATAGCCATGGGT  
GAAGGTCTTCCTCTAGTTCTCACCTTAATTAGCATTCGGTGAGAATGCCTGCATGTTGAA  
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTTGTTCCCATTAATATTATCATC  
TCTGATAGAGCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAACAAGGCGCCTCATCG  
CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT  
CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT  
AAACTCTGGCGTTTAGCGTACGAAGGAGATTATCCTAAAAGGAACCTCCCTAGTAATAGT  
GTAATTTGGAAGGGCATAGCATGTCTGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC  
AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA  
TATTCAATTGGGACTGCCTAATTCAAGGGCCTCCAGATACGCCATACGCTGATGGTGT  
TTAATGTCTAAGCTAGAGTTTCCCTAAAGACTATCCGTTATCTCCACCTAAACTTACTTCA  
CACCCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATTCTAC  
ACTCCCCCTGGTGATGATCCTAACATGTACGAATTAGCGGAAGAAAGATGGTCGCCAGTGC  
AAAGTGTAGAAAAAATCTATTAAAGTGTTATGAGCATGTTGAGTGAGCCCAATATCGAAA  
GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC  
AGGTAAAGTTATCCATTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216)

MSKTAQKRLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPDPYADGVFNAKLEF  
PKDYPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKIL  
LSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)

GTCCTTCCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG  
TGTTTTGACAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTACCAGAAGTAC  
TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACCAG  
AGTAAACACTTCTACCAGTATTTCTTTACGGTTCCGATCAAAACCATCACTCATTCGGTC  
ATTCCTTACCGTACGATAAAACCAAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC  
ATCCGTAATAGTTTTTTTCTATTTTGGACTTTTGTAAAAAAGGATTAGGGATACGTTG  
CTCATAAAAAAATTGACGAAGATTTTAGATAATTGGCAAATAAAAAATGAAATAGTATCAAT  
ATACCGAAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA  
TATTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG  
TTCCCCGAGCATCTGTATTCGTGCCAAGAATCAGCACACCATTTATTTTGCATAATTATA  
TCTCTAATGGCAGAATGGACCTTTTTTCCAAAGAATTCACAATGGCCGCGTATCCAAAT  
CTGATCTTTGGTCAAGCAACAAGGAAGGAGCTCTTAGTATCTCAAAGGAAAAAAGAG  
CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCTCTTTAC  
ATCGTATATCTGGCGTTTTACTGGCTCTTGGATTCTATGCTTTCACAATTACTTTGGGTG  
TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA  
AGATGCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC  
ATTTTGGTAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG  
GGGTTATAAAAAACCGGATCAATCGTTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC  
TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)

MKATIQRVTSVFGVPRASVFPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN  
KEEELLVSQRKKRPISPHLTVEPEMSWYLLSLHRISGVLLALGFYAFTITLGVTTIMGM  
DTTFQDLNKWYHEKMPKWSQWVAKGSAAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS  
IVLAGTLVLGTYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:  
714-1121 (SEQ ID NO 219)

CCGCTTAGCGCAAACCTATCGTGAACCTCGCTGCAACAACCTGAGAGGGCAAGGATATACATA  
AAAATAGCCTACAAATTCTGAACTCTGTAAAGGAAGCCTCATAAATAAAGGTAGATAGTA  
AAGTATACAAGAGAAGAATCCCAAGATGTCAGCTGTCCCAAGTGTTCAAGTATGTTTTCA  
GTTCTGCAGAATGATGTTTGATAGTATCGATAATGGAGTGAGATCAAGAGAAAAAATG  
AATATGTCAGCCAACCAAGTTCTGAGTAGGCAGTAAATGAGTACGCATAGTGTATTTATC  
CAAAGGAAAGAATTGTTATTTTTACAAGCCGAATTGAGATCCAATTAGGCAATGTTTTGG  
GGAGAGTATTTTGACAAGATTGGTTAAACTACTACGGTCAGTTCCGTAACCAGTACGATT  
GTACACATAAGGAAACAACCTGTAAAGATAAACAATAAGGGCTTCCAATGCCATTGTAAGA

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TATCATATTTCCTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG  
AAGGTTGCGCAACTAAAGAAGTTGAAATTTAAATGGCAAGCGCTACATTTTCATCCATTT  
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCATTTTCTCTCAATGAA  
ATAATTGTTACTAACATTGAATTTCTCGTAACATAATTGCATTACTTCTTTAGACTTTTG  
GTAAGAAGAAATCAGCTACTGCTGTGTTGCCCATGTCAAGGCCGGTAAGGGTTTGATCAAGG  
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC  
CATTATTGTTAGTTGGTTTGGACAAATTCTCCAACATCGATATTAGAGTTAGAGTTACTG  
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGTTTAGTTG  
CTTACCATCAAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACCTT  
CTTACGACAGAACCCTTGTGATTGCTGATTCTAGAAGACCAGAACCAAGAAATTCGGTG  
GTAAGGGTGCTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)

MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF  
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQYVDEQSKNELKKAFTSYDRLLIAD  
SRRPEPKKFGGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)

GTCCCATCATTTCTTTACACCTCGTACTGTATTCATGATCATCTATCCATTTTACATACCG  
CTCCCTTTAAGATACGTTTATTCGTAACCTCCATTTACCAATCACTATGAGCCGTCACG  
TTTCCAAAAAACCTAAACATATGATGCAAACCTCCAATGAGACTCAACGTAAACATGCAA  
GTAAATACAGAAGGTTAAGAGATAGTTGTCTTAAAGGGGTACCGAAAGCATTTAGGGGAG  
GCTTAAGGGAGGGTGCCGATCCTATGAAGTATTAATACGTAATGCCAAAAGGAATTGTTG  
AACATCTGAAGTGAGTAGATTAAATCGTACAGTAATCGTACAGTACTATGTCTTACTGATG  
TCGGGAATCTCAGGGGCGACCGCCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAT  
AAAACCTCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT  
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTTCAGA  
GCTCAAAGGAAAAAATTGCAGGGCGATGCAAAGGTAGTGAGTGACGCTTTTAAGAAAAATGG  
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAGTGAAAAACACAACATC  
AAGAGCAATACAACAAGCTCAAAGGGGCGGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)

MNTDQQKVSEIFQSSKEKLQGDQKVVSDAFKKMASQDKDGKTTDADESEKHNYQEYQYNKL  
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)

GGTTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT  
TCGATGTGGCAGTGTACGAGAGCCATTCTGTATCGTTGACAAAGTTTGCATGACTTCAT  
GTTGTTTTCGTAGCAGTATTCGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTTG  
TTCTTGGTCCACATTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCTTT  
TGTTCCGATGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCTGTAAAGTCG  
CCGTTTCTCTTTAACCATTTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCACCATTA  
CCGCCTTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC  
CTTCTCTTAGCCAATGACTCCAAGCTGGCTGATAAAAAACAACTAAACGGTAAAGCCAC  
AAATCCGAAATGTATCACCATGATCACCAGCCTGCTAAGTGCCCTCTATTGATCCGTA  
TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTTATATGTGCATTGCAAAAGCATAAACA  
AATCTTGGCAGCCGAAGCCGGCAATCCACTTCGAAACGCACGGCTGAACATATAAAATA  
TAAAGGACATGTGGAGAGAAGCTTCTCTTCTTCACATTTTCGATTTTCATGATCTAAAGT  
GGTTCTTTTACAATAGAAGAGCACCAACACGAAATATGGCTGTGCGGTGGTAATAACTGGA  
GCATGTGGCTGCGAATGTACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA  
CGCTGATCAGTTTGGAGCATGGGAATTTTCCCACCAATATAATCGCAATATTTTTGTCA  
CTTGGTGGAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAACGG  
TATCTCTCTCACGAGGAGAGGAATCGCAAGGTTTGACCATTTTCAGACCTGTTCCCAATG  
TCAGTAAATTTGCTTCTTTTCCCAGAGTGCCCAAGGAGCCCCAAGGGGCTTTTACCA  
ACTGGAATATGACTACATCAAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA  
TCAAATTTACCCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTCAACT  
CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT  
CTAATGTTACCTCTAAACAGGATCACGTCCAACCAGTTGCCCTTAAGAAGTTATCTCAA  
AGGATATCAATTTCAATTCGTAATTTAGAATAATTAAGATAATGAAGACCCAGAATGAAG  
TCGTTGATGAAACAAGCGCATATTACATGGAAAAACCAGGTTCTTATATTGAATTTACCA

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TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCATTTTTTAGATCCTTCTT  
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAAAATCAATATACA  
GTAGTGTTGACATGATCTTGCAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA  
AGATTTCGAATACATTTTCCAAACTCAACTGTGGTGGAACAGAAAACTAATTGCAGGTC  
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA  
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTAAAGG  
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA  
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)

MITQPAKCPPLLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE  
ASLP SHFAFHD LK WFFHNR RAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDR TLISLSH  
GNFSHQYNRNIFVTWWKSLFEASTAFRRASGLTVSPLTRRG IARFDHFRPVPNVSKFASF  
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNNMTISLRCPFNSLGGLNQ  
CSHSNSCKAYQNASNVT SKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDE TSA  
YYMEKPGSYIEFTISEFNVNGTF SAPLSFLDPSLLADLDEMIRNYKYELKSIYSSVDMIL  
QNYGSLPITFHRNKIRIHF PNSTVVETEKL IAGLNIATGVIYADTSPDISLEGTNLNALV  
NVNDSGSVWSFVKEPSFSPRSASFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2: 963-1228 (SEQ ID NO 225)

ATCAAATATTGATCGAGTT CATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA  
GCACTTATTTTTTTTGGATTTAGATGTGAGACATACTAAAAAAAAGTTGCTATCAAGCC  
TATAATTTGGCTACGTTGTCTTCCGGTGTTTTTCAATTGATTTAAGTTACAACACTCAAA  
TCTGGGTAATTTGATCTTTTTTAATAATTATTTTAGTGACATATAGTTCTTAGAGTTTCGC  
AGATTTATTTTGTCAATTTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC  
ACATCGCGCATGTGTGGGTGTATATGCCCTTTTCACGATTTTTAAGTTGCGTCTCAAAAT  
AGTTTCCGAGTTGGAAGCCTGAGTTTTTCAAAACAATATAGGAATTAAAGGTATACGTCT  
TTGGATACATGTTATTTGAAATGGGGTAGAAGCTAGCACAACTGAAACCAAGAAAACACAG  
ATCATAACTAACCGTTCAAGATGTTGATGCCAAAGCAAGAAAGAAACAAAATTCACCAAT  
ACTTGTTTCAAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT  
GGATAGCAAAGATGATAAATGAAAATACAATTAAATTGAACTTGAATATCATTA AAAAGTG  
GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCAATGAATCCG  
AAAGAAAAGTGCAACCTAAGCAGAATTCATTATTTACGCGTCCATTTTTATAATGTTT  
GAACTTTTGAGTCCCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTTACT  
TTACAGTTTCCGGAGTTTCCGTATTATTGCAAAAGGACCACAAACAATTGAAATCATGAT  
ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT  
AGAAGGTGTTGTCGTCGCTAAGAAGGATTCAACCAAGCTAAGCACGAAGAAATTGATAC  
CAAGAAGTTGTATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC  
TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACCTTGAG  
AGAATACTTGAACCTGCCTGAACACATTGTCCTCAGGTACCTACATTCAAGAAAGAAACCC  
ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)

MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS  
WQYYYYTLTEEGVEYLREYLNLP EHVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)

CCCTTCGCTAAATCATTAAGAGGTCATT CATGAAGTTAATTCAGCACCAAAGTTGGACTG  
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTTCAGATAATTGTCGTCGC  
ACAAGACTGCCCTCCCGTCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG  
ATGTACATAACTTGAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCTCTG  
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTTCGTTCTTCTTATTTCTTGT  
CTTAGGCATTTCCGCTTTAGAAAATTTCGTTGGGTGGTTTCTGCGACGGGTATCCCCTTCG  
ATTTTGCATAATGATCTTCAATTCTACAACATAAAATCAAGTAGATACAGGAAAATATTCC  
ATAAATTATAGTGTAATCGCCCTGTATACACCTTATCGTTTCATCTCAGGCAAGTTAAA  
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAAGCTCACTGTAGAGACAGAAA  
CAGTTGAGGCACCCGTGGCAAATAATCTTTTATTGTGCGAATAACAGTAATGTAGTAGCAC  
CTAATCCTTCTATTCCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAAATAGTTG  
ATGATTCTGTCGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTGCCACCA

TAGATAACAATTTAATGGATTCCGATGCCACGTCACATAATCAAGATCATTGGCATTTCAG  
ACATAAACAGGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTAG  
AACATATCGGC'TCTGTTTCATCAACTAATAATAAGTAACAATGCCCTAATCAACCACA  
ACCTCTGTCTATCTCATCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT  
TGTTGGTAGCTTCTAACCCCTGCGTTTGCTTCAGATGTTGAACTCTCGAAGAAGAAACCTG  
CCGTATCTCCAATAATATGCCCTACAAGTAACATTGCCCTTTATCAAACAGCGAGATCCGG  
CGAATATTTCATGGTCCATCATCAACTTCCGCATCTAAAGCGTTCAGAAAGGCTTCGGCCCT  
TCTCCAATAACACGGCAGCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC  
CTCTTTTACCTCTACCTTCACTATCACAACAAAATAAGCCAAAAATAATAGAGAGGCCCA  
CAATGCACGTCACCTAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA  
AGGCGAAGAAATGCTCCCGCAATTCAACCACACACGATAATGGTCCAGTAGCAAATGATG  
GGCTGCGTATACCGAATCAC'TCGAACGCAGATGATAATGAAAATAACAACAAAATGAAGA  
AGAATAAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAAATATGCA  
CTACATCTACTAAAACAGCGCCTTCAACCGCACCTTTGGGCAGTACAGACAATACTCAGG  
CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA  
CCAGCAGCAACAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA  
TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTCTAACATAATGCAATAAATGACG  
ACTCACATGAGAGTAATTTCAGAAAAACCAACAAAGGCGGATTTTTTCGCTGCAAGGCTGG  
CTACAGCTGTAGGTGAAAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG  
CAGCTAATTCGACTAAAAACCTAATATTTCCCTGACTCCTCCAGCCAGCAGCAGCAGCAGC  
AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA  
GCGCCCCAT'TGCTAAACAATAACAAAAAAT'TATTAAGCCGACTGAAAAAT'TCAAGACATA  
TTAGCACTGGTGCCATAT'TGAATAACACAATCGCGACTATAAGCACAAATCCGAACCTTGA  
ATTCTAATGTGATGCAGAACATAACAATCTGATGTCGGGACACAATCACCTGGACGAGT  
TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG  
TACAATCGGTAGATTTCGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGC  
CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACATTTACTTTTCATCCA  
CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAAATTCGCAGGAATTGG  
AACCAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTCTACTTTGAGACAT'TCCT  
CTGCTAATAGAAATCTAATTTATGGTGACAACAAAGGCCCTTTAGAACAAACAGTGTCAA  
AGATATTTGATTCAAACCTTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC  
ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAAATAGTG  
TGAAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCATGGTTTAAACTTTT  
ATGGTGATAACAATGTTATTGAAGAGGAAAAATAATGGTGACTCGTCTAATGTAAATCGAC  
CGAACACACTAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG  
ATATTCACCTCCATGTTTATTATAATCATAAGAACGATTTAGAAACAAAACCGCTAATAT  
CCGATTATGGTGAAGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT  
GTTACTATGGCTCAGCATCCAACACGCACGAACCTCCATTACATGGAAGGATGCCTTCAA  
GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT  
TGAATGAATATACCCCTTAAGAATGAAACGTGGTCAAAGACACCTATCAAGAACAAACA  
ATAGCATAATGAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCCAATA  
TCAATAATAACGATATGTTGGTTACTCACCACCAACTTTTACTCAAGGAAGTCCCCAT  
TTGTGAAAGTAAAGAATTTTCTTTTATCTTTCGATTTGTTATATCATCACTATTGATGACAG  
GATTCATTCTGGGATTTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG  
TGATGGATAATGTGATTTCAAGTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT  
TTAATCCAGGATTCTTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTCGAAAAA  
GTTCTTACCTGAAGTGCGATTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA  
TTTTTACAAATAACGACAAATCTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG  
GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAACTAGAGACACCATTAAGT  
TCCAGGGCGGCGCATTTAATAGGAACCTACGATGTGTGTCAGTCTCGAGTGTCAAGCTTTTAA  
GTCCTGGGTCTCGTGAAGCCAAGCACGAAAACGACGATGATGACGATGATGATGGCGACG  
ATGGTGACGATGAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAATGCTAGAG  
ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA  
TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTCAATACGCAAAAATCTACGGCTA  
TTCAAAGGATTCCATGGTCCATCCTGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVETETVEAPVANNLLLSNNSNVVAPNPSPSASTSTSPLHREIVDDSVATA  
NTTSNVVQHNLPTIDNNLMDSDATSHNQDHWHSINRAGTSMSTSDIPTDLHLEHIGSVS  
STNNNSNNALINHNPLSSHLSNPSSSLRNKKSSLLVASNPAFASDVELSKKKPAVISNM



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PTSNIALYQTARSANIHGPSSTSASKAFRKASAFSNNAPSTSNNIGSNTPPAPLLPLPS  
LSQQNKPKIIERPTMHVNTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH  
SNADDNENNNKMKKNKNINSKGKNERNDTSKICTTSTKTAPSTAPLGSTDNTQALTASVS  
SSNADNHNNKKKTSSNNNGNNSNSASNKTNADIKNSNADLSASTSNNNAINDDSHESNS  
EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQQQPPKQ  
QQQQQNHGITSKISAPLLNNNNKLLSRLKNSRHISTGAILNNTIATISTNPNLNSNMQN  
NNNLMSGHNHLDLSSIKQEPHQLQQQQPPMDVQSVDSYTSNPDNSNVIKSPDKRSSL  
VSLSKVSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN  
YGDNRPLR'TTVSKIFDSNPNNGAPLRRYSGVPDHVNLEDYIEQPHNYPTMQNSVKKDEFY  
NSRNNKFPHGLNFYGDNNVIEEENNGDSSNVNRPOHTNLQHEFI PEDNESDENDIHSMFY  
YNHKNLLETGPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGRMPSRNNNDY  
DFMVGNNNGNQQNLNEYTPLRMKRGQRHLSTRNNSIMNGSIHMNGNDDVTHSNINNNNDIV  
GYSPHNFYSRKSPFVKVKNFLYLAFVVISLLMTGFI LGFLLATNKELQDQDVVVMNDVIS  
SSDELIFDITVSAFNPFFSISVSQVDLDIFAKSSYLKCDSDNGDCTVMEQERKILQITTN  
LSLVEESANNDISGGNIETVLLGTAKKLETPLKFQGGAFNRNYDVS SVSVKLLSPGSREA  
KHENDDDDDDGDDGDDENNTNERQYKSKPNARDDKEDDTKKWKLLIKHDYELIVRSGMK  
YEVFFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAATTTTGGATTTACTGCTCCTCTTTTAAGAAGACAAGTG  
TGTGATATCGTAGCGGTAGGAACCAATTTTGCAATCGATTTACTTACAGCCAAGAAAATC  
TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTACACGTTGTGCTTGCCAGGAAC  
TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGCATCTGATGT  
GTAAACTCATGTGGTGCAC'TGGTGTGTTTCCAAAGACTGCACTATTAAGTGGGAATTTT  
TTTTTCTTCTAGTGAATTTTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATTATTTAA  
ACGGACGGCAAACATGAAAAAAAATTACCAACCATATTTCTATTTCCCTTTCCCTTTAC  
CTATTTCTCTTTTTGAAATAGTTTCATTTCTCTCTCTGAAACGACAATAAACCAAACTCTA  
GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAAACCGAACAAACAATTGAAATCCCAG  
AAGGTGTTACTGTGACGATTAAGTCCAGAATCGTCAAGGTTGTGCGTCCAAGAGGTACTT  
TGACCAAGAAGCTTGAAGCATATGTATGTTACCTTCACCAAGGTCAACAACCAATGTATCA  
AGGTTGCTGTTTCAACCGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCGTTAAATCTT  
TGGTTGACAACATGATCACTGGTGTACCAAGGGTTACAAGTACAAGATGAGATACGTCT  
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCTAAATTCATTGAAG  
TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTCCCAGTTAGAGATGGTGTACTA  
TCGAATCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG  
TTTCCCAAAATGCCGCTGACTTGCAACAAATCTGTCGTGTTAGAAACAAGGATATCCGTA  
AGTTTTTGGATGGTATCTACGTTTCCCACAAGGGTTTCATTGTGCAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPEGVTVSISKRIVKVVGPRGTLTKNLKHIDVTF TKVNNQLIKVAVHNG  
DRKHVAALRTVKSLVDNMITGVTKGYKYMRYVYAHF PINVNIVEKDGAKFIEVRNFLGD  
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICVRNKKDIRKFLDGIY  
VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACTGGGT'TTTTGAAGACCAGAATGGAGATC  
TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAAC  
AGTAATGGAAATGGTAATGATGACACCTTAATCAGAGAACCGGAAGCACTGGGGCGTAAG  
ACGAGTAATGGAGGGCGAATATGATTACTAAGTTAAATAAATCAGATACAGTATTTAAAG  
TTCTTTCAAAAAAGATAATGTCATATATTTTACTATCTACGCAGTGAAAGAGTTCCTTC  
TAATGACACACTATTCAC'TTCGGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT  
TATCCCGGAAATGCGATGAGATGAAAATGCATGAAGTAGCGTATATATTGATTGCATGAG  
GTTGGACTTGAAAGGGCATATATACTCGGTTTTATCATTGATTCAAGTGT'TCCCATAAAT  
AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT  
ACAGAAAAGCGCAAGAAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAAC  
AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAAGTAGCAGAAGATGAGAGTTTACAAA  
AGGATTTAGATATGACCAAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG  
ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC  
GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAACTGCTATTTCCAAATG  
CTGTCAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTAAAAAAT

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CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACCTCTTTGACCA  
TATCACATTTTCCACATGGACCCACTGCACAGTTAGTTTACACAATGTTGTTATGAGAC  
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT  
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCAATGCGGGG  
CCAAAAAGATTCCGAAAGAGTAATCACATTTTGGCAATAGGGGTGATTTTCATTAGCGTTA  
GACAGCATGTATATGTGAGAACAAGAGGGGAGTAGAGATTGCCGAAGTTGGTCCCTAGAT  
TTGAGATGAGGTTGTTTGAAGTGGGTAAGTCTTAGAAAATAAGGACGCTGATGTTG  
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLYRKAQELQDSQLQQRQIIKQALAQGKPLPKELAEDESLQKDFRYDQ  
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG  
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVVMRHDIIINAG  
NQSEVNPFLIFDNFTTALGKRVVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVVYR  
TREGVEIAEVGPRFEMRLFELRLGTLENKDADVEWQLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:  
990-1418 (SEQ ID NO 233)

AAACACCTACTTATAGACACGACCAAACCTTTCCACAACCTTTTCATCAGAGAGAAATGTTG  
ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACCTACCTGTCATTCTGCATAG  
TAGTAGTTACGAAAGGCACAGAAAATAACAAAAAAGTCAATTTTCTACGGT  
CTCCATCCGTACCTCTTTAAATCCGTACATTATTGTTTGGCTTAATTTCAATATTTCCGA  
AAAAGCGAGCGCCCTGGTAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC  
CAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTTCCAGCCTGGCTTTAGGGAAGAA  
TGGGCTCACCTAGGCGTTCATAATACGCGGAGGGGAAATACCAAATGCTATTGATTATGG  
TAAAAATATGTGTTATTTGACTTTGTATATACAAACAGAGAAACCAACACACTAAAG  
ACTAGACACATAACTGACCAATGTCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA  
GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC  
TAAAGGCTGACTTGAGACCATTGCAAAATCAAATCTATCAGAGAAGTATGTTAAAGCTTAT  
ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGTTCTTTGTCAGTAATTTTTT  
CAAAAAAGAGTGATTTTGGAGCAGTATCTGTATGAAATTTTCATGTGTTTCGAGAAAAATAG  
TAATTTCCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCT  
CCTTGGTCAGTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA  
AGGAGAAGAATCACAAACCCCTTTTTTGTATGAATGAACCAATTCAGTTACTAACTTTAT  
TTCAACGCTGCTTGATTCCTTATTGTTTAGATTGATGTCACCGGTGGTAAGAAAGCCTAG  
TCCTTTTGTGCCAGTTCAGCTTTGTCTGCATACCATAAGGTCCAAACCAAATTTGACCC  
GTGAATTGGAAGAAATTTCCCTGACCGTCATGTTATTTTCTTGGCTGAAAGAAGAATCT  
TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA  
CTGCTGTTTCACGACAAGGTTTTTGAAGACATGGTTTTCCTCAACTGAAATTTGTCGGTAAAA  
GAGTTAGATATTTGGTTGGTGGTAAACAAGATCCAAAAGGTTTTGTTAGACTCCAAGGATG  
TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA  
AACAAATGTTTTTGAATTTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)

MSSVQSKILSQAPSELELQVAKTFIDLESSPELKADLRPLQIKSIREIDVTGGKKALVL  
FVPVPALSAYHKVQTKLTRELEKKFPDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA  
VHDKVLEDMVFPTEIVGKRVRYLVGGNKIQKVL LDSKDVQQIDYKLESFQAVYNKLTGKQ  
IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:  
987-1333 (SEQ ID NO 235)

TTCATCACCAATATAGACTAATGCGTTTTGGAAACGCCAAACCGCAGTGACAAATAGCAAA  
TATGTAGCTGTCATATCGGCATATAATAACAGTTTCTACCAAATGCTGTCCTACATTCA  
GAGATCTTACATCCTTACATCTAAAGTAAACCTAGACATTTACTTCGAGTTATACTTTT  
TTTTTATTTATCTATTTTCTCTTGGCGACATTTAACACCTGAATTCGGCTAACGCCA  
GGACTGATCCTGCCAGGGAAGGGAGCTTTGTCTAGTGCCAATAGGCCGACCAGTAGGAA  
GGTTACAGCAGCTGGCCCGCAGAGTGATTGGGTACAGGAAATAGCGCAACCTTCTCTTT  
TGCCCCGGGAAAGGCGGTCAATCTACCTTCGAAGGGCTAGTACATGAGCGCGAAGGAGGC  
AGATAATAGCACCATTAAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA  
AACAACAATTATCAGTAAAAATGGGTATGTTATAACCATAATTCTAATGGTGAATAAAA

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TCAGGACCAATAAAGAAAAGCTAATTTTGATTTTATTGTCAATGAAATTTTCATAATCGTC  
ATGAATGCATAAACAGACACACCTAGCAACTGTATAATCTGCGCCTAAAAAGGGCGTATA  
CACAAAACTAAACGATGCGCAATAAAAGTTCAGCAGTCAGCAATGAAACCGAGATATGCA  
GCAACAGAGTATCATATGCATGGAGGATCCTTTCTGTTTTTCTGATAATATGCTCTGAAA  
AAGCTCCAAACAGCACAGTAGCCTATTTGTGAAGCTCAAAAAAGGCTTCTATTTCCCTCG  
CTATCTTCAGATTGTGCAGTGATATTCTTTGAGGAAGGAAACGTAGAGGGGATAAGTTGG  
ATAACTGTTATTTCTTTTCAATATGCTAGATTTTGCTTACCACCTTACTGATTTTTTCTA  
ATAATAAACTTTTTTACTAACATTAGTACGATGTCTCATCTATTTCTTCTATTTAGTTAA  
CGTTCCAAAGACCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACA  
CAAGGTTACTCAATACAAAGCTGGTAAGGCTTCCTTGTTTGCCCAAGGTAAGAGACGTTA  
TGACCGTAAACAATCTGGTTTCGGTGGTCAACCAAGCCTGTTTTCCACAAGAAAGCTAA  
GACTACCAAGAAGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACCAGAGCCCAATT  
GACCTTGAAGAGATGCAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGC  
TTTGCAATTCTGA

YNL162W, 116 aa (SEQ ID NO 236)

MVRCLIIYFFYLVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGF  
GGQTKPVFHKAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGKKQKGQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)

GGTCCACGTCAGTTCCACACAATAACATTTACGTAGTGTTACGCGGAAGCAGTTACATCT  
CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC  
GTTAGTATTTTTGGCCGCCGGTAAATTTCTCTTGTTTTTTTTTCTTGATTTCACTTCTTTT  
CATGTTCCCTTTGGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTGTTTCCGT  
AACATCCATACCTTTCCCTGTATAATATTCTTGCTGTAAAGTTTGTTTTTTTTATGAAAAA  
AACATTTTCTTTTCTTGAGATGAGGCGCCGCGAGCCTTTCTCCCATGGGCAGTGGTAAAT  
TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTTCATACATTTTAAGCAATT  
TCTAGTTTGTAGATATTGTTAGATTAGTTTTTGAACATTGTTTTGATAACTGAAAATAAA  
ACAGCAAAACAACTACAAAAATGGTCGCTTTAATCTCTAAGAAAAGAAAGCTAGTCGCTG  
ACGGTGTCCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTGAAGAAGGTT  
ACTCCGGTGTTGAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA  
GAACTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACCTTTGTTGGTTC  
AAAAGAGATTCAAGTACGCTCCAGGTACTATTGTCTTATATGCTGAAAGAGTTCAAGACC  
GTGGTTTGTCCGCTGTGCGTCAAGCTGAATCTATGAAATTCAAATTGTTGAACGGTTTGG  
CTATCAGAAGAGCTGCTTACGGTGTCGTGATACGTTATGGAATCTGGTGCTAAGGGTT  
GTGAAGTTGTTGTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTTGCTG  
ACGGTTTCTTGATTCACTCTGGTCAACCAGTCAACGACTTCATTGACACTGCTACTAGAC  
ACGTCTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA  
AGAGCAGAACTGGTCCAAAGGCTTTGCCAGATGCTGTCAACCATCATTGAACCAAAAGAAG  
AAGAACCAATTCTTGCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAACTGAAGCTC  
AAGCTGAACCAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)

MVALISKRRKLVADGVFYAELNEFFTRELAEEGYSGVEVRVTPTKTEVIIRATRTQDVLG  
ENGRINELTLLVQKRKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY  
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG  
VLGIKVKIMRDPKASRTGPKALPDAVTIIIEPKEEEPILAPSVKDYRPAEETEAQAEFVEA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)

CTTTGATAAATTAATACGGTAAGATACCGTGTGAACCTATTATAATAACTGCCACGCTTAT  
AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT  
ATCGTGGAGCATAACTACAACAAAGAATACACAGCGTCACATAGAGGGTTTTTGAGAGGA  
GAAGTTGAAATAGGACTTGATCTTGGGGGAGAGGGGATTTGAAAGCACCCATTCAGGAGT  
ATGTGTCTGTAATTGAAGTGTTAGCGCGCGATTACCTGTAATAAGAGTGATGATTTGAT  
AGCGCCATTTCTACATCATATGGCAAATGTTGAAAACTGTACGCGCGAACTAAATTTTT  
TTTTACATCCCACTAAATGAAAATTTTAAATCGATGCCCATTCCAAATATGCTTATTCTGA  
AGGACGGCTCTGACAAGGGCATATGCGTTAAGATTGATTGTTCAATATTCATAAAACAGG  
ATCTTTCAAGGGACGATAAAATGGATGAGCAAGTTATTTTTTACAACAAATACCTCAGGAA  
CAATAGCTTCTGTACACTCATTTGAACAGATAAAATTTGAGGCAATGCTCCACTCAATCAA  
GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTTTATTGCTCAAGCACAAAAAGCAT

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TAATCAATGTCTACAATCTGTCTCAGGTTCTTTCAAAAGAGAATCTGTTGAACAGCGCTTAC  
CATTACCTGAAATCCTAAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA  
GAATTC AAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT  
CCACCGAATCGGGTAAATTTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA  
AGCCTATGGCTCATTACCAAAGTATCACCAAGATTAAGTCCATTTTAAACGGCAAGTATA  
TTATTACTTCTGGTAACGATTTCGAGAGTTATTATATGGCAAACCTGTTGACTTGGTATCAG  
CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG  
ATTTCCAAGTTTCTTCTAGTCAAGGAAAATTTTATCATGTACTGATACGAAACTCTTCA  
CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA  
AGCAGAAGGCAAACGAAAATGACGTTAGTATTTGGTAAGACCCAGTATTGCTTGCACAT  
TTACAACCTCCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA  
TTGGTACTGCGGAAGGTTGTTTTCATTGAATTTATTTTATAAACTAAAGGGTAATGCTA  
TCGTTAATCTGTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC  
TAGTGCAACGTAACCTACTAAGTGGCGGCGAAAATGAAGATTTGGATGCATATATGCAA  
TGGGCCAACTTGTCTGTGAGAATGTCCTAAATTCAAATGTGTGCATGCCTAGAAATATCAA  
TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTTGCGGAAATTT  
ACTCAAAACAAATCATTAGAATATCCAACTTTAACTACATCACAGGATTAGTTGGAG  
AAGTGACCAATCTCTTAACCAACCCTTACAGACTCGAACGTGGAAATTTACTTTTGAAG  
GAGAATCCAAAGGCAAACAACCTAGTAATAATGGTCACAATTTTATGAAGATACCAA  
ACTTACAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC  
AGATAGGAGAACCAGAAGCAGAGACAGATCCTAACCTCGCATTACCACTTAACGACTTTA  
ATGCCTATTTGGAGCAGGTCAAACGCAAGAATCGATATTTTACATATCGGTAAGGTGT  
CAAGCAATGTAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG  
CCGCTAAAGATGAGGAAATTACAGAACTTAAGACCAACATAGAAGCATTAACCTCATGCCT  
ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA  
AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTNTSGTIAVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL  
SGSFKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL  
YIWELNSGILLNVKPMAHYQSITKIKSILNGKYIITSGNDSRVIWQTVDLVSASNDPK  
PLCILHDHTLPVTDVQVSSQKFLSCTDTKLFTVSQDATIRCYDLISLIGSKKKQKANEN  
DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKILKGNATVNLQ  
AGVNTVQKGRVFSLVQRNSLTGGENEDLDALYAMGQLVCENVLNSNVSCLEISMDGTL  
IGDTEGKVSIAEIIYSKQIIRTIQTLLTSQDSVGEVTNLLTNPYRLERGNLLFEGESK  
PSNNNGHNFMKIPNLQRVIFDGNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV  
KTQESIFSHIGKVSSNVKVIDNKIDATSSLDNSNAKDEEITELKTNIEALTHAYKELRDM  
HEKLYEEHQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCCGTACGTCAAGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCGTTTGT  
TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTAAAGTTTCTTTTACCAATTA  
GTGCTCACTTCTCTCGTCTTTTATTAGGTGTGTGTGTGTGTGCGTAATTTTTCGCTG  
ATTACTTTTATATAGTGTAGTTTGTCTTGAATGTAATAAAGACTTCTGTTTTATTTTGT  
TTGTTATTTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA  
CTACAAGAAAACCAAGCTTCTATTACTTTGTTTCTTTCTCTTTTCTTTTGAATAAAA  
GAATTTTCTTTAAGGAGTAACCTTAAGCATTTAGCTGCACATTAACACTTTTCTTTT  
CTTCTAACTCACACACTTTTGGGAAGAACATTTATTTTTCGACCTTCTTTCCCAATACC  
CAGCGCTTTTAAATTGAAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG  
TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT  
CATCGGACGGTAGTTTAACTACTACCACCTCTACTCATACCACTCACAAGTATGGTAAGT  
TCAACAAGACTTCCAAGTCCAAGACCCCAAACCACACTGGTACTCACAAGTACGGTAAGT  
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATAACCGGTACTCACAAGTATGGTAAGT  
TCAACAAGACTTCCAAGTCCAAGACTCCAAACCATAACCGGTACTCACAAGTACGGTAAGT  
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATAACCGGTACTCACAAGTATGGTAAGT  
TCAACAACAAACCAACATGACACTACCACCTTATGGTCTGGTGAAGAGCCCGTAAGAACA  
ATGCCGCCCTGGTCCATCTAATTTCAACTCCATAAAATGTTTGGTGTACCGCTGGTA  
GTGCTGCCGTAGCCGGTGCCTTATTACTATTATAA

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YNL190W, 204 aa (SEQ ID NO 242)

MKFSSVTAITLATVATVATAKGEHDFTTTLTLSSDGS�TTTTSTHTTHKYGKFNKTSKS  
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS  
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS  
NFNSIKLFVGTAGSAAVAGALLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACACATATATATATTTTTTCATTTTAAATGTCTTAGCTTTTGTPATCTTAGATGAA  
GTTTTAGTTCTGTATATCACGATCAAGATATCATACAATCATAAATTCAATTTATTCTTCT  
GTTTCCCCTCTTGAGGCATCAAACGAGTGTGTTGACTGATACACACCAACATACTAAGGCA  
ACTTTTCTGGCTGCCCCAAAGCTGTGGCACGTATGAACTGCTTTTCGGCTGCATAAAACA  
ACCATGTGGAGTTTTTACTGTATTCGCATTTTCGCCCCGCTAGCATTTCTTCGTTTCATGCTA  
AAAAAGAGGCGTGGGCTAATATTCAGTATTAATAATTCCGGCACCCGCACAGCCCATACC  
GGAAAAGGGGCTGGTGTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGG  
AAAGACTTTAATTTGTCTTGCTAAACACTTGTAAAGCCTTCCAAATATAGATCACTTAAGA  
CAATCTAACAAGTGTCCAAAATGTCTGCAACGAATTCTACTCAAGTGGCCAACAAGGTC  
AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGTCTCCAAACAACGGTCAATATGGTG  
CCGACAAATGGTAACCCCAACGGTGAACGTGGTATTATTTCCACTATTGTAGGTGGCAGTG  
CCGCTGCGTACGCTAGGCTAAGGTGTGCAACAACCATTTCTAAGTTGAGTGGTGTGCTGG  
GCGCCATAGGTGGTGCATTCCTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC  
AACAAGAGCAATACGGCAACTCAAACCTTCGGAGGTGCTCCTCAAGGTGGACACAACAACC  
ATCACCGTCAGACAATAACAACAATAACGGTGGATTGGCGGTCCAGGCGGCCCTGGCGG  
TCAAGGTTTCGGAAGACAAGGCCCAAGGATTTGGAGGTCTGGTCCACAAGAGTTTGG  
TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTTCGGCGGCCAGGTGGC  
CAAGGATTCGGTGGTCCAAACCTCAGGAATTCGGGGGCCAAGGTTCCTCAAGGATTCAAT  
GGCGGTTACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGQQGQYNQNNQERTGAPNNGQYGADNGNPNGERGLFSTIVGGSAGAYAGS  
KVSNNHSLKSLGVLGAIGGAFLANKISDERKEHKQQEQYGNNSNFGGAPQGGHNNHHRQTIT  
TITVDLAVQAALAVKVSSEDKAHKDLVLVHKSLLVQVAKDSVVQILKNSAARWPRIRWSK  
PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTTCTTTTCAAAAAACCGTAAAAATTTGAGGTCACACCAACTAAATACAAA  
TTGTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACCTCAATA  
TAGTAAAGTTTTCATCAGCAATCTTATCTGAGTAAATATTATCTACGATCTAAATATAGGAT  
GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC  
CTTTTACAAAGTGGATACAGGTTCCTATCACTACCGCCATTTCACTAGCAAGTAGAGTA  
TTGAGAAAACGGTAAACTTTGAAAGTTGCAGATGCAGAATATATATCTGGTTTTGTAGTT  
CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTAAATATAAGTAATGAA  
CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTTAATC  
AGCTAGTGCATACCAAAAACAATGAGTAACCAACACAGCCCTCAGCCATTTTGTGTTGGACA  
CCAAATTGGTGAAACTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCAACAATAAAAAACA  
TATTCGCCGAAAAAGCATTATATTTGAAGCTCGCTCTTGATTATTTCTTTCTTCAGAAAGA  
ATTTACTAGAGTTTTGCGTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG  
ACACTATATATATTTTGTGCCTGTTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA  
ATATATTGGAAATATGTTTGCCAGGTTTGTTCAGGGAGGACTTGAGGGTTTTTAATA  
ATACTTTTTTACACATATCACGATAACCGCCTACGTATTTCTCCAAGAAGACTTTTCTCAAT  
TGTTCAAAAAAATCAAACTAAGGCTTCTGTACTATGTTTTACAGTTGAGGAAATTTTTC  
TGACAAACCAAGAAATTTTACCTCAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA  
ATAAAGTACAGACAAATGGGCGCAACGGCACGATTTTCATAGTCACTCTAGAAATAAAAC  
TGAACAAAACACAAATCACTTTCTCCTCATTTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA  
GGGAAAAATCAGGCGCCAGCATAAAAAATAACCTATTAGTGATAAAATGACTGCACATG  
AAAGGAACCACTCGAATCTGTTCAACAAACATACTAATTTTCGGGTGACTTATACTCAA  
TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPQPFCLDTKLVLLEELQEGKQFNNKNIFPEKALYLKLALDYSFFRKNLLEFCV  
HLDKIKGVIRPNYDTIYILCLLEVLLNLVFTDNILEICLPRFVSREDLRFVNNTFYTYH

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DNRLRILQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNQ  
PQRHDFIVTLEIKLNKTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPE  
VQQTILISGDLYSIALAVTSIESALITLDDL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTTCTCGAGAAATTGTGAACAAAAGAAAGACACAGAAGATGATAAGAG  
AGAGAAACAACGAAGAAAGAACAACAATGTTGGGGTTCACCCGAGAGATATTGACATACT  
GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA  
TATTCTCTTGTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA  
TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTCTGGA  
CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCGGGTAAACGGAA  
TTGTGATAATTAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA  
TTAGCAACTATAATAGACTAGTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT  
TCCAAGAACGCAAACTTAGAATGGTCCGGATTCTTCCCATAATTTTGAGCGCCCTATCTT  
CGAAATTAGTGGCGAGTACAATATTGCATTTCATCCATACACTCAGTGCCATCTGGAGGCG  
AAATCATATCTGCAGAAGATCTTAAAGAAGTTGAAATTTTCAGGGAATTCGATCTGCGTTG  
ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG  
GTCAAGAACTCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAAGAGG  
CAAAACTAAATGATGAGAAGAATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT  
CAGAAGACATGAAAGCATCGCCTGGTGACTATGAATTTTCCAGTGATTTCAAAGAAATGA  
GAAACATCATAGATTCTAACCCGACTTTATCTTTCACAGGACATTGCCAGATTGGAGGATA  
GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC  
ATGAATTCGCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG  
AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAAACAATCCTCCTGTAGTCCAGTTCA  
TTAATGAAAAGTTTTCCAAATTTTAAAAGCAAAATCATGGCCGCTCTGTCAAATTTGAATG  
ATTCTAACCCACAGATCCTCTAATATCCTAATAAAAAGATACTTGTCATTTTAAACGAAT  
TACCTGTACATCCGAAGATCTTCCTATATACTCTACGGTTGTTTTACAAAATGTATATG  
AAAGAAACAACAAGGACAAACAGTTACAAATAAAAGTCCTGGAGTTGATCAGCAAAATTT  
TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAAGAAATGCTG  
AGAATTGGTTCGTCAAATCTGCAAGAGTGGGCAACGAGTTCCAAGAGATGGTCCGAGACA  
AAAGTATGAATGAATCATACATAACAAGAACGTTTTTTACACCCCTTTACAACCTGAAGAAA  
TTTTTCAAAGTGACATCACGATCAACAAAGGGTTTTTTGAATTGGTTAGCGCAACAATGTA  
AAGCCAGGCAATCTAACTTGGACAATGGGCTCCAAGAGAGAGATACTGAACAAGACTCAT  
TTGATAAGAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA  
TAAAAAATTTTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSSKLVAstilHSSIHVPSGGEIISAEDLKELEISGNSICVDNRCYPK  
IFEPHRDWQPILPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS  
PGDYEFSSDFKEMRNIIDSNP TLSSQDIARLEDSFDRIMEFAHDYKHGYKIITHEFALLA  
NL SLNENLPLTLRELSTRVITSLRNNPPVVEFINESFPNFKSKIMAALSNLND SNHRSS  
NILIKRYLSILNELPVTSEDLP IYSTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE  
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFDFDTLYNLKKIFKSDIT  
INKGFLNWLAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE  
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAAGTACATGATTTTTGTTTGCATTGATGACTTGTTTATGACTAACATATTTAATTT  
TTATTTGTTAACCGTAGGGTTTTATGAAGTGCTGACGAATCCTGTTTATTGGAAGCATA  
TTTTACTGTTTGGCGTTTGCTATGCCCTGATTTTTGTCACTATTGCTGGTCTCTTTTATG  
TCACACTTGTACCGCTTTTAGTGACATGGGCCATACTGTTATTAGGGCCTCTTGGTGTGA  
TACTGGTTCATATTCAATGGATTTTACAAACGAATGTCTTGACTGCCTTTGTTTGTAGAA  
CACTGGTCTTGACCCATATTACGAATCAGATATTTGATATATCTTTGGTGTGCAAGACC  
AAGATGAATTTCTAAACGAGGTGAAGGTATTGCCTAAACCACAAAAGCCACATAGAAAAA  
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGGAAGTCGGATTTTTAAGA  
TTCCCGAGATTACTATTACGAATGTTTTTAAAGTCTCCAATTTTACTTCACTAACATTAC  
TGTCGCTAATTCCTATTGTAGGACCAATCTTGGCAAATCAACTAATGGCCCCAAAAAGAA  
CCTTTACCTATTTGCAGAGGTACTTTTTACTAAAGGGATTGAGTAAGAAACAGGCCAAAG  
ATTTTCAGTACGAGCATTACGCAAGTTTCATATGTTTCGGTATGTCTGCCGGTCTACTAG  
AGTTAATACCCTTCTTCACAATAGTCACCATATCTAGCAACACTGTTGGTGCAGCTAAAT

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GGTGTACTTCGCTACTAAAGGGTGAAAGAAAGAAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFFKVSNFTSLTLLSLIPIVGPILANQLMAPKRTFTYLQRYFLLKGFSSKKQAKDFQYEHY  
ASFICFGMSAGLLELIPFFTIVTISSTVGAAGWCTSLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)

ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCTGGAGGAAT  
CATAGGCAAAGAAAGAAAAGAAGATTCATCTTTAAACTACCTTTCAAGCCTTTATTC  
GTTCTCTCGTAAAGGACACACGAAAAAATAAACAGTACCTTGCAGAAGGAGTGCAGAGTT  
AGGTCGCAGGGAATCCTTGAAAGCCAAGAGTTTTTTTTCCGTAATGATCTCCCAAAGCAA  
CCATCAACATTGTGGTGCAAAGTTTAGTGTAAGATGTTCTACTGAACATATCTTAATAGCT  
GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAACAACAAAGTAATGTTCAACTTTTCGTA  
ACTACGGAAAAATAATATATAAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT  
CATCTTCTTTTCCAGTTTAGCCATTATCAGCACATAATACAAAACACACTCGTACACTC  
GCTTCAACTATAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG  
CTTTGGCTTCTGCCCAAACCTCAGGAAGAAATGACGAATTGAACGTTATTTTGAATGACG  
TTAAGTCCAACCTTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT  
TAAGCAGTCTGCCATCTGGTGTTTAGACATCGGTTTAGCTTTGGCTTCCGCCACTGATG  
ACTCTACACTACTTTGTACTCTGAGGTTGACTTTGCTGCTGTTAGCAAGATGTTGACCA  
TGGTTCCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACCTCTA  
CCACCGCTGCCCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCT  
CCAGTGAAACTACTTCTTCTGCCGTCGCTTCTCCAGTGAAGCTACTTCTTCTGCCGTCG  
CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGCTGCTTCTTCCAGTG  
AGGCTACCTCTTCCACCGTCGCTTCTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT  
CCTCTGCTGTTTCTTCCAGCTGTTGCTTCTTCCACCAAAGCCTCCGCCATTTCTCAAATCA  
GTGATGGTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAACTGAAAACGGTGCTGCCA  
AGGCTGTCATCGGTATGGGTGCTGGTGTCATGGCCGCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)

MAYIKIALLAIAALASAQTQEEIDELNVILNDVKSNLQEYISLAEDSSSGFSLSSLPSG  
VLDIGLALASATDDSYTTLYSEVDFAAVSKMLTMVPWYSSRLLPELESLLGTSTTAASST  
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSAATSSAVASSSEATSSSTV  
ASSTKAASSTKASSAVSSAVASSTKASAIQSISDQVQATSTVSEQTENGAAKAVIGMG  
AGVMAAAAML

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)

CATTGATCTCGAGCACAGCTGCTCTTTTCTCTCAATGAATTACGTTATATGTTAATCACA  
CAAGCATCAGTTTTTTCATCGCAAAGAAAATATTTAGAGTTCTTGCAATTCAGATGTACC  
TCAATTAATACTCAATCACCTCCTATGTTCTTGCTGGTAGTACTGCTTTTTGTCTTAATT  
ACTGCTGAATCAGCCTTCTAGAAGACCGTTCGTTCAGCCGCTCGCCCCCTTTCAAAGC  
TTGCGCGGCTGAGTTTTATGAGGGGCGGCTTTTTTGTGAATGGCAATCTACCATTATTAG  
TAGCAATATGATTTGCAGATAGATACATATATATCTTCTGGGTTCATGTCTCGTTACCA  
TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAATAATA  
GGACTCCTCATTAATAAAGGCTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG  
CAAGTCAACCTTAATTAATTATGATTTCTGTTTGCCCAAAAATGACTTGCAAAAATGCT  
ACAGAAGCCTCACATTCGATGTTCCAGGACAACAATTCCAAGAGAGAAATGAACAAAACC  
TTAAAAAACGGGCCAAAAAGAAAGGAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC  
CTTCCACCCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG  
TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTTCGCCAA  
ATTTGCAATATTATTTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG  
AGAACAAATCTGAATCCAGTAGTTTTCCAATGAGATCCTCAAAGTTGTTGGAAAAGAATT  
CTGACATCAAAAAATATTTCTTGGTATCCAAGAATGGAAAAATAGTGAGGAGAGACTATC  
CAAGCAGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAAAGAAGCTGGA  
TAAAGTTATGGCGCCAAAGAAACTACAAATAAATAAATGAAAGGCTGAATGACAAAAAAAT  
GGTTTACTTACCCAGAACTTATCTTCTCTGAAGAGCGTATTAAACCGTTATATAGAGGAG  
ATGATAGTGCACCATGTACAAAAGAACAAAAAGAAAGCATAAAATACTTCAACAAAAGG  
TCGGATATCCCAATAACCCTAAGACAATAGTTTGTACATTAAACGGAAAAAACATACGT  
GGGTGCCCCAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA  
TAACTACACTGCCAAAAATGATTTCTAACAGGAAAAAACTGCAAAAGATGATACAGAAT

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GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTTTGATTATA  
TTTTACAGCTAGTAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAAATAATTGTAG  
GCAAAATTAAGTCTGGTAGATGTCATTAATGTCCATACTCCAGATTTCTTAGTTC  
TTGCTACTTTAAAGCACGAGCGAAATGAGAATCTTATTACATATAAATCCAAAAAGCTGA  
CAGATGTCTTTCTTGTAGTTATCCGATTCCACATTTGTTGTTCCCTCGAAACGAATGT  
ATTCGTTTCGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA  
TGAAGCACGAACACACTGACGTTGAGAGCATGAGCAGTTCAATGTTCAAAAAAATACAA  
TATCAGATATTTCTTCACATATTTCCGTAGATTCGTACGCCGAAGATTTCAAAGGCAAG  
GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCTCCAGAAAATTGACCGGTC  
TCGCCCAGCATTCAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA  
AAGATAGAGAATGTACTAAGGAAAAATTTTGTGAAGAAAATGATATCATAATTAGAG  
AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA  
GTCACGGTGACCAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTCGAAAAACA  
CAAAGTTTAGAAAATCTTTAATACCATATTTCTTCTCAGAGGAACAAAATACCACAACAA  
CTATTAACTCAGTAGCTCGCCTACGTCCCAAATCAAGTTTGCAACCTCTGTAAAACACA  
AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT  
CCTTCGACAAAGAAAATTTCTTTGATCCATCTGATAAAAGCAGTAGTGTGATAATAGCA  
TTCTTTTGAGGAAAGTTAAAGTGCCGGTGCTGCTTAAGAAAAGTCAAACTAATGACTCCT  
CAAGTAGTGCAGGGTCAAAGAAAAGCTCGTCTAGTTTGTAGTACTGTGAACACCTTCACTG  
GGGGTGGAGTTGGGATTTTAAAGGTGTTTAAAGTGGAAGTCTCTGGAAATAAATCAT  
CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTTTGAAGTGATGATCGTAACGACAAGA  
AAAAGAAGAAGAAAAAAGAAGAAATCATTTGTTCTTATTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQQFEERNEQNLKKRAKKKGSFQPSVAFDTPVSTAGYS  
SIDDSREGFKGVFPVNYTMEECYDDETSFSPNLQYYLRDTFQSSPFLNTRKENKSESS  
SFPMRSSKLLKNSDIKKYFLVSKNGKIVRRDYPSTPVIVNETLMINRFEKNWIKLWRQR  
KLQINERLNDKKKWFTYPELIFSEERIKPLYRGDDSAPECTKEQKRKHKLQKQVGYPNP  
KTIIVCHINGKKHTWVALDWTVYKFARNLDHIVITTLPKMISNRKKTAKDDTEWAPGYQK  
EVIDQKLNDFIDYILQLVKVKISVKITLIEIVGKIKKSLVDVINVHTPDFLVLATLKHE  
RNNELITYKSKKLTDFVPVSYPIPTFVVPSKRMYSFELNLQREVNEHYVSKNHMKHEHTD  
VESMSSSMFKNTISDISSHISVDSYAEDFKRQGYIKKQFNSTNDSIPRKLTLGLAQHSRR  
KITGDIEKLQDDEKDIRECTKEKLLLKKIDIIRESLKSSLAIETLPGKNVSQSSHGDIQS  
SFKNALIGNGSKNTKFRKSLIPYSSSEEQNTTTTIKLSSSPTSQIKFATSVKHKDGRAAL  
GKARNLPDIRHSISFDKENSFPDSKSSSVDNSIPLRKVKSAGALRKVKTNDSSSSAGSK  
KSSSFSTVNTFTGGGVGIFKVKFSGSSSGNKSSSRNSSSGDVFEESDDRNDKKKKKKKK  
KKSFLFLFGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AATTTTCCCCCGTCATAAGTTCCTATACACGGCTGGCTCTGATGGCATAATTTTCATGCT  
GGAACCTACAAACCCGCAAGAAAATAAAAAATTTTCGCCAAATTTAACGAAGACAGCGTGG  
TTAAAATTGCTTGTTTCGGACAATATTCTATGTCCTGGCAACTTCTGATGATACTTTCAAGA  
CAAACGCCGCAATTGACCAAACATTTGAACATAAACGCAAGTTCAATATACATAATATTTG  
ACTATGAGAACTGATATCTTCGTGAAGATTCGTGTAGTATGATAGAACATTCAGAAAAA  
AAATTCAGATTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAAATCA  
CATACATAGATTAAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATCAATCATCTTA  
TTAAGGTATCTTGTTTAAGCCCAAAAGTCTGCTCCCAAATTCCTCACTGTAGCTACTAAA  
ACAACCTATACGCAAGAAAGATGTCATTGACAGCCGATGAATACAAACAACAAGGTAACG  
CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTTCTACTAAAGCTATTGAAG  
TTTCTGAAACTCCAAACCATGTTTATATTTCTAACAGGTCCGCCTGTTATACTTCTTTAA  
AGAAATTTAGTGACGCATTGAATGATGCTAATGAATGTGTCAAATCAATCCATCTTGGT  
CTAAGGGTTATAATAGACTCGGTGCCGCCACTTAGGTCTTGGCGATCTCGACGAAGCTG  
AAAGCAACTACAAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCCAAAGAAGGAT  
TGGATCAGGTTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC  
AGTTGTTGTGCTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCACAAAAACTAGCGAAA  
TGATGAAGGACCCTCAATTAGTGGCTAAACTGATTGGGTACAAACAAAATCCGCAAGCTA  
TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATTGATGGGGG  
TTGATTTAAACATGGATGATATAAACCAATCAAACCTCCATGCCAAAGGAACCGGAAACCA  
GTAAAAGCACTGAACAAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG  
AAAATTCCTCTAAAGCACCACAGAAAGAAGAAAGTAAGGAATCCGAGCCAATGGAAGTTG



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ATGAAGATGACTCTAAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTTACA  
AGGCACGTCAATTTCGATGAAGCTATAGAGCACTACAACAAGGCGTGGGAACATGCATAAAG  
ATATTACCTATTTAAACAACCGTGCTGCTGCTGAATACGAAAAAGGCGAATACGAGACAG  
CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG  
TCATTTCCAAATCATTTGCGCGTATTGGTAAATGCCTATCACAAATTGGGTGACTTGAAGA  
AAACTATAGAATACTACCAAAAATCATTTGACCGAACATCGTACTGCTGACATTTTGACCA  
AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCTTG  
AAAAGGCGGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA  
ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTAGAGGATATT  
CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTTCCTGAAGCTATCGCAGATTGTA  
ACAAAGCCATTGAAAAAGATCCAAATTTTCGTGAGAGCTTATATCAGAAAGGCCACCGCAC  
AAATTGCTGTTAAAGAATATGCTTCCGCTTTTGGAAACACTAGATGCGGCCAGAACCAAG  
ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGGAAATTGATCAACTGTACTACAAGGCAA  
GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCAGAAGAAACCTATCAAAGGG  
CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAGTATTTTGC  
AGCAGGCCCAACAGAAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA  
AAAAGATTGACAGCTTGATCGCTGCTGGTATCATCCGGACTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTADEYKQQGNAFTAKDYDKAIELFTKAIEVSETPNHVLYSNRSACYTSLKKFSDAL  
NDANECVKINPSWSKGYNRLGAAHLGLGDLDEAESNYKKALELDASNKAKEGLDQVHRT  
QQARQAQPDGLTLQFADPNLIENLKNPKTSEMMKDPQLVAKLIGYKQNPQAIGDQLFT  
DPRLMTIMATLMGVDLNMDINQSNMPKEPETSKESTEQKKDAEPQSDSTTSKENSSKAP  
QKEESKESEPMVEDEDDSKIEADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN  
RAAAEYKGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTIEYYQ  
KSLTEHRTADILTKLRNAEKELKKAEEAYVNPEKAEERLEGKEYFTKSDWPNVAVKAYT  
EMIKRAPEDARGYSNRAAALAKLMSFPEAIADCNKAIEKDPNFVRAYIRKATAQIAVKEY  
ASALETLDAARTKDAEVNNGSSAREIDQLYYKASQQRFPQPGTSNETPEETYQRAMKDPEV  
AAIMQDPVMQSILQQAQQNPAALQEHMKNPEVFKKIQTLLAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAGTACAGCTGCCTTTATTTCTTGTGGTCATTTATTGCTTTTATTTTCAAGTCA  
GATATACAAGAAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA  
ATACCATACTCTACCAACATTATTTTAGTCCGACGTTTCAGTCCCTGTAGGTGTTCCAAATC  
CTTCTGGCATTGACTTCTGTGCAGAAACCCTTCAAATGAGTTCACCTTTACGTCAGATC  
GCATAACAACCGGTCAATATTTTTTTCTTTTGGCTAAACCCCTACTGCAAGCACTTTTA  
AGAAAAAGAACAAATAAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTGTCTTTTCGGAC  
AAAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCTATATAAG  
AAGGGCGCACATCGTCCCCCTAAGAATAGCGAAGCGATATTACACTGAACACTACAATG  
TCAAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA  
AGGACTCTTGTGATTTGTGGGAGCACCTGCCTTCCAAGCTGTTCTGGCGGTGAAAAGTGCA  
AATGTGATCACAGCACCGGAAGCCCTCAATGTAAGAGTTGTGGTGAAAAATGCAATGCG  
AAACCACGTGCACCTGTGAAAAGAGTAAATGCAATTGTGAAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECKKDSCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE  
KSKCNCEK

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:  
1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCAAACATATGATATGGTATTAAAAAATGAA  
AAAAATTCATTATTCTTTAGCGTAATTATTGAAGAAAAAACAGTGCGCGCGGTAATTTTT  
TGTCACCTCAGTAACTAGAGAGAAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC  
TCTGCCTAGGATTTCTCTTATGCTTTCTTTTACCAATCACTTTGTTCCGGCGAGGCCCG  
CGAAGCTCGCTTTCTTTTACGCTAGCAATCATGTTCTTGCCAGCGTCGTAGACTACTGTA  
TGGCAGTTGCTGCAC'TTGCCATGAATATCCTAGTGAAGCCTCTATGCAATAATCCAGTTA  
CTGCGTTAGAATCCTGGTAAAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT  
TGATTGAAAATTAGTCCTTGGCACTTGGTATATATCTTATTTTAAAGAAAGCTGAAAGGAA  
GAAAGATCATCACGAACAACATGTCTGCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA  
CTGAATTGGAATTACAAGTTGCTCAAGCTTTCGTTGAATTGAAAAATCTTCTCCAGAAT

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TGAAAGCTGAGTTGAGACCTTTGCAATTCAAGTCCATCAGAGAAGTATGTTATTAATTTG  
AATCTAAACTTAAGAATAATGGAGAGTAACAAAGGAAAAAAGTGTGAACGGGACGATACC  
AGAATGTTTCAATCTAGAAAAGTATAAAAGATAAGGACTAGGACTCAAATGTATTTGGCT  
GACTATCGCCTGAACCTTGATGCTAAGCAAATACCATATCTTCAAGAAAAAGCCTACTCC  
AGTGTTTAAGAAGAAGGGAACGATTTACTAGATCATGCTATACGCAGTAAGGTTCTGATA  
GTTAATTACAATCGGTCCAAGTTCTAAGCGGTGTCGTCCATGCATATATCATTTACAAGT  
TACTGGCGTCAACTCTTCAAATATTCAAATATCACCTAATCAAACCTTACTAACATTTTC  
CTTTTTTGTTTTCTTCTTTTATAGATCGACGTTGCTGGTGGTAAGAAGGCTTTGGCCAT  
TTTTGTTCAGTCCCATCTTTGGCTGGTTTCCACAAGGTTCAAACCTAAGTTGACCCGTA  
ATTGGAAAAGAAATCCCAAGACCGTCATGTCATCTTCTTGGCTGAAAGAAGAATCTTGCC  
AAAGCCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACCTTGACTGC  
TGTTTCATGACAAGATCTTGAAGACTTAGTCTTCCCAACTGAAATCGTTGGTAAGAGAGT  
TAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTGTGTTAGACTCAAAGGATGTCCA  
ACAAATCGACTACAAATTTGAATCTTTCCAAGCTGTTTACAACAAATTTGACTGGTAAGCA  
AATTGTTTTCGAAATTCGAAGTGAACCTCATTAG

YOR096W, 190 aa (SEQ ID NO 260)

MSAPQAKILSQAPTELELQVAQAFVELENSPELKAELRPLQFKSIREIDVAGGKKALAI  
FVPVPSLAGFHKVQTKLTRELEKKFQDRHIVFLAERRILPKPSRTSRQVQKRPRSRTLTA  
VHDKILEDLVFPTEIVGKRVRYLVGGNKIQKVL LDSKDVQQIDYKLESFQAVYNKLTGKQ  
IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)

ACCCATTTTACAAATTTTTTTTGGCTATTTGAGCCATAGTACCCATTAATAGGTCTCGTCC  
ATTCCCTTGTTTTTTTTTTTATTGTTTCAATTACACTACATAATTAATAATCACATCACTT  
TCACTCTCACCTTAGTCGTTCTTTATCAACCAAAAAATAAAAAATGCTTCAATCCGTTGT  
CTTTTTTCGCTCTTTTAACCTTCGCAAGTTCTGTGTCAGCGATTTATTCAAACAATACTGT  
TTCTACAACCTACCCTTTAGCGCCAGCTACTCCTTGGTGCCCCAAGAGACTACCATATC  
GTACGCCGACGACACCACTACCTTTTGTGTCACCTCAACGGTCTACTCCACGAGCTGGTT  
CACCTCAACTTCAGCCACCATTACCAATGCGGCCCTCCTCCTCCTGTCCACCTCTTCGGC  
CTCTGGATCTGTAACCCCAAGATCCACCCATGAAATTACCTCCACCTCGACTATCACGTC  
CACTTTGCTGCTAACCCTTCATGACTCCACTACTTTGTCTCCATCATCTACTGCAGCAAG  
TGTCAGTGACGAAGATTCAAACAACAAAGATGCAAAGGTCAAGTCCTTTGAACAGGCTTC  
AACTTCCAATGGTTGCGTCCCAATCACAAAGTTTGTCACTGTCAACCAATGAGCCCGTTAC  
CCAGTACGTTACAGTACCCCCAAATACGACTACACAATACGTTACTGTCAACGGTGCACC  
TTCTGTTACCCTACCTCTCCAGGTAACGTACAATGGTACAACACCACTTCGATTACTAA  
TTCGACCAGTTGGTGAATTATGA

YOR248W, 100 aa (SEQ ID NO 262)

MTPLLC LHHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSLSLSPMSPLPSTLQSP  
QIRLHNTLLSPVHLLLPLPLQVTYNGTTPRLRLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:  
990-1255 (SEQ ID NO 263)

AACTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCTAATGCA  
AACACACGTCCTTTAAAGATCCCCGTGATAGGTTTCATTAAAGGCAACTTCCATACACGTT  
GAAGTGCCAAATTTTTCCCTACATCCAAGCATTCCTGGGTTTGTATGGGTGTTACACCGGT  
TTTTCTTTTTTATTTCAGAGAAGTACAATTTTAGCGGGTTTCAAATTTCCCCTGTGTG  
CGAGAAACGCTCCGGTACGCCTAGGCTCACTCCGGTCTTCTCCCCATTTCTATCAGCGC  
GATAGGCATACTGTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA  
ACGCACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACCTTAGATTAACTGGTAT  
TAAGATTTGCAATTTTGGGCTGGATTATTAAGGTGAGTAGCAAAGTTTAGCAAGAACA  
GTACGAACCTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT  
ACTTATTCCAAGGTATGTTTTAGAATAACTTTCAGAAAGCATGAAGATACACGGAAAGTC  
AAGCGAGGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGCATTACATACACGATGTT  
TCAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG  
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA  
AGGCCATCGACCCTGGAGACGTATGAAATATGGTATACGTCCTATATTTGGGCAAGAAAA

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CGGTAAAAC TGT TTTACGCGGAGATCCAAC TTTTGATCCTTACCGAGTACCACGAATCAT  
 CTATATGATCTTTTACTA ACTTATCTTCAATTTCAACGGAGAGATGTAAACATCATTCT  
 CTCCTATGATAATTTCTTTT TATACAGAAGGTGTTGTTGTCGCCAAGAAGGATTTCAA  
 CCAAGCCAAGCACGAAGAAATTGACACCAAGAAC TTGTATGTCATTAAGGCTTTACAATC  
 CTTGACTTCTAAGGGTTACGTCAAGACTCAATTTCTCATGGCAATACTACTACTACACCTT  
 GACTGAAGAAGGTGTTGAATACTTGAGAGAATACTTGAAC TTGCCAGAACACATTTGTTCC  
 AGGTACCTACATTTCAAGAAAGAAACCCAAC TCAAAGACCACAAAGAAGATATTAA

YOR293W, 105 aa (SEQ ID NO 264)  
 MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTFQS  
 WQYYYYTLTEEGVEYLREYLNLP EHVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:  
 915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTCATATCTTAAAGGT  
 GCTGATTGTTTGTAGGCACGAAGTAAACAAGCTCTTCCCCAAAACAATAAATACGGT TTT  
 CGGGACTGTTTACCCGTACATTTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTT  
 ATCTCTTTTCAAGTAAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC  
 GCGGCCTAGACAGTTACTTCCCAGGCCAGGGCCAGGCCACACGGACAGAGGCAGATTCCA  
 AGTTGTTCCGCATAGTCTGTCTAGCTCTTCTCAATTTTCCGCCAGATTCTGTCTAATTT  
 CTTTCCGCTCGAGTTGGCAACAGTACGAAGAAGTAACTCTAATAGATAGATATAACCGTT  
 TTTGAGGGCATTATTTTTCGAGAAGATAATAGAAGAGAACCGTAACAAAGGAATCAAGCA  
 AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT  
 TTTATATGGTCAAGTCAAATTTGAATGAACATATCGTGGAAATTTAAAACTACTGAAGAATA  
 CCCAATAAGTCAATGCAACCTGTGAATGTTTTTCTGAAATACGCCGAATACTGAATACG  
 ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATATG  
 GTTAATATCATTTGAGAAGTCTTACATGAGGACTATAGAACTACCATCCAGGAATPATA  
 GAGGAAATTAAGTGAATCAGAGATCTATTTTGAACAATTCATTTACATGTAATTGTCTGC  
 AATAAAGCAATATTTTGAATATGCAAGTTTACTAACAAGAATAAATCTTTTGTATT  
 TTTATCTTTAAGTGGCTCATTTTCAAAGAATACCAAGTCATTGGTTCGTCGTTTACCAAC  
 TGAATCCGTTCCGAAACCAAAGTTGTTTCAAGATGAGAATTTTGTCTCAAATGAAGTCAT  
 CGCCAAGTCTCGTTACTGGTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG  
 TGAAATTTGTTTCCATCAACCAAATCAACGAAGCTCACCCAACCAAGGTCAAGAAGTTCGG  
 TGTTTGGGTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAATCAGAGA  
 CGTATCCAGAGTTGCTGCCGTTCGAAACCTTATACCAAGACATGGCTGCTAGACACAGAGC  
 TAGATTTAGATCTATTACATCTTTGAAGGTTGCTGAAATTTGAAAAGACTGCTGATGTCAA  
 GAGACAATACGTCAAGCAATTCTTTGACCAAGGATTTAAAATTCCCAATTACCTCACAGAGT  
 CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)  
 MYLAHFKEYQVIGRRLP TESVPEPKLFRMRIFASNEVIKSRWYFLQKLHKVKKASGEI  
 VSINQINEAHPTKVKNFGVWVRYDSRSGTHNMYKEIRDVSRVA AVETLYQDMAARHRARF  
 RSIHILKVAEIEKTADV KRYVVKQFLTKDLKFLPHRVQKSTKTF SYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAATAGTATATATATGTAAAAAAAATTTCTGCTTCATGTATATA  
 CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT  
 ACATCTTGGCATATTAATGGTTATTTCCGGGGTTTGTTCGGCTCAACGGTGATATAAAA  
 AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTGTTTACAACATCTTC  
 ACATTTCCATTGTGGAATCATTTTATTTTTTTTCAAGAATACCTTACCCGCAAGCAAAC TTT  
 CAAGCAAAC TTAACAATTTGCAAAAATTTTATCGAATTTCTCCGACGACATATTATAAAAGT  
 TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCTTGTTCATTTGTTTTCCTCAAT  
 TCAAAAAC TTTACCGGAGCAGTTTAAATTATCTTACTGTGCAAGAAGTCAAAAAC TAGACT  
 ATATATTTATGAGAAGAAAAATGTCTGACGTTGAAGAAGTTCGTTGAAGTTCAAGAAGAAA  
 CTGTTGTTGAACAAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTGAAGAA  
 CCGCTTTGGTTCCAGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA  
 GAGGTGAAGCTTTATTGGTTGTTTGGTTCAGCTCTGTTACTGAAGCTAACATTATCAAGT  
 TGTTTGAAGGTTTGGCTAACGACCCAGAAAACAAGGTTCCATTGATCAAGGTTGCTGATG  
 CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA  
 AGGTTGTCGGTGCCCTCGTTGTTGTTGTCAAGAAGTGGGGTGCTGAAACTGATGAATTGT

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CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVEEVVEVQEETVVEQTA EVTIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV  
VLVSSVTEANI IKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV  
VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTCGATGTCGCACCAGATTGGGAATCTTACGA  
CTATGCAAAGTTGGATCCAACCTAACGACGACGACAAAGAATTCATCAATAACATGTGGGC  
CTGGGATAAGCCAGTTTCCGTCATGCGCAACCAAGGAAATTTGTTGACGGTAAGGTCTT  
AAAATAATCTCTTCGTACTATCCTTCATGTCGCCTTTTATTATAAAGTATGCTAGGTAGT  
TTTATCTATATCTTATTTATGACGCAATATAGGGTAACAGAGTTTTTCTGCTCTGAAACT  
TCCGCAGAAAAAATCAAGTTTTCTTTCGTATCTTGGATTATTGTTATATAATAGAT  
GCATGTATTATATGTATAGCAGTGATTTGCTTATTTTCTTGATTCTGAGGAATCGAAGAA  
GTAACCTTAGCGTTTCTTCCGTTGAGCAGAGCAGTATAATAATCCTTCAAATCTTTAGGT  
TACGGGGTTTTCTGTGCGATGACCGAAGAACTATTACTATAGATTCTATTTCAAATG  
GGATACTGAATAACCTGTAAACCACATTTGATCCAGGACATTGTAGCTCGGGAAACCACTC  
AACAACAATTGTCTGAAGACAAGATATCCGGATCTTCGCAGTTATTATTTCGACCCGAACG  
GATCTCTCGATATTAATGGACTACAGAAGCAACAAGAGTCCTCTCAGTATATTCACCTGTG  
AGAATTGTGGCAGGGATGTGTCCGCAACAGACTAGCAGCTCATTTACAGAGATGTTTGA  
GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDSISNGILNNILTTLIQDIVARETTQQQLLKTRYPDLSYYFDPNGSLDING  
LQKQQESSQYIHCENCGRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:  
901-1605 (SEQ ID NO 271)

GTAAGCAGAACCCGGAAGAAGACAAGAGGTTTCATTTCAGAGAAAACATCCGTACATTTCGAG  
TTCTCATTTGAACCCATACATTTCAACTATTTTTACATAGTTCGTTTTTCATGTGTAAAAT  
TGTCATCGACGCGCCGGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCACT  
GGGGCCGTGCATTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCCGTTCCCACTTGGAAAG  
ATTGGCGTAATTCACGCTCCTCTATCGATTCTAGCGGGAAAGTTATCTCTCCTGGTAAG  
CGTTGGAGGAATGCCGCTACCTAGGTAAGTCTACTGGGTGGGAATTCCAGTACCGACGTC  
TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTTCATATACAGTGTACCAAGGATAA  
AGTGGTTAATGCTTATTCGTCATTGAATTTTTATATTTGCTTAAGAGAAGTGACAAAAGA  
GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGGCAACA  
GAGAACTTTATATGTGGAAAAATGGCATGAAAGTTTGAAAGTGAGAAAGAACTAAACAGA  
ACCAGACGTCGTAAAGATTTTAGAAATTTTTTATGGAAAGAAGCAGGAAGACTACCATAT  
ACTAATTGATGCGTTTGTGGCGTTATTTTTAAACAAACAGAGCGGGTTTACATATACTGT  
TACTACAAACCGTGAAATTGAAGCAGTTTCATATACTTGGAGTATAGTCAATAAAAGACAA  
GCTTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCCTATTCAAACA  
TTAATTTTGCAATAGTATACTAACAATTTTCTTAATAACCTGTTGAAAATTTAAAATAG  
TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAGACCTTCGAAATTGATGATGAACAC  
CGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAAGTCGATGGTGAAGCCGTTGGT  
GACGAATTCAGGGTTACGTCTTCAAGATCTCTGGTGGTAACGACAAACAAGGTTTCCCA  
ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAAGCTTTCT  
TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAAGTCCGTCAGAGGTGCCATTGTT  
GGTCCAGATTTGGCTGTCTTGGCTTTGGTTCATTGTCAAGAAGGGTGAGCAAGAATTGGAA  
GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA  
AAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTTCGTGATTTTCGTTCATCAGAAGAGAAGTC  
ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA  
AGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTCAGAAACGCTCAAGCTCAAAGA  
GAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTGTCTGAAAGAAAGGCTGAG  
AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEV DGEAVGDEFKGYVFKISGGNDKQG  
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRSV RGAIVGPD L AVLALVIVKKGEQE

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LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT  
PQRLQKRHRQRALEKVRNAQAQREAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)

GTCTCAGTGATGCAATCATCATGGCACGGGCATTAATTAAGGTTAAGGAACCACTTCTCT  
ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA  
GTCATTGCCATGGATTATTTCATCTCTTTTCGCTGTTCTCTTTCTTTTCAAGTTTGTCTATC  
ATCATGCCCTTACCTTTTGCCTTTCCATCTTTCTTTTGTCTGCAAAATAAAGGGAAGAGGG  
GTAAAAACGCAAGGAAGAACAAGAAGAAGAGGGTAGTGCAAGAAAAAGAAAAGAAGAAAA  
AAAAAAAAGTAATCTTGATACCGTGAGCAAATAAGCTAACGGAAAGCGTAAGAAAGAA  
GAGCGTGTTTGGGAAATAACACCACAGCATAAAGCTAAAATTCAGTTTATATAATCTAT  
AGTAGTCCATAGAAATTGCGAATAACGGAAACAATAGTCCACCAAGCAAGCATAGGGA  
GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTTCGATGTGCCCGTAGATTGGT  
TGATAAAGGTAAGAGTAGACGGAAGACAATAACGAAGCCATCGAGGCCCTTCTACGTCGC  
CAGCCTCCTCTTCATCTACGTCCTCTTCGAAAAACGGAGACAATAGCACGAGTGGTAACA  
GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCATCTGTATCCAATGCAGCACTTTGTA  
ATACTGAGAAACCAGATTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA  
ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA  
ATCCGGTACTACCGTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC  
AATTTGTAAGGAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAACTCAA  
GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTTGGCAAGGGAAGCACC  
CGCCAATTTCTTACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAA  
AGACTAAAAGGTCGATTTTGGATCTTTGTTTAGCAAACGGTCTACCTCTTCTTCAGCTT  
CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG  
GCATTAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATCACCATTGAGAG  
GAGTGGCACCACAGCTAGCAAGCCACAGACACCTATACCTCCCTCCCTGCACCTTGCGAG  
TAAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGCCGTCGATAAATTCGAAT  
CCGATCCTCCCAACAACCTTCTTCAAGAACCCCAAAAAAGGGAACATCCTTATCCCTG  
ATGACATGATAAGCGAGGTTCCTTCTATTTCCGTTGGGTATTTCCAGTAGCAACCAATCGG  
CCAAGTCAACCAATTCACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA  
TACTCGCCCTGGAATAACAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG  
CTCATTTTGTCTGCTAATAGAAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG  
CAGGCGGTAAGCTTACTGAAAAGTCATCAGAAGGCACCATTACGAAGCAAAGAGAAGAGG  
TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACC  
TCTCAAAAGCCGGCATTGATAAGCCCATTTCATATGCATGAGCACTATTTCAAGGAACCTG  
ATCAAGATAAGTACCAAGACGGTCATTTCTATTGAAAAAACAAGGTTACGCTGGATGTTA  
TTTACACAAGATGCTGCCATTTAAGGGAATTTTACCATTCCGCTTACCCTAAGACAAG  
TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTFTTTGAACCCTAAGCCTACCTTGA  
TCGATATTCTTTTCTTTTGTGATTTTCATCACCATTGCTCCCATTCACACGATTGTTTTCG  
ACAATGTAGCTTTTAAACCAGGATATGTTTCAAGATAATTTATTTCTGCTTTGGTAAACTCCA  
CAGTTTTTGGACAAATTGAGTTTAAAGAAATGTACGAATCGACCAAGATGGATGGAAATTAC  
TATGTAAGTTCTTTTGTCTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA  
TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAACTTGTTTACTG  
ACGTCTTGTCTCAGAGATCTCACAAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT  
TTAGCAAAATTCCTTACTCATGCTTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAAA  
ACTTTCCAGAATCGGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC  
AGGATTGTCTGAAATTTATCTTCAATTTGGATGTCTCAATATAACGTCCAGGGTGTGGATC  
TAGCGTTTAATGATCTGTCCACTATGATTAAAGCCAATGGTTGGTAAACTATCTGCTCTAT  
CATATGATAACTTAAGATATTTCAATTTTGAACAGCACTAATATTTTCGACTTCTTATGATT  
TAGCTTTGCTCTTGAAATATCTTTCTAAGTTGCCTAACTTGATTTTTTTTGGATTTGAGTA  
ATTTGTGCGCAATGCTTTTCTGACATTTTACCCTACATGTACAAGTATTTACCAAGATTTT  
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAGGAAGTACGCTGTG  
TTTGTAAATATTTTGATTAAAGTGCAAATCGCTCTCGCATGTGTCAATGACTAATCAAAACG  
TTGAAAATCTCTATCTAATGAACGGCACAGATTCTCCGTTTCAACAACTAACACAGACG  
CGCATTTGGATGTTTCGAGCACATTGGACGTTTAAAGGCCAATTTGCTAAAAATAGTTTTT  
CATCCACACTTTACGCATTTGCTAGAGACTCTCCAACTTGATTGGTTTAGATTTTGA  
ATGATTTGATATCAGAAGAGATTCAATCAAGAATAGCACTGTGCTTGATGAGAAATATGA  
AACGGACCATGGATTCGACTTTCCAGTTAGATGAATTGGATTTCGCAAGATGATTTGCTAT  
TCGATGGCTCTTTTAGTAATATGACCGCTGAAAGTGTTTTAGAAAACTGAACCTGTTAA  
CGGATAAGAGTACAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAAATATA

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TTGAAAAGTTCATATCTTGCACCATAATGTTTCAGCATACAATAGATACTATGTTTCGAAA  
AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAACCTTGTAAGATTACTCCTTT  
TGGAACAAAACCTTATGCAATATACTAGAATTGTTTTCGCATAATCCGAATCTGAATGATG  
TCCTTGGATCCAGCAGGGATGATTTCGAAGGAAAGTGTGACTCCAGCGAAGATTCAAAAT  
TACCAGCATTGAAGCACGTGAATCCGGATACCATGTTCCCGAAGAAAAAATACAACCTG  
AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAACTATTG  
ACGTTTTTCACAGGCAAACCATTTGGTGTTCGAAGCATACATCATCTAGTACTTCTGTAGGTT  
GTAAAAAGCAGGAAGAAGAAGGTGAACCTACATAAATGGGGTTTCTTCGTTTCAGCAGC  
AGAGGTCTTTTATACCCTGAAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA  
CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA  
ACAATGAAACTGCTACCACTAGTTTATTTAGCCCAGCTAATCCTAAGATTTTACCAAAAA  
TTCCATCCGGTGCTGTCTTAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG  
ATGATTTGATTTCAGAACGTTAATCTCAACAACATAGAATTGGAGAACATTTATGGTGAAT  
CCATTCAGAAATCAGCGTTTCGACATTTACACCAGGCGTGGATTCTGATGTATCTGCGCCCA  
ATACCGATAAAGGATCCGTAGAAACATTCGCTGCAGTCTCAACTGACGACCCAAATTGTG  
AAGTCAAAGTCACTGCTACCTATGACAAACTATTAAATAATTTGTCGATGGAGAGGTCAA  
TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDVPVDWLYKKGSRRTNTKPSRPSTSPASSSSSTSSSKNGDNSTSGNRSSNDKP  
RARSSSVSNAALCNTEKPD LKRNDGNTSASDTDNIPLLTPINSGNRSDSADIDNPATVDA  
IDLIDNDDNGSSTQFVRKKRSTSISNAVSSSKPRLASSAINATASSSVGKGKHPPISSPS  
NATLKRSNSTSGEKTKR SIFGSLFSKRSTSSSASTAKKPLPVVNTSTTENESGGIKAVAT  
PDP RVKEISSPMRGVAPTASKPQTPIPLSPALAVKDLSTVSLKRVSFVDKFESDPPQQL  
PSRTPKKGNI LIPDDMISEVPSISVGISSNQSAKSTNSNIKGPLYTKKSKEYILALENQ  
KLALREAAKHQQEAHFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPPNVE  
ADRELENNKLAENLSKAGIDKPIHMEHYFKEPDQDKYQDGH SIENNEVTLDVIYTRCCH  
LREILPI PSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITIAPIHTIVFDNVALNQ  
DMFRIIISALVNSTVLDKLSLRNVRIDQDGWKL LCKFLLNKS LNKLDISQTKIKSDLAE  
SLYRHNMDWNLF TDVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI  
RIGLAGATTSNISQDCLKFIFNWMSQYNVQGVDLAFNDLSTMIKPMVGKLSALS YDNLRY  
FILNSTNISTSYDLALLKYL SKLPNLIFLDLSNLSQCFPDILPYMYKYLPRFPNLKRIH  
LDSNNLT LKELAVVCNLIKCKSLSHVSMTNQNVENFYLMNGTDSVPVQQTNTDGDLDSSS  
TLDVKGOFAKNSFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST  
FQLDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVVKDDTKRYLLKKYIEKFHIL  
HHNVQHTIDTMFEKRKSGELPLQEKENLVRL LLLLEQNLCNILELFSHNPNLNDVLGSSRD  
DSKESVDSSSEDSKLPALKHVESGYHVPEEKIQPENDVITARPHLMATDSGKTI DVFTGKP  
LVFKHTSSSTS SVGCKKQEEEEGELHKWGFVQQQRS LYPENESTRQTPFASGDTPI NTET  
AGKSTSSPSVSTSNNETATTSLSFPANPKILPKIPSGAVLRSAIMKAKGIDSIDDLIQNV  
NSNNIELENIYGESIQNSASTFTPGVDSDV SAPNTDKGSVETLPAVSTDDPNCEVKVPAT  
YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAAGCGATTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC  
TCAAACAGCATTATATCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCCTGTC  
GGTATGAAAATTTAAAAATATATAATAACATAAGTTTGCATTCATTAATATTAATATAAA  
TCAACGTATCAACCATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG  
CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTTCGCT  
CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTAAATAA ACTTAGA  
TGTTTCTTTA ACTTATTCCGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG  
CTGTGCAACATTATAAAGGTGCTTTTAAACTACTAATCGTATATTTCAGCAGGTCAGAAC  
GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCCGCCTTTATCAA  
GGAACAATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAGATTTCACTCTTCCTTTA  
CGTTCCTTAAGTAACAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAGG  
GCAGTAAAAAGGCAGCGTACCATCGTCAACCCCGGAACACGAACATACTGCACCACTTA  
TAAAGCAAAACAAGACAATCACAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTTAA  
AAAAGAAAAGAAGCGATTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC  
AGAGTGACATGACCACAAATGTACTCTATTCTGGATATAGACCTTATTTCATCAATCCCA  
ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG  
AAGATTTAAATGAACCTCTATCACCATGGATTTCTCTGCCACTGGACTTGAATTCCTTT

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CAGAGTGGGAGAATATACCTAGTGAACACTACTGAAAAATTTGAAGCCTTTTCATCCACCTA  
 AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG  
 TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAAATGGATGAATTTTCAAAGAGAAGAG  
 GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAACTTGAGGGAT  
 GA

YPL159C, 253 aa (SEQ ID NO 276)

MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKSRRKKGSKKAAY  
 HRQPPEHEHTAPLIKQNKTIKKEHSDVRGSHLKKRSDFSWLPRVPSTSHLKQSDMTIN  
 VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP  
 SELLKNLKPFPHPKEKSMNTNELIHVSARKNTLVDNKTSETLQRKMDEFKRRRGKGRKKS  
 VVTLQLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2:  
 569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC  
 TGCGGTTCTTCCATCCCCATCTCTTCCACATATACCGGGGGTTCTGATGGCATTCCCTATA  
 GCTTGCTCAAAGTCCTGCGAGTTAGCTCATCTTGTGAGTTATTTGCTGGTTCTTCAACA  
 TTCGGAAGAGTAGTGTAGCCCCTAGTATTACCATATCCTTTGTATACTCATATGCGAAC  
 TTGTCTAATACAAATGTATACCAAAAATAACAGCTTGAAAAAAATCTCAGGGTCTTTTCAT  
 TGAATAATCTCATTCTGCTATTTTAAGTTTTTCGTTTGCAACCCGAGACTGTCGAGCTAG  
 AAAATTTTCATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAACTTAT  
 GCAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC  
 AATGGGCTTCAATATAGCGTATGTCCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA  
 GATCTCTTTTGTGTTGATACTAACCAGTAAAGTTGAGAGTTATAACAATGAAAAATAGGA  
 TGCTGTGCGACTTTTTTTATCCACAGTTAGGTGGAGTCGAATTCCATATATATCATTTAT  
 CGCAGAACTAATCGATTTGGGCCATTCTGTGCTCATTATAACTCACGCTTACAAAGATC  
 GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA  
 TTTTCAGAGAAACCACTTTCCCCACTGTTTTTTCAACATTTCCAATAATAAGGAATATTC  
 TTCTCAGAGAGCAGATCCAAATGTTCATTCTCATGGTAGCGCTTCCACGTTCCGCTCACG  
 AGGAATTCTTCATGCTAATACTATGGGATTGAGAACTGTGTTACCGGACCATTCACTCT  
 ACGGTTTTAATAACTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA  
 ACATAGATCGGGTTATATGTGTTTCTAATACATGCAAAGAAAATATGATTGTTAGAACAG  
 AATTAAGTCCTGATATAATCTCAGTAATTCCCAACGCAGTGGTGAGCGAAGATTTCAAAC  
 CAAGGGATCCTACTGGTGGCACCAAGAGAAAAACAAAGTAGGGATAAGATAGTGATCGTGG  
 TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTTACTTACTCGCATAATTCCGAAAG  
 TTTGTTCCCTCACATGAAGATGTCGAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG  
 ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAAACGTGTGCAACTCTTAGGCTCTG  
 TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT  
 TAACAGAAGCATTGTTGATCAATCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTGTAA  
 CGACACAAGTCGGAGGAATTCCCAGAGTGTACCAAATGAGATGACTGTTTATGCAGAAC  
 AGACATCCGTTTCTGACCTTGTTCAGCAACAAATAAAGCTATCAATATCATAAGAAGTA  
 AAGCTTTGGACACTTCCTCTTTTCATGATAGCGTGTCTAAAATGTACGACTGGATGGACG  
 TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA  
 AAGATTGGATGAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC  
 TTTATCTGTTATGTGGAATTGTAGAGTACATGCTTTTTTTTCTCTTTAGAGTGGCTATACC  
 CCAGGGATGAAATCGATCTAGCTCCAAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA  
 AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)

MSSSHKVESYNNENRMLCDFFYPQLGGVEFHIYHLSQKLIDLGHSSVVIITHAYKDRVGV  
 HLTNGLKVYHVPFFVIFRETTFTVFSTFPIIRNILLREQIQIVHSHGSASTFAHEGILH  
 ANTMLGLRTVFTDHSLYGFNNLTSIWVNKLLTFTLTNIDRVICVSNCTKENMIVRTELS  
 PD IISVIPNAVSEDFKPRDPTGGTKRKQSRDKIVIVVIGRLFPNKGSDLLTRIIIPKVCSSH  
 EDVEFIVAGDGPKFIDFQQMIESHRLQKRQVQLLGSVPHEKVRDVLQCGDIYLHASLLEAF  
 GTILVEAASCNLLIVTTQVGGIPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT  
 SSFHDSSVSKMYDWMMDVAKRTVEIYTNISSTSSADDKDWMMKMANLYKRDGIWAKHLYLLC  
 GIVEYMLFFLEWLYPRDEIDLAPKWPCKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTCGTGGAAA  
ACCAGCATTTTCGTAGAAAAAGTTGATACGATTACAACGGTTATAATGAAAGTCTATCAA  
TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA  
ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT  
GAGGCGAACAAACACATCTATACATATATATACATCTATATGGATATAAAAACGACTAAT  
TCAACGTTGTTTTTATCAACCGAGCTTACTCTTGTACGGGTAACCGCAAGGATAGCTAGT  
TGCGGATGGTATAGCGATTTGGCTGGCAGCATGATTAAGGAATCCAAACATCTAATGGAC  
TAGCACATTTCTATCGATTTACGGGTCAGGTAAACATAGATATTGGGATATATCATATATC  
CTTACTGAGTAACATAAATTATGGTTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG  
TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTTCGA  
CTAGGTCGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTTCGCTAGAGTTTTTAACACATG  
ATGGCACCCCTGGATAATGATTATTTTAATAAGCACAACGTTTCTCAGAAATGCAAGAGTT  
CTGATGCACTTTTCAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAACAAGAG  
TAAAGTCCAATCAAGGAAAAAGATCAGCATCCTTTTCATAGTCCGGTGCATAATACCGCTGC  
TCAGTCCAAAGAACAGCAGTCATTTCTAATACTGGAACCTGCTGGTTTCGGCCTGAAACCAC  
GAAGAAGTAAAAGTACCCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA  
GTGAATCTACTACTGACGAGGAGGTGGAATGTTTTTCGGAAGACAACATTGAAGATGGAA  
AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAGAATGTGC  
AGCAATTAATCAGAATGAATTACAATCCCCGGATTCAATAGATGAACAAGAAGAAGATA  
AATCAGGTACTGATGGAAAGGAAAAATCAGAGCTGTATCCTTACCATTACCTCATTTTAT  
CTTCCAATAACTATTTTCGGAGAATCAAGCCATTCTATAGAACATCAGAAAGATGGAGAAA  
CATCTCCAAGCTCAATTGAAACAAAACCTGAATGCAACAAGTGTAAATCAATGAAGAGGGGC  
AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAAATTTGA  
GGGCCTCATTTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAAA  
AAATTTCTGATGTTGGTAATACCTTAGCTGCACATAAAAAGTAATCAAAAACCAAGTCATT  
CAGATGAACAGTTTTCATCAGGAAGATCACATTGATGCCCTAGGAGTAATTCATCAAGAA  
AAAGCGACTCGAGCTTTATGTCTCTTAGGAGACAAAGTTCTAAACAACACAAATTATTAA  
ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG  
AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCAGTCGACTGGAG  
TTGAACGTAGATTTGAAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG  
ACTCGGTTGAGCATATGGCTTCAGGTGATACTTTAATGAACCTGGATGATGGCAAATTCG  
GCAAGAGCAAAGAAAAATGGTGGAAAGATCTCAACTTGGCCAAAATATACCGAATCTCAGT  
CTACTTTCCCCACCATTGCTAACATCGGTAGTAAAGATAATAATGTACCACAGCACAACCT  
TTTCGACCTCCATATCGAGTTTAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC  
ATGGTTCAAGAATGAATAATATTTTTCACAAGAAAGGTAATCAGAATCTACTTCTGAGAT  
CCAACGATCTCAACAAAAATTCATGAGCCCCGGCCTCTCCATTGTCCAACGAACATATTA  
CATCTAGTACGATCCCGTAGCGATGCAACACAGACAATCCAACCTCAGGTGCCAAATTTA  
ATAGCTTCGCCCAGTTCCCTTAAATCAGATGGGATTGATGCAGAATCAAGAACACAAAGAA  
AATTATGGTTGCAGAGGGAGAATTCTATTATGGACTTAAGTTCACAAAATGACGGTAGTG  
ACTCTATCTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATG  
AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTTGTTGAGAGTACAAC  
CTATAATAACGGGAAATGCAAATAATATCAGGAAAAAAGCCATAACGATGCTCAGTCAA  
TCGCACATTTCTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTTACTAACT  
ATGACAAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAAGATTTCAGGCAGTGT  
TGTCCGGTATATGGAAAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA  
AGAATAGGACAACGAGTACAAACCACAGCGTTGGCCACACTGCTTCACAGAATGCACGTA  
ACTTGCTGAGGGGCCCGATGGGTTCCAGCACGACTTTGCACCACCAACGCGTCATTAACCT  
CTCTGCAGCCGACTACGAGGGCAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA  
CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLNASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND  
YFNKHNVSQKCKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS  
HSNTGTAGFLKPRRSKSTQSVLSLRDAQESKKSESTTDEEVECFSEDNIEDGKVNNDKV  
IAEHVMPEEKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG  
ESSHSIEHQKDGETSPSSIETKLNATSVINEEGQSKVTKEADIDDLSSHSQNLRLASLVKA  
GDNISEAPYDKEKKILDVGNTLAHKSNOQKPSHSDEQFDQEDHIDAPRSNSSRKSDDSSFM  
SLRRQSSKQHKLLNEEDLIKPDIDISSAGTKDIEGHSLLENYAPNMILSQSTGVERRFEN  
SSSIQNSLGNIEHDSGEHMASGDTFNELDGDKLRKSKKNGGRSQLGQNIIPNSQSTFPTIA  
NIGSKDNNVPQHNFSTSISSLTNNLRRAAPESFHGSRMNNIFHKKGNQNLRLSNDLKN



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SAAPASPLSNEHITSSTNSGSDANRQSNNGAKFNSFAQFLKSDGIDAESRTQRKLWLQRE  
NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA  
NNIRKKSHNDAQSIAHSSSDTDHKDEDDLFTNYDKKFDDLYPHILASAKIQAVLSGIWKS  
ESYLFNKDVNPINKNRTTSTNHSVGHTASQNARNLLRGPMGSSTTLHHQRVINSLOPTTR  
AVNRRMENVGYMHTQPQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:  
668-1212 (SEQ ID NO 281)

TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGTCATATGTATTATGCAGGTTTCATT  
TGTTCCCTCCCTTATTTCTTTTCATAGTATTTATTTTTATTTATTTATTTATTTTTTTTT  
GGATTTTATTTTATTTCTTTTAAATGCTAAGAAAGTAATTCCGCATAATTAAACGTGTG  
CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA  
CTTCTAAAATTCGCGCTCAACATGGCCGTATTGTACATTATATCGTTCATCATTATATC  
GTATACAGCCCGCATTACCCGACAACCTCCGTCTGCAACGCGTTGACCAGAAAACCTGAACA  
AGAGATCGCATAAAAAACCAAAAGGAAACGAATTAATTGTCAAATAGTTAATTGTAATGGA  
TCCTCTAGAAAGGCAACAGTAGATTTATTTCTTTCTTTCTAGAAACATCATTATAACT  
AACAATATAAATTGGAATAATGGCTGGTGGGATATTTTTGGTGGTGTATGTTATCAC  
CCTGTTACCGTTTTTCGGATACTTAGTTTTATTTCAATGTGGTAAACATTGAATGTTTTCA  
GCTTAAGATCTATTTTTTTTTTCTAGAAGAAATTGCGTCTTTACTAACTTTATTTTAC  
TGACAGTTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACTACTT  
TTCTTGGGTTTGGATAATGCCGGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA  
TTGGCAACCTTACAACCAACATGGCATCCAACCTCTGAAGAACTGGCTATTGGTAACATT  
AAGTTTACAACCTTCGATTTGGGTGGTCATATCAAGCTCGTCTTTATGGAAGGATTAT  
TTCCAGAAAGTTAATGGTATCGTCTTTTTAGTCGATGCTGCTGACCCTGAAAGATTTGAT  
GAAGCACGTGTCGAATTAGATGCTTTATTCAACATTGCCGAATTGAAGGACGTTCCCTTT  
GTAATTCTTGGTAACAAGATCGATGCTCCAACGCCGTTTTCTGAAGCGGAGCTACGTTCT  
GCTTTAGGATTATTGAATACCACCTGGCTCTCAAAGAATTGAAGGTCAAAGACCAGTTGAA  
GTTTTTCATGTGTTCCGTTGTTATGAGAAATGGTTATTTAGAGGCGTTCCAATGGTTATCT  
CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)

MAGWDIFGWRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE  
ELAIGNIKFTTDFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA  
ELKDVPPFVILGNKIDAPNAVSEAE LRSALGLLNTTGSQRIEQRPVEVFMCSVVMRNGYL  
EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)

TTCTTTACAATTCACCTTGCAATTATTGAAGGAGTGCTATTCTTCGTTTTGCCACCCTTTT  
GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCTTGCAGACAGCGCAACAT  
CCAACCATCCTAAAGGTATGGGTGTACTGACGATGCGATTATTTTCATTAAGTTCTGTCTT  
TTTTGTATAAATGAAAAAGAACGGTGAAATCCATAGAAATACAGAGAGCGACGCAACA  
GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAAGCTTT  
TTCACTTTGCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCACTCAGCTAT  
GCGAAAGTTTCATTGTTTGATACATCTTGATAGTAACCGCAGGCTTCTTTCTTAGTTTCAT  
ATTTTATTGTATTTCAACTAATATTATTTTTTTTTTTCAGTGGAAGGGAAGGTGAACCAAGA  
ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAACCCCTATGCGTGATTTGAAGA  
TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAAATCTGGTGACAGATTGACCAGAGCCT  
CCAAGGTTTTAGAGCAATTATCTGGTCAAACCTCAGTTCAATCCAAGGCCAGATACACTG  
TCAGAACTTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC  
CAAAGGCTGAAGAAATTTTGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA  
GAACTTCTCTGCTACCGGTAACCTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA  
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC  
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACCGTTGGTAACTCCCACAAGA  
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGATGCTGATGTTTTGGACA  
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKAQNPMDLKIIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR  
RNEKIAVHVTVRGPKAEELERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI  
GIFGMDFYVVMNRPGARVTRRKRCGTGVGNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457)

TATATGACGGCAAGTGTCTCACTGTTGCATTACGCGATGTTTCTTTTCTTTGTTCTTGTAAAG  
CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC  
ACCGCTTTTATPAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCCATTATTTCTCA  
AAGTGATGCGAATTTTCAGAGAACACATTAACCTGGGGGCCATAAACGCGACGTGCTACCATT  
TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT  
ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTTACT  
TTTCGATTTCAATTTGCACTGCATGATGCTTTTCTTAGGTAGTTTTTTGTTATTAAATAGTA  
TCATAAATTCCTTGCTCTTTTACATAAGAATTAGGAAAGTACAGAACAAAGAGCAAATTTAATA  
TATAATGTCCGGTGGTAAAGGTGGTAAAGCTGGTTCAGCTGCTAAAGCTTCTCAATCTAGAT  
CTGCTAAAGCTGGTTTAAACATTCCCAGTTGGTAGAGTGCACAGATTGCTAAGAAGAGGTAAAC  
TACGCCCAGAGAATTGGTTCCTGGTGCTCCAGTCTATCTAACTGCTGCTTAGAATATTTGGC  
TGCTGAAATTTTAGAATTGGCTGGTAAATGCTGCTAGAGATAACAAAAAACAGAAATTATTC  
CAAGACATTTACAATTGGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAATGTT  
ACCATCGCCCAAGGTGGTGTGTTTTGCCAAACATTCACCAAACCTTGTGCCAAAGAAGTCTGC  
CAAGACTGCCAAAGCTTCTCAAGAAGCTGTAA

YBL003C, 132 aa (SEQ ID NO 458)

MSGGKGKGKAGSAAKASQSRSAKAGLTFPVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAA  
EILELAGNAARDNKKTRIIIPHLQLAIRNDELNKLGNVTIAQGGVLPNIHQNLKPKSAK  
TAKASQEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459)

TGAACGGGTGCAAAATTTACTTTAACACCCAAAAAGTATATGCGTATATATATATATTTATC  
CTTGTTATTTTGTAAATTGAGCTATGCAACATAAGATTCTCGCGATGTAAGAACTACTTGC  
TAATCAAGAGAACTTCAACAATTTTCCATCGCAGAGACGAAAAAACTGGAAAAAATAAAAA  
GAAAAAATTGAAAAAGAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT  
TCTTGACATCATCAACACACCATCGCAGACCCACGTGGCCGCTTCGTGTGCCCTTGAANAATC  
AGCCTTAAACGCAATCTCATTCGCGTTCTGTGGAAATTGTCTCGGACTACACGCTGGGCGTG  
CATCACCAGTGAAAAATGCCGTACCGCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA  
GAAATAGACTTCTGGGTTTACACCCCGGAATAATACTAAAAACCAAACCTGGTAAATAGGGCT  
ACAGATGAGCAGGAAAACGTTGCCGGAAGTATTATTTATCCGAGAGAATAATTGATGAAG  
AAGTAGCGGTATGCACAGTAGCGGCGGAAGTATTAGCAATTTTACTCTGGTGTGCACAAGA  
GTGTTTCATCATTTTTCACGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA  
GAGACCGTACCACACGTTTAGAGCAGCCAGGTTGCGAAACTCTTCTAAGATGGTTTCCAGCA  
ATTGTGTACTATCAGAATGTGGACAGTTTAAAAGGTTGACTGCGAATTTGTCCCAAACCGTA  
TCACCGTTCGATTTTTTGAATTTGATCAAAGCACCCTCCTAATAGCACAGCGATGCTGTGA  
GTGTGCCAGTGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460)

MSRKTLPEKVYLSERIIDEEVAVCTVAAEVLAIFTLVCTR VFIIFFTARICHGIWPSSPSER  
PYHTFRAARLRNSSKMVSSNCVLSECGQFKRLTANLSQTVSPSHFLNLIAKAPLLIAQRCEC  
ASNGC

YDR529C, 884 bp, CDS: 501-884 (SEQ ID NO 461)

GAGTCTCCGGAGTTGACCAAGTCATACAATGTGCTACTGACCAAGAAATGGATCTGTGTAGT  
TCCAAGATCGCATGCCAAGAGTGGACCGCCATTGATGTTAAACATTAACTCCACGGGGTACT  
GTGGTATGATCCTCGTTAAAGACAGAGAAAACTAGAGAACCTCACTGAAGATCCTCATCTT  
TCACTATTAAGGTCTATTAGCCATATGTACATTGTCTATAGATGTGTAACCTGCGCTGTGATC  
TTGTTTTGACCAATCAGGAGCGACGCGCTTTTTATCGGGTCACCCCGCGGGGGGCTGACA  
ATTTACTTTCATAGAGCAGTAATAAAAGGGAAGAGATGTAAAAGCTTGGAAAAATAGCAGTA  
AAGGTTGTTGTTGGACAATTTATCAGAATATTAGTAACCTGTAATTAAACGTTCCAGAAAGAA  
CAAAATGCCACAGTCTTTTACGTCTATTGCGAGAATTGGTGACTATATTTTGAAGTCACCG  
TCCTCTCCAAGTTATGTGTTCCAGTTGCCAATCAGTTTCATTAACTCGCAGGTTACAAGAAG  
TTAGGGCTCAAATTTGACGACTTAATTGCAGAGGAAAATCCCATCATGCAGACCGCTTTAAG  
AAGACTCCCTGAAGATGAATCTTATGCCAGAGCATATAGAATAATCAGGGCTCATCAAACCG  
AGTTGACTCATCATTTACTGCCAAGAAACGAATGGATCAAAGCCCAAGAGGATGTTCCCTTAC

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CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGAAGGACGAGTTAGACAACAT  
AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462)

MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRR  
LPEDESYARAYRIIRAHQTELTHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIE  
VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTTTT  
TTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCTGTGT  
AGCCTAATGTTTAATGCCTAATTTTTTCTTAAATGCAGCAACATACATATGTTGAGTCGTA  
TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACATTTTAAAC  
ATCCGTACAACGAGAACCATAACATTAATTTTTTAAATATTCTTTTTGTTTTTACCAGCCTTC  
TTTTTATTTTTATCCGAAGATCTTTTGGAAACCCGCTCTGCGAATAGCGAAGCTAGGATACCA  
AATTGAAACTTGGACATAACTCATCATTAAGAAGTATACTGTTAAGAGAGGCATTTCATTTTC  
GTGTATTATAACGTTTAGCATCAGTTACCCCTGAAAGCCCAACATATACAAAAATACGCGTC  
CAAGATGTCTACTAAAGCCCCAAACCCCTATGCGTGTATTGAAGATCGAGAAAATTTGGTCTGA  
ACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCTCCAAGGTTTTAGAACAAATTA  
TCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTGTCAGAACTTTCGGTATCAGAAG  
AAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTCCAAAGGCTGAAGAAAATTTTGGAAA  
GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAACTTCTCTGCTACCGGTAACCTTC  
GGTTTTCGGTATTGACGAACACATTGACTTGGGTATCAAGTATGACCCATCCATCGGTATTTT  
CGGTATGGATTTCTATGTCTCATGAACAGACAGGTGCTAGAGTCACTAGAGAAAGAGAT  
GTAAGGGTACTGTTGGTAACTCCACAAAGACAATAAGGAAGACACCGTCTCTTGGTTCAAG  
CAAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRN  
EKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFPGIDEHIDLGIKYDPSIGIFG  
MDFYVVMNRPGARVTRRKRCGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465)

GCAACATTACCACCTTGTACGGAGCGTCAGAAAGAACGCACCTCATCATTATTATGAGAACA  
GTACGATAACTTCTGTCTGAGATACGCTTCGTTGTTATAATACAAGTGAAACCGCCACGGAT  
AATTAGCAGCAATTGAACACAAGGGATATCATTTGTGTGACCTTTGTTCCTCTCATCTGTC  
TGTGAACCCCTTAGTAACCTATTAAATGTTTATTTCATGAGACTAGTCAAAACATTCAATAACA  
GT'TTTTCTATATGAGAAAAAATGAAAAAGCAACAGTACGATTATT  
ACACTGACTATGCTGCAGTTTCCGCAATAGCAAAATTGTGTCACATTACACGAAAGAAAGAA  
AGAACGCTATTTCTTATAAGAGCAAACCTGTTGATAAGTTTATAGCAAGAATAAAAAAGGGTAA  
AAAGTCATTGATAATAACCACTGCTGTGACTATATATAATAAGAATCGAACTGTAAAGTTAA  
AGCAATGGTGTTCGGTCAGCTGTATGCCCTTTTCATCTTCACGTTATCATGTTGTATTTC  
AACTGTGCAAGCAGATTTCATCCAAGGAAAGCTCTTCCTTTATTTTCGTTTCGACAAAGAGAGT  
AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC  
TATCGCTGTTTTTGAATTTGACAATTTCTCATTATTGGACAACCTTGATGATTGACGAAGAAT  
ACCATTTCTTCAATAGATTCTTTGCCAATGATGTCAGTTTAACTGTTTCATGACGATTTCGCCT  
TTGAACATCTCTCAATCATTTATCTCCCATTTATGGAACAATTTACTGTGGATGAATTACCTGA  
AAGTGCCCTCTGACTTACTATATGAATACTCCTTAGATGATAAAAGCATCGTTTTGTTTCAAGT  
TTACCTCGGATGCCTACGATTTGAAAAAATTAGATGAATTTATTGATTCTTGCTTATCGTTT  
TTGGAAGATAAATCTGGCGACAATTTGACTGTGGTTATTAACTCTCTTGGTTGGGCTTTTGA  
AGATGAAGATGGTGACGATGAATATGCAACAGAAGAGACTTTGAGCCATCATGATAACAACA  
AGGGTAAAGAAGGCGACGATGATATTTTAAAGCTCCATCTGGACTGAAGGACTACTAATGTGT  
TTAATAGTTTCTGCGTTGCTATTGTTTCAATTTGATTGTTGCACCTTCTTGGATATCTAATTT  
GGATATCACATATGGTGCCTTGGAAAAATCAACAAACCAATAAAAAAACAATTA

YGR106C, 265 aa (SEQ ID NO 466)

MVFGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDTISTISSTADVISSVDSAI  
AVFEFDNFSLLDNLMIDEEYPFFNRFFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPES  
ASDLLYEYSLDDKSIVLKFKFTSDAYDLKKLDEFIDSCLSFLEDKSGDNLTVVVINSLGWAFED

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EDGDDEYATEETLSHHDNNKGKEGDDDLSSIWTEGLLMCLIVSALLLFILIVALSWISNLD  
ITYGALEKSTNPIKKNN

YGR182C, 854 bp, CDS: 501-854 (SEQ ID NO 467)

CCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAACGACTTAGCGAAGCT  
TATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCATTTCAGGTACTAAC  
AATGCATAAAATTATGAGTAGTCTTTTTCATCACTATATAAAACCTTTTCAAACGAAACGCT  
GTTTTTGTGTTGTTACTATCTTTGCAGGTGCCTTTGTTTCCAAACTGTATTTGATACTGCTAT  
TACTTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGTCAAGGCTCGAATAG  
CTGCAGGCGATGGAGACGACGATGATGAGTAAACGCTGATTATGTCACACATATACGTGCAA  
ACGCTCTCTCTCTCTCAAGCTATATAAGTGGCACTCGTCTTATTTATTTATTTTATTTT  
TGGCTGGTGTTCATGTTCAACCCAACCTCATAAAGGCACTCAACTTCATATTTTGACACAA  
ATCTATGTTCTCGCCAAAGCGCATTCAAAATTTTCAGAAATGGAAATAGACACGAACGAGCCTGTC  
TGTCAGATGTTTCAAAAATCCTTATTATAATTTTATATTCTACTAAAGGAAAAAGAGAATTA  
GGAAAAAGAATAACTCATTTTATGTATATACATATATTTTGTACATATCTATACCAAGCAAG  
TATAGTGCAATACTGTTCTTCGACGTTATTAAACGTAATAGCATTTTCTTGGTATCCTTTGA  
ATCTTATATACAAGTACGAGTACATACTGCGCAGTAAATTGATCCTGATGGTGTGTTTAGAT  
TTCGCCAGAAGCGGAGGCGTTCTGGATTCTGGAGATGTAAGCCTTTGA

YGR182C, 117 aa (SEQ ID NO 468)

MSRQSAFKFQNGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI  
VQYCSSTLLNVIAFSWYPLNLIYKYEYILRSKLILMVCLDFARSGGVLDSDGVS

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-  
914 (SEQ ID NO 469)

AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATAATGATGACTCTGATGAGC  
GAGAGATTTGGTAGATTCAAGCCCTCTACTATGTTTTATAGTTGACATATTTGTATATAAAA  
ACTTATACATTATTAAACATTTGCGCGTCGATTGACTTTTATTTATTATTAACAAAGAAGTA  
ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCCTTATCTAGCGAAGGC  
AACTTTTGAACCTCCCAGTTGTTAATATGTATCATTATACACGACCCAATCAAACGCGGGA  
AGTCAATGCCGAAAGAATTCTAGGACCTAAAAGCTGCTCAATCCTTGGGCTTTCCCTAATG  
ACATCCCCTCTCAAACCTTTAGCTTAGCAGTTGTATTTAATGTCTGTACGGATAGTCAATA  
ATCGTTGAAGGTTGATTTTCATATCCTTCGCAATTTTCGTAAAGCAACAATAGCAATACGGAC  
TAAATGGTATGTTGGTGTGTGTGTGTGTGCTGCTTCACATTTTCAGGCTAAAAATGTTATCCGT  
GGAATCTTCCTTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAAC  
GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA  
TTCAGGTTACTAACAATGCATAAATTATGACTGCTTTTTTCATCACTATATAAAACCTTTT  
TCAAACGAAACGCTGTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAAACTGTA  
TTTGATACTGCTATTACTTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT  
CAAGGCTCGAATAGCTGCAGGCGATGGAGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470)

MSFSSLYKTFFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD  
DDDE

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 471)

GGGCTTTTCCAGTGCCGCGGCCTCGAGATCCAGGCACCAGGAAGTAGGCACGCTGTGTATTC  
TAACACATTGAAGGGCCTAGGCCCGCTGACGTGGGGTCTAGTTCCACTTTTTCATTACCTTT  
TCTCGGTCTTTTCTTGCTCCCACAGGCCGTTAATGGCCTGAAACAGTTTGTGACTTTGGAC  
TTATGATAACGATGTTTGTCCGGGTGCCACCGGATTCTATCGCGGCGAATCAAGTCTAGTCT  
GTTTGCAATCCATCAAGGCACTGCTCATTGTGTAAAATTGTTCTACGCTTTTGTTCATCAATCA  
TATCTAAACTCACAGCCGCTAGGGTAGGTGTGCCTGGCAGTGGTAAGGTAGCCGGCTCGTCT  
TTGGTCATGCGCCAATACTGTGCAACGGCCGCGCGTAGCGTTCTTCGGCTTCAACCTTAGA  
GCTGATACCTTTTGCCTGGTCAAAGGCGAAAACGTCTACCTCGCTTTCACTGCTGCTTTCCG  
TTTCATGACTTCGTTTCAAGCGGTCTCTTTCGCTCTCGGTTGTAAACACACTTGTAGCCTGCT  
ATGCTTTTACCCTGACTCGAAAAGCGTAGCCTCATGACTAGTTGTACCAACGCCCTTTCTTTT  
CTTTTTTTTCTCTTGACACTTCGGCGTATTCATCGCCACTGGTACAAGCCGTATGGTGTCTTT  
TTTGCTCATTTTTCGTTTTGACGTTGCGATGGTTTTCGCGGACCAATCGCATGGGTGGTGGTGG  
ATGTTGTCTTTGCTAGTTGCAACGTAGTCTTCTTCTCCTGCGCTTTCTGACGAAAATTGG  
CCTTACGTATCTTTTTTTCGGCGTCTGTTGTCGTATCGCTGTTTCATATAATCGTCTGCTCACTCA

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TATCGGCGCTTTTACTGCATGCTGTCTTTTGAAGAGAGTTTCATTGAAAAGTAGTGAAGAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAAAGCTTACATACGGAAAGAGAAAAAAAAAAAA  
AAGAAATTTTAA

YKR040C, 167 aa (SEQ ID NO 472)

MTSFQAVSFALGCNTLVACYAFTVLEKRSMTSCTNALSFLFLLTLRRIHRHWKPYGAFL  
LIFVLTLRWFRGPiAWVVVDVVFASCNVFFSPALSDENWPYVSFFGVVVVIAVHIIIVVTHI  
GAFTACLLKRVSLKSSEEKKKKKKKKKEKSLHTEREKKKKKF

YOL127W, 1343 bp, exon1: 501-513, intron1: 514-927, exon2:  
928-1343 (SEQ ID NO 473)

TCCTTATCTTGTATGCCCCGATATAGCAACCTTGTGTGGTACCAATCTAACGGTTTCCGTACTTT  
GCAATGAAGAGATGAGGAGGCATGGGTCACCTATTTAATATGTACGGGTGTTTACATGGAGT  
TGCTTTCTTTTGTCTCAGCAGTCATTGTGCGCCAAAAAAGAGAAAACCGTGAGCCGAA  
GTCCACGCTCTGGAGTTAGGCTCTCCCATTACGGAGAGAAGCATTTCCTCAGCCTGGGAGCC  
CCGTTGGAACAGTCAGGCTAAACTGGGCCTTCCTACCCACTGCTTGCTGTTTCTCACTGGAC  
GCACAAGGGGATTTTCTTCTACCTTCGGCTTGCCCTCACTGCGTTGGGGCTTCCCAATGCAA  
CTTCGTTTCGTATGCATACAATCTTTTAGATATTTATCTTTTAAATTTATTTTAAACAATTTT  
AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA  
TAAATGGCTCCATCTGGTATGTGAAC TGCAATATTAATAGCACGAGAAAATTGAGAGGAAG  
ATAGATGGGAACTAGTAGAGTTGATATTTGATGAGATACGAAAACCACACGTAAATAAACTAT  
CCGACGACAAGAATAGTGCATTAAGGACTTGATTAAGATATGGTGAGCAACGTAATTATCGG  
GCTCAACAGTTTATTAGCAATCGTTTTTGATAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT  
TACTACCAACAGCCATTAACAAATCCATTAGAGTGTTTCGTTTCGTTTTCTGCTCAGATTCAA  
GAAAATTATTCCATCCTCATTATACTTTTTTCTTCTATTTTCGTGCTCCACGTCGAGGTATCA  
AGGAACATAGTTTACTAACATTAACGAATTCATCTCCTATGAATTTACTTTTTGTATAGCTA  
AGGCTACTGCCGCTAAGAAAGCTGTCGTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC  
AGAACTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC  
TTCCAAGGCTGTTCCACATTACAACAGATTGGACTCATACAAGGTCATTGAGCAACCAATCA  
CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTTCCAAGTTTCCATG  
AAAGCTAACAAATACCAAATCAAGAAGGCCGTCAGGAATTATACGAAGTTGACGTATTGAA  
GGTTAACACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT  
ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474)

MAPSAKATAAKKAVVKG TNGKKALKV R T SATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV  
IEQPITSETAMKKVEDGNILVFQVSMKANKYQIKKAVKELYEVDVLKVNTLVRPNGTKKAYV  
RLTADYDALDIANRIGYI

**FIG. 2:**

YBL051C\_homolog\_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

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AGAGAACGTATTGAAGAGGAGAAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA
TCAAATGCTTCTATGGCTTCTTTATTGTCTAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT
GTGGCTGGCACAATCCTTCTCATACCCTGAAAGAATGTTTTTAAATTTACCTTTTAACAATTCC
CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAAATGATCTTGAAGTTTGGGAATTGTACACTCAA
TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG
AATATTTCTCAACGGAAAAATCATATCAATTTTATGTAATTTATTTGAATTTATTAGAATTGTTTGAT
AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGATAACTCAACAATCTATT
ATTCTTAATTTCAACAGGTGTCTGGGCCAACTCACCCGCAACAACATCAACAGAATCAACTTCAA
CAACAGCAACAGCAACAACATCAACATCAACATCCTTCACATTTCATCATCGATGATGAACCTTCAT
CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCCCTGAATTTATTAAGATCCCAATCGCAATCAGCA
TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC
CAAAATCAACCACCACAACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG
CAATCTATTCAAAGCCAACCACATTCTGCGAGACCTTATTCTCAATCATATAATATTTATCAACAA
CAACAGCAACAGCAGCAACAACAAGCTCAACAACAAGCTCAACAACAACAACAACAACAACAATTAAL
TATCAACAGGGACACCAGTCACAAGTTTCAACACCTACATTGAATTCTTCTAGTGCTGCTGCATTA
CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCAAGTAGTTTTGCT
CAACAGCAACAACAACAACAACAACAACAGCAACAGCCGCCACTAACTTCATCAATCCATGATTCCT
CCAACACCACATCATCATTTTACCCTTCAACAGCAGCCACCACAACCAATCATTACCTATCCAAT
TACCATCAGGGGGTTGGATCTCAACCAAAAACCTCCATTGGC
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YBL051C\_homolog\_1 409aa (SEQ ID NO 286)

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RERIEEKREKRGQLEEQHRSASNASMASLLSAASTTAATKNLSVAGTNPSHTTERMFLNLPFNNS
SFNAPPVEINFNDLEVLTYQLVLYRDDITKSTFELAI SPANLNISQRKII SILCNYLNLLELFD
NGLIIIRRKPGYIAQCITQQSIIIPNSQQVSGPTHPPQHQQNQLQQQQQQQHQQHPSHSSMMNLH
QLGGT LAVPAHPELLRSQSQSALPLPRLRQQTSTPIQQNQVQHQQNPQQQQQQHVQPPQNYNQ
QSIQSQPHSARPYQSQSYNIYQQQQQQQQQQQAQQQAQQQQQQQLQYQQGHQSQVSTPTLNSSSAAAL
LRSSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPPQPNHYLSN
YHQGVGSQPKTPL
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YBL051C\_homolog\_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

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ACTTTTTTGTATTCAACTCTCTAACTCTTTCTATTTTTTTTTTTTCTATATACACTGTAAATC
AATCAACAATAGCAGGATATCCATTTCATATACAAATAGATAAACTGTTAATTAATTAATTAAGT
ATTTGATTTGGGAAAAAACAATTTTATATTTGGAGAATTGAATTTCAATCATTTTAAACAATTCA
AAGCTTTAATTTCCACCTATCAAATTTTATTATTTTGTGTTTCATTATTTTTTTTTTCCCTTTC
TTTCTTTCTTTCTTTCTTTTGGGAACAAAGTAATAGCCGATAAAATAAATAATTCACATAGCCCA
ATTCATATTACATTGACTTTTGACAAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC
CGAATCAAATGGGCACGTGAATGCAACGTCGTCCCTCTCTATCATCATTATCGTCAGCCTCGGGCT
ATTCTTTCTTCCAAATTATGGTGGAATCCTACACCAATCCCAACAATTCCAATACCAATAACAATA
GTAGTGGCAATAGTAATAACAACACTCATGGCAATAACACTCCCAATATCAACTCAAAGATTGA
CAAATAATAGGAATTTACAATCCTTGTGGATAAACCAACCATCTATTGCTCCTTCTAATGTTGTTT
CTTGGGTGGAACAGCAACAACAACAACCCCTTGATCTGTTGGAAAAATAACTAAAACAGACTCCA
GTAATGATGCTTCTGCTACTAATAATAATAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA
ATGCCAATGCCAATATCCATGCCCAACCCATGTCAACACAAATGTTAATGCAACACAACAGCAA
CTGATTATTAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA
AAAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA
CTAACAATAGTAGTACAGGAAGTTCTAACATTGCAACATGCTTCCTTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATAGCACCACAAACAATACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCCATTTGCCATTAAAAAGCAACAATTGT
TAGATGTGATGACAAATTAACCTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG
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99/161

TGTTTCGTGGATTAGCATTGCGCAATTTACATCTACAGATGAGACATCAGCAGTAGTAAACCAAT  
TGAATGGAAGAGAAATAGGTGGAAGAAAATTACGTGTTGAATACAAAAAATGCTTCCGGCACAAG  
AAAGAGAACGTATTGAAAGAGAGAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTG  
CATCAAATGCTTCTTTGGCTTCTTTATTGTCAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGA  
GTGTGGCTGGCACAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAACAATT  
CCCTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTTGGAATTGTACACTC  
AATTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCCAGCATAT  
TTGAATATTTCTCAACGGAAAATCATATCAATTTATGTAATTATTTGAATTTATTAGAATTGTTTG  
ATAATGGGTGCTACTAATTAGAAAAAAACCAGGATCCATTGCTCAGTGTATAACTCAAAAATCTA  
TTATTCCTAATTCTCAACAGGTGTCTGGGCCAACTCACCCGCACCACCATCAAAAGAATCAACTTC  
ACCAACAGCAACAGCAACACACATCAACATCAACATCCTTAACATTCATCATCGATGATGAACCTT  
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YBL051C\_homolog\_2 550aa (SEQ ID NO 288)

MDFRNLSTTPNQMGTVMQRRPSLSSLSASGYSSSNVGGNPTPNPNNSNTNNNSSGNSNNNTHGN  
TPKLSTQRLTNNRNLQSLWINQPSIAPSNVVPWVEQQQQQLDLSLENNTKTDSSNDASATNNNNVN  
VNVNANANVNANANIHAQTHVNTNVNANTTATSINASTILNTTPSINDTNDNAKKINVSMISNNNN  
NNSNNNNNNNTNNSSTGSSNIANMLPSVSNATTTMNSNSINSTNNNTTINEADDDDELIPTAIVIKNI  
PFAIKKEQLLDVMTKLNPLPYAFNYHFDNGVFRGLAFANFTSTDETSAVVNQLNGREIGGRKLRV  
EYKKMLPAQERERIEREKREKRGQLEEQHRSASNASLASLLSAASTTAATKNLSVAGTNPSHTTER  
MFLNLPFNNSSFNAPPVEINFNDLEVLELYTQLVLVYRDDITKSTFELAISPSIFEYFSTENHINLC  
NYLNLLELFDNGLLLIRKKPGSIAQCITQKSIIPNSQQVSGPTHPHHHQKNQLHQQQQOHTSTSTS  
LTFIIDDEPSSIGWYISCSSAP

YBL066C\_homolog 3254bp PathoSeq: 1..94/2146..3254, public:  
95..2145; CDS: 501..3251 (SEQ ID NO 289)

ATAAAAAAAGAAATACAATTAATAAATTTTCTCTGTGAAAAGGCAATTTCTGGGTCTAGTAGTA  
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CAGTTTCTTTTTCTTTTATATATTTTTTCTTACTTTCTCTTCTTCTTCTCTGACAGTATATTAATA  
AATATTTCTTTTAACTTATTTTTCAATCAAGAAGGTACTGAAGATATCAATTAACCTCAGTTAAA  
TCCATATTACCAGTTGTGGAATAATCAGAAGAAAAAAGAGAGAAAAATCACGGGAATTAC  
GTTCTCAACAGAAAAATAACAATAATTTTTTTTTTATTTCATTCCAAGGTATAACAAGAACGTTAGGAA  
TAATATAAAATTATCACCAAAGCTGCCATCAACGTGTGTCGACAACCAATCGACTCCTCCCTTAAC  
TAGAACCATAGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAGAAAGGTAAAGTGAGAA  
TTTTGCCTAAACCATCCCCCTACACCAACCAACCCACAAACCCCATTGCCATTACTTCCAGCTCAAA  
CTAAACCTGTAAACTCAAAAAGAAAATCAGCAGCCAGTACACCTGGAAATGAATCAAGAAGAAATCAA  
GAAAATCAAATTTACAGCTTCAACACCCCAACAGTGTACACCAACATCAGTCGGAACACCTCCAC  
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TCAAATGTAATGCTTCAGATAATTATCCAAACCCATGTGAAAGATGTAAAAAATGGGTTTGAAT  
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ATGCATCGCCAATTCCTTCTGTGACAAGTATTCACAAAAATGCACCGTTGACTCACGAAAAATCCG  
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TCCAAGCCTTGATCATACTTTCAATATGGCCGTACCTAATGAAAAAGTTTTGGATGATTGCTCTT  
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TTTCGCTATCTATTTTCCAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG  
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GATTTAACTTCAATTTGAAGAAGGGGGGCAATTGAAGTATATTATTTGTATATTAAATTGATGA  
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ATTTATCAGCAACAAGAATCGTGACAATCGTTTCTAAAATGGTGAATGACATTTTATTGATTGAAT  
TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTCATGTTGTTCAAATTACATTTGTCAA  
GATATTTGATTGACAAGTATGTGGATAGTGTGCTAGACAGCTGATTGTTACTGTGCATCGTTTATTTA  
GAAACACGTTGAGTTTCTGGAAAGATTGCAAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA  
ATTTGAACATGGTGTGTATAATTATCCTGAAATATTTTTAAATGATCTGGAAAATGAGGATTCAA  
GTATTATCACCAGAATGAGGTCACATTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC  
ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAAAGAAAATCT  
TGCCCTTGCCATTTTACAACCAAATCATAAGGATGATTTCAAGACAATTACCACGACATCACCTA  
ATGGAAC TACTATTACATTTAGTTCCAAC TATGATCAAGCTATGAATCAAGCAAACTGAAATCTT  
TTGATTCCAGCAAACTGAAATAAATGGTATTCCCTTACCTATGCTTGAAGCTACTGGTTCAA  
CAAGAGAAGTTTTAGATTTCTTTACCCTCGCAATCTTTACCATCACAAGCACCAACTCTTCAGCAGT  
ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAACAACAACAACAAAAGCACCTGCAGC  
AACTGCAGCAATACCAACAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC  
AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCTTCAGCAACCAC  
CTTTTATTTTGGCAAAC TACCCTTACCACAAACTTATTTGCCAAAGATTGATGAAATGAATATGT  
CACCAGAAGTAAACAAGAAAACCTCTGTTGCTCCATTTGCATCTCAAATCACCAACTTTTTTGTATC  
AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTTTGGGTTGGTTTGTATGTA  
ATATGATGCAAGAGAAATAA

YBL066C\_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLLPAQTKPVNSKRKSAASTPGNESKSKSRKSNSTASTPNSA  
TPTSVGTTPPQKTSKPTGHRPVTSCFQRQHKIKCNASDNYPNPCRCKKMKGLKCEIDPEFRPRKGS  
QIQSLKSDVDELKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYTSA  
NSSPQVAFSNASPIPSVTSIQQNAPLTHENSNDNSPYALNTPENIEELQPISEFILGDVTLPLNRRAN  
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW  
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQGLHRGGEFIEFQSRNQVSLGP  
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLLNARVDKSLPKNFRCLISLSIFQCKLVNI  
MGISVTRPDGLLEPSNRAGSLSLDRELERLRFKLQFEEGPIEVYLYIKLMICCFALPGTPIE  
DQVKYVSFAYLSATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMLFKLHLSRYLIDKYVDSARQ  
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENESSIIITRMRSHLTAS  
LFYDLVWCVHEARRRSVLDKGKRQAQPNKKILPLPFYNQITKDDFKITTTSPNGTTITTLVPTDQ  
AMNQAKSKSFDSSKPLEINGIPLPMLEATGSTREVLDSLPSQSLPSQAPTLLQQYPMQDDQQQQEPS  
QQQQQKHSQQSQYQQQQQSNQQQPHLQHQRQFQQSPPPQFSMISSTPPLQQPPFILANSPLPQTY  
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YBL078C\_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:  
450..533, exon 2: 534..908 (SEQ ID NO 291)

TTATTATTACTATGACACACACTTACTCTCTTCTATGTCTCCGCTTACATCACACATCATACGTTT  
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CTTTTTTTTTTATTTATTTATTTTGTATTTTGTATATTAATCAAAC TATATCATTCATCTATATA  
TACATCCCCATCGATTTCATCTGACATAATAGTATGTATGATCATAACAGAGGGAATACCCCTTTT  
TATTATTACCAAGGTCATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTGTAG  
ATAATTGCCACTCAATCTTTAATTGACCATCGACCACAAAAATAATATGGAAATAATACTAACAGA  
ACTTAGAAACATCACTCATAATGAGATCACAATTCAAAGACGAGCATCCTTTTGGTATGTATTACA  
TGATTTTTTAGTCCTCTGAATCTTCTCCGATCATCATATACTAACATTTTCGTGGGTGTATTCTT  
TAATAGAAAAGAGACAAGCCGAGGCAGCAGAACTTGCTCAGAGGTTCAAGGATAGAGTACCACTCA  
TCTGTGAAAAGGTTGAGAATTCCGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG  
ATTTGACTGTTGGTCAATTTGTTTACGTTATTAGAAAAAGAAATCAAGTTACCAAGCGAAAAAGCCA  
TTTTCATCTTTGTCAATGACATATTACCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC  
ACAAGGACGAAGATGGTTTCTTATACGTTTATACTCTGGAGAGAATACTTTTGGCGAGAACTAG  
CAATTGACATTTTCATCATTAGATTTTCAAGTGATATCCCTGATTATGTTTAA



YBL078C\_homolog 135aa (SEQ ID NO 292)

MRSQFKDEHPFEKRQAEAAARIAQRFKDRVPICEKVENSDIPEIDKRKYLVPVDLTVGQFVYVIRK  
RIKLPSEKAIFIFVNDILPPTAALISTIIYEEHKDEDEGLYVLYSGENTFGEKLAIDISSLDFSDIP  
DYV

YBR073W\_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

GTGGCACATCCCAGGAAGTAGAGCATGGACAGTTCGTATGGTATTGCTGTGCATACGATACAAAAA  
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CGTCCCTAAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT  
ACTTTTCATTTTCCATTTGTTATGCTTACGACAACCTGAAACCATGCTACTTCATACGTTTGTATTGA  
TGTTTTCCTTATTTGGTTGCCTATGGGATCTACGCTTATTTGCCTTCAAGTATCATGTTTGAACATCT  
CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT  
GTCTACTTAGTTTTTATAGTTTTAAAAAATTTGTTAATAATAAACCCAAAGTTTCTAACAGGCTCTGTTT  
GCTCGACTAAAAAAGAATTTTGTCAAACGCGTATCAGAATGTTTACCCTTTTTTTTTTTTACCACAG  
ATCAAATGAATGTTTCGACCTAATGCTCCGTTTCGGCCTCCTAGACCAATAAAGGGGGGTGTTGCGG  
TGGTGCAGAAAGTAGTAAAACGAAAATTGCCACTACCACCAATCCTAAACCTGCAAAGATTTTGA  
CTACCGATCCCGGCTCAACAAAATACGTGATCCAATGGAGAAAGAAAACCTCAAAGAAGAACAAAA  
CATGGGACGGTGATGGGTATGCCGTGATTAAACAGCTTTGAGAATGGGGCATGCGAGATATCTATCA  
AGAAGTCTGATGGCAAACCTATGGGGAAAAGAGTGTTTACTGCGACACCTAACCTTGACGACGTGA  
TTAGTGTGGGACCCCTATGAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCCAGACAG  
TGACACGTGTTACCCACCAGTTCAAAAAGGTTGCTCCTCCACAGCTAGTAGTCGGAAACCGCTTT  
ATGACGACTGTGCCGATGCCATCGCGTTGCCTCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA  
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AGTGTTTAATGGGGTACCGTGGGTTTGGCGGGCAGGGTGTTTGTAGCAGATGAAATGGGGTTGG  
GGAAAACGTTGATGACAAATCACTACAATCTGGACGTTTGTCTCAAACAAAACCCGTTTATGGAAAAAG  
GTGCACTGGTAAATAAGGTATTTGGTGGTGTGCTCCTGTACGCTTATTTCCAATTGGAGACAGGAGT  
TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTGTTGACGCTCAACAACCCAAATGTCAAACGAGA  
AACAGGATATACTCAATTTTGGAAAGTTGAATGTGTACCAAGTGTTAGTGGTGAATTATGAAAAAC  
TTGTGGCACATTTTGTATGAACCTCAGCGGTCAAGTTTGATTTGTAGTGTGTGACGAGGGCCATC  
GTTTGAAGAATAGTGCAAATAAAGTATTGAATAATCTTATCAAGCTCAATATTCCGAAGAAAATTG  
TTTTGACGGGTACGCCGATTCAAACAGAGTTGGTAGAGTTTACACAGTTGATCTCGTTTCTCAACC  
CGGGTGTGCTTCCCGAGCTAAAATTGTTTTCAGCGAAACTTTATAACACCTATATCTAGGGCCCGAG  
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TGACTCAGAGTTTTATTCTTAGACGTACACAAGCGATTTTGGCTAATTACTTGACACAGAAAACCTG  
ACATTTTGTGTTGTTTGTTCACCTACATCGTTGACGCTCAAGTTGTTTCGACTATATAACCAACTGA  
AGAAATTTAATCAGTTTGAAGCATTTACCATGATCAATTTGTTTAAAAAGATTTGCAATTTCCCTTT  
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CCGGTAAAAATAAACATTTCTTGTGCGCTTGGCTATTGGAAAATTGCTTCGCTTGGGGAAAAGATTGTCT  
TAATTTCCAACCTACACCAAGACTTTGGACTTGTGGAACAGGTTTTCGCGCAAGGTCAGCCTAACAT  
TTTCGAGATTAGATGGGTGACCCCCAACAAATGTGCGTAGCAAGTTGGTTAATCAGTTTAAACACGA  
ACCCCGACATAAACGTATTTTTATTGTCGTGCAAACTCGGCGGGATGGGGATCAACTTGGTCGGGG  
CTTCGAGGTTGATTTTGTGTTGACAATGACTGGAACCCAGCGACCGATTGCAATCGATGTCGCGAA  
TTCACAGAGACGGACAATTGAAACCGTGTTCATTTATAGGCTATTCACCACGGGGTGTATTGACG  
AGAAAATCTTTTCAGCGACAGCTCGTGAAGAACAAATTGAGTTCCAAGTTTTTGGACAATGACGCCA  
CGTCCAAATCTGATGTGTTTGAACAATGATGATTGGAAGAATATTTTGGAGATAGATACATCGACAA  
TATCCAATACTCATGATTTATTAGAGTGTGTGTGTGAGGGCGACGGTTCGATGTTGAGTCAGCCAA  
CCATAGAGGAAAGCGAACCACCCCCAAAACAAGCATGGGTACTGCATTAGAGCTTAAGAAGAAGA  
TTGACGATGGTGAGGCGCTAAAGAGGACGGCTGTTAAATTTGCCTTGAACGATTATCGACACTACA  
ATCCAGAGGTGAACCGTAATTTGGATTTGATTCTGCGCTACACCGAATTGCTAACAAATTCAGCT  
ATGAAAATAAGCAATTGCCAATTACATTTATAATGCTGAGAGTAACTAATTAA

YBR073W\_homolog 796aa (SEQ ID NO 294)

MFTLFFFTTDQMNVRPNAPFRPPRPKGGVAVVQKVVRKLPPTTNPKPAKILTTDPGSTKYVIQW  
RKKTSKKNKTWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK  
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADIALPPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTTIWTLKQNPFMKGAVVNKLVLVPCPV  
TLISNWRQEFRKWLKANKLVNLTNNPMSNEKQDILNFGKLVYQVLVNVYEKLVAHFDELSAVKF  
DLLVCDEGHRLKNSANKVLNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPKLFQRN  
FITPISRARDINCFDPEVKKRGEEISQQLIELTQSFILRRTQAILANYLTQKTDILLFVPPTSIQL  
KLFDYITNLKKFNQFEAFTMINLFKKICNSPSLLADDELFFKKIVEEFNLGMASGKINILVPLLE  
IASLGEKIVLISNYTKTLDLLEQVLRKVSFTFSRLDGS'PNNVRSKLVNQFNTNPDINVLSSKS  
GGMGINLVGASRLILFDNDWNPATDLQSMRIHRDQGLKPCFIYRLF'FTGCIDEKIFQRQLVKNL  
SSKFLDNDATSKSDVFDNDLKNIFEIDTSTISNTHDLLECVCEGDGSMLSQPTIEESEPPPKQAW  
VTALELKKKIDGALKRTAVKFALNDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS  
RVTN

YBR086C\_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

AAAGAATTTCAAATTTAGT'TTTAGGTGATAATTATCGTTCGTCTTTCCTAACCTACCAATTTTGA  
CTTTGTGTACTCATACGATGGTTGTTATTAGTTAAAGT'TGCTTTGCTTTTCAATTTCAAT  
TCACAATTTGAATTTCAGAATAGAATTAGT'TTACCTTTTCTTACAATCGGCTAAGATTTTTC  
TTCTTCTAATTTAGTTTACAGAATAGAAAGAATAGT'TTGCTTGT'TTGCTCATATTTACAATCAAT  
GGTTAT'TGGTGT'TTATTATTTT'TTGGTTTCTCTT'TTACCCCCCTTCCGTCTAATTGAGTTA  
TTGTTTGGGAATAATTTATTACTTATTCAATATATTTT'TTCTTCTTCCCTTCTTCAACTTCTT  
TTTATACATTTCAATCAACCTTCCAACAATCCTATAATTACTTACTTACTTACCTTCTTCAATTGGATTA  
ATTGGATTTGAATTTGT'TACAATTTGAATTTCAACTTCAACGAGATGACTT'TACCAATTCAGGATTTAGAAC  
CTGATTATTATATTTCCGTCAATTATCCTACCACCGATAATGGATCACCAACCCACAAGCTGAAA  
AATCATTTGAAAACATTAATTGATTTATTATACGATAAAGGGTTTGCCGCCCCAAAT'TAGACCTGGTG  
ATTTAGACCATTTGT'TAGTCTTTGT'TAAATTTGCTTTCATACAAGT'TTCTGAAGAAGCTGAAAAAG  
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TTATTTATCAATACTTAACTTATCCACACGATTTGT'TGCTGGATGTGGTATTACTCTAATTTCTGGGG  
ATTGGAATTTGTTCACCGATTTGT'TCCAATTACTAATGCCTT'TAATGAAACCACTTTAGTTGAAG  
ATTTAAAAATTAATGTTACTCAACCAATTTATCAATTTGCCACTATCAAAAAGACATATGGAGTTG  
AAGTTGCTCTTTATTTTGAATATATAAAACATTACACTTTT'TGGTTATTATTGCTTTTCTATTATTG  
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GGGGGG'TTTTATTTCTTGCATCATGGCATAGAAAGAGAACAACTTTGGTTAATGTATGGGTGTTT  
AAAATAGTCATTTAATTTGAAGAACATAATTCGAATTTGGCTAAAGTCAATGAAGATGAAAGAAA  
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CCATTGCCTTTGGTGT'TTGT'TGGTGT'TTGTATTAGTTATCAATTGAGTTGT'TCTGTATTGAAATCT  
TTTAAACCGATATTTATGATGGCCCCGGGAAATCTTTATTGACTTTATTACCAACGGTTTAAATCA  
GTGTATTTGTGCCAATTTTGACCATTTGTTTATAATGCTGTCACGGATATTATTATTAATGGGAAA  
ATCATGATAACCAATATAGCAAAAATAATTCATTTCTTGT'TAAACCTTTGTGTTGAATTTCTTGA  
CTGGTTATGTTCCATTAATCATCACTTCAATCATATATTACCATT'TGCTCATTTGGTGCAACCTC  
ATTTAGGTGATATTAAAACCACTATTGGCACATATGCTGGTGAAAATAGATTCTACACCAAATACT  
TGTTGAAATTTAAAGAGTCAAGAAGAATTTAAAATCAATCAAGGTAGATTAGATGCTCAATTTCTTT  
ATTTCAATTGTCACAAATCAAGTTATACAATTTGGTATTGAAATATATTCTCCCATTTGGGT'TAAGAT  
TTGTATTTAATTTTATTGAAACGAAAATTCAGAAGAAACCTCAATTACAACTAAAGATGATAACC  
CTGATGAATCTATTTGGTTACATAATGTCAGATTATCGTTGAAACTTCCTGAATATAATGTTGATG  
ATGATTTTAGAGGATTAGTTT'TACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG  
CACCATTGGTTTGTATTATTTTCAATTTAATTTT'TTCAAGTTGGATAATTTTAAATTTATTGAATG  
GTAAATATTTCAAACCACCACTTCCAAGAAGAGTTGATTTCTATTTCATCCATGGAATTTAGCCCTTT  
TCTTGT'TAGCATGGATTGGATCAATTTATTTCCCCCGTGGTACGGCATTTTACCGTCATGGTACTG  
CTCCACCAAAATCTATGGGTCAATTTGCCCTTGATAAAGCTAGTGTTCATGTTTTCATCCTCAGTTT  
TCTTGGTTTATTAATGTTTGT'TTCAAGATGGAATTTTGGATTTTGAAGTTATCTTTTATTGAAAT  
TCTCTTCTTTGTTCAAGAGTCAAGTTGAATGGGAAAATGATTTTGTGATAATGATAATGAATTTGA  
GACATGATTATTATTCTGGGAAAGTAAACCAACTTATAAAGTCCACTCGGATGAGTTGTGGGAGA  
AGTTTACCCCAACAATCAACTTTGAATTTCACTGGTCTTAAACCAACCGCAGAAACTGATGATAAAG  
TTGAAAAAATGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTACTGCTA  
CTT

YBR086C\_homolog 714aa (SEQ ID NO 296)

MTLPIQDLEPDYIISVNYPTTDNGSPTPQAEKSLKTLIDLLYDKGFAAQIRPGDLHDHLLVFKLSS  
YKFSEEAEDLIKNEYFGVTGKDDVLASKLRITTYQYLTYPQSVGGCGITPNSGDWKFVTSIVPITN  
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLSIIGLVSHFRKDKRFS  
LTFAFINLLWGVFLASWHRREQHLVNVWGVQNSHLIEHNSELAKVNEREYEEKSTYFHANNTNGF  
RFLKQLAFIPIALVFVGVLSYQLSCFCIEIFLTDIYDGP GKSLTLLPTVLISVFPILTIVYNA  
VTDIIIKWENHDNQYSKNNSILVKTFVLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA  
GENRFYTKYLLKLSQEEFKINQGRLEDAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK  
PQLQTKDDNPDESIWLHNVRSLKLPYNNVDDFRGLVLQFGYLMFGPVWPLAPLVCIIIFNLIFF  
KLDNFKLLNGKYFKPPVPRRVD SIHPWNALFLLAWIGSIIISPVVTA FYRHGTAPPKSMGQFALDK  
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFKSQVEWENDFVDNDIKLRHDYYS GKVKPTY  
KVHSDDELWEKFTPQSTLNFTGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C\_homolog\_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS:  
399.1781 (SEQ ID NO 297)

CGGTAATTATGTACAAAAACAAACAATCAACATATTAATCGTTATCCCAACTTTGTACAGTTT  
CTAACACCTTTTATTTTGTGTTATACAAATTGCACAATCAATTACTATAACTTTTGTGAAACGT  
GGGCTCTGTTTAGTTTAACTTCTGTAGTTTATTATTTCCGATTGGGTTAGCTCAATAACTGCATT  
TCGTACAATAATGTTAATTCATTTCTAAATTCCGATGAACCGAACACACAAAAACATCCAGTTCT  
GGAGAGATTTTCAAACTTCTATTATAAATAGAACCCCTATAAGTCCATAATAATTCATTTGAAGG  
ATTATTTTCTTTCCCTTTTCTGATTACTTTTCACCAATTTTCTTCTCTCCAAAAAACACCTTCT  
TCATGGTTTCTGTCTTCTAAATTAATCAATAACGGGTGTTATTAACTAGTCAAAGTGTCTTCCAAG  
ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAATATACTCAATTTTCTTGGCGGTAGTG  
CCCCTTATATTCAAAGAAACGGATATGGGATTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTC  
AAATTCATTTGTATTCAAGACATGGTGAAAGATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAG  
CAATTTATGCTAAATTTGAAAACACAAAGGTACTTTTAAAGGTGATTTGTCAATTTTAAATGATT  
ACACTTATTTTGTCAAAGACAGAGTAACTATGCTAAGGAACTAGCCCCAAAAATTTCTGAAGGAA  
CCTATGCCGTTACAACCAATGCCCTTGGCTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT  
ACAAGGAAAACCTCAACTTTACCAATCTTCACATCCAATTCTAACAGAGTACATGAAACTTCAAAGT  
ATTTGCTAGAGGGTTTTTAGGTGATGATTATGAAGAAGGTAAAACCTGTCAAGTTTAAACATCATCT  
CTGAAGATGCTGATCTTGGTGCCAAATAGTTTGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAAC  
TGAGCAGTAGTACTGCCAAAAAATATAACACAACATATTTAAATGCTATTGCTGAAAGATTAGTTA  
AACCAAACCCAGGTTTGAATTTGACTACAAGTGATGTCAACAAATTTATTCAAGTTGGTGTGCTTATG  
AAATCAACGTCAGAGGAAGTTCAACATTCTGTGATTTATTACCAATGAAGAATTCATTAAGAAGT  
CTTATGGTAACGATCTTTCCAAATATTATTCTAATGGTGCTGGTAATAATTACACCAGAATCATTG  
GTTCAAGTATTTTGAATTCATCCTTGGAACTTTTGAAGGACACTAAGAAGTCTAATCAAGTATGGT  
TATCATTGCTCATGATACTGATTTGGAAATTTTCCATTCTGCTTTAGGATTATTGGAACCACTG  
AAGATTTACCAACATCTTACATCCCATTCCCTAACCCATACGTCCATTCTTATTGTTCCCAAG  
GTGCCAGAAATATACACAGAAAACTTCAATGTAGCAACGATGCTTATGTTAGATACATTATCAACG  
ATGCTGTCGTGCCAATTCCAAAAATGTGCTACTGGTCCAGGGTCTCTTGTAAACTTGATGATTTTG  
AAAATTTGCTTAAAGAAAGAATTGGAGATGTTGACTTTGTTAAACAATGTGGTGTCAATAGTACCT  
ACCCATCTGAGCTTACTTTCTACTGGGATTATAAAAATGTCATTACAGTGTCTCTTTAGAATTTGT  
AA

YBR093C\_homolog\_1 461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ  
IQLYSRHGERYPKSNKGSLEAIYAKFENYKGTFGKDL SFLNDYTYFVKDQSNYAKETSPKNSEGT  
YAGTTNALRHGA AFRAKYGS LYKENSTLPIFTS NSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS  
EDADLGANSLTPRSACSKNKESSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE  
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDKTNSNQVWL  
SFAHDTDL EIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND  
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYSAPLEL

YBR093C\_homolog\_2 1871bp public: 1..1752, PathoSeq: 1753..1871;

CDS: 501..1868 (SEQ ID NO 299)

GAGTTTTATGGGATTGGGTTTTTCAATTAAAGACTCTTCGTGATAATGCAATACCAAAACCAAAAT  
TTATTTAACGATGCAATAATTATTTCAATGTGAGCATCCATGAATCAGTGAGAATCTTTATTATG

GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACTTTATATCTTGGTGTTGGGATGGTGCCACA  
AATGGAGATTGTTGAGTGATACATGAAAAATACGTAGTTAAATTTTGTCTTGTCTTTATTTATTTA  
GCCACTTTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA  
AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAAATTACGGGGATTTAATTCG  
CGACTCACCCACGTCTCACACAGTATGTGCTTTTTTCATAAGTATGATTGAACCCTAAAATATC  
AACTTTTCATAATAAACATAAATCTTTCCAGACAACATAAATGGTTGGTTTATCACGAGTACTTAATG  
CTGGGTTTATTCTAAGTGGACAATCTGTTTTCCAGGATGTTGCTGCCCCACATCAAGCATCAATTG  
AACAAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAAATTCAGGGTATGGGA  
TTTCTACTGATATACCAGAAAAATGCACTATTGAACAAGTTCAAATGATTAGTAGACATGGTGAGC  
GATTTTCCTAGTAAAGGAGATGGGAAATACTTTAATTCAGTGATGGAAGTTTCAAGAGATATGGTG  
AATTTTCATGGAGATTTATCTTTTTTAAATGACTATGAGTATTTTCGTTACTAATCCGATTAATTATG  
AAAAGGAGACTACTCTTAAAACTCAAAGGTCCATATTTTGAACACTACAAATTTATTACGACATG  
GAGCTTATTTTAGAAAAAGATATCAATCACTATTTGACCAAAAAGGAGAAGCTTGTTGTGTTTACTA  
GTAATTCCTGGAAGGTGTTATCAAAGTGGTGTCTATTTGCTCGAGGATTTTATAGGAGATGATTACT  
CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAATGGGTGGTAATTCATTGACAC  
CAAGATACGCTTGTAATACTTTGAATCAAGATTTACACAAAAGATTTGGTGAATCAGTACGATAAGA  
CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC  
AGGCTCTGTCATTATTTCTTTGGTGTGCCTTTGAGATTAAACGTTAGGGGTATTCTCCATTCGCA  
ATCTATTTACAAAAGATGAATTTATCAGAAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA  
CTGGTCCAGGTAATAATATGACAAAGGTAATTTGGCTCACCTATGGTGGAAGCGTCGTTGAAAATGC  
TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGTATTTGACAT  
CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCGTTGATCGAGTACCATTTCCTCAATCCATATA  
ATGCAGCAGAATTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATGAAATGTGGTGAAAAGC  
AATATGTTAGATTTATTGTAATGATGCAGTTTATCCATATCCGATTGTAGTGGAGGTCTTGGGT  
TTACTTGTGAATTGAATGATTTTATCAAATTAGTTAAAAGTCGTTTACATGATGTTGACTATAAGC  
TTCAATGTGAAGTGGACGACCGACCGGAATTGACATTTTATTTGGGATTATAAAGACAGAAAGTATA  
ATGCGCCGTTAATAGATCAGTAA

YBR093C\_homolog\_2 456aa (SEQ ID NO 300)

MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ  
VQMISRHGERFPSKGDGKYFNSVMEVFKRYGEFHGDLNFLNDYEFVTNPDPYIEKETTPKNSKGPY  
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNSGRCYQSGVYFARGFLGDDYSEDVFEFVVDED  
KKMGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDNPLDLSDQVSSSLFLWCAFEI  
NVRGYSFPCNLFTKDEFIRSGYRNDVGNYYQTGPGNNMTKVIGSPMVEASLKMLQEDSKIWLTFTH  
DTDIEMYLTSGLIVPPGDLVPDRVPFPNPYNAAEFFPQGARTYTEKLKCGEKQYVRFIVNDAVYP  
YPDCSGGPGFTCELNDFIKLVKSRLHVDVYKLQCEVDGPAELTFYWDYKDRKYNAPLIDQ

YBR093C\_homolog\_3 1888bp PathoSeq: 1..1656, public: 1657..1888;  
CDS: 500..1885 (SEQ ID NO 301)

TGTAGTATAAATAAGGGTATGAAATACCAACATCCCAGAATATCAACGAGATAGAAGAGAGGAGTT  
TCAATATATATCTTGTGAATAATACTTCGTTCTAATTCATATACACAACCTAGACGTGTACACGC  
TCAATCTCAGGTAAAGAAAGTTTATATTCATCACTATATAACAACAATCAGGCTTTGCAAAAAA  
CATTTAAAACATAACTGTTAATATGGAAATATAACGCCTCGTAGTTCTACGCACGTGGCATCCTT  
TATCTATTTATTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG  
CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAT  
AAAATAAAGTAATATAAATAGGTATGCATTTTCCCTACATTTATTTTCTCTTTCTATTTTAATTTG  
TTTCTTAAACAGCAACAACAACAATTTGAAATTTCAAAAAATGGTTTCTGTTTCTAAATTTATTGAACAA  
TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA  
ACAATATAACATCGTCAATTTCTTGGCGGTGATGCCCTTATATTCAAAGAAACGGATATGGGAT  
TTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAAATTGTATTCAAGACATGGTGAAAG  
ATACCCAAGTAAAGTAATGGTAAAAGTTTGAAGCAATTTATGCTAAATTTGAAAACCTACAAAGG  
TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTATACTTATTTTGTACTGATAAAAACAATTA  
CGAAAAGGAACTAGCCCAAAAAATTTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTCA  
CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTCACATTACCAGTTTCTC  
TTCCAATTCAGGTAGATGTTACCAAACTTCAAGATATTTTGTAGAGGATTTTATAGGTGATGACTT  
TAAAGAAGGTA AAACTGTCAAGTTTAACATCATTTCTGAAGATGCTGATGTTGGTGCCAAATAGTTT

YBR093C\_homolog\_4 461aa (SEQ ID NO 304)

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MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ  
IQLYSRHGERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT  
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS  
EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE  
INVRGSSPFCDLFTNEEFIKNSYGNDSLKYSSNGAGNNYTRIIGSVILNSSLELLKDTENSNOVWL  
SFAHDTDLLEIFHSALGLLEPAEDLPTSYPFPNPYVHSSIVPOGARIYTEKLQCGNDAYVRYIIND  
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVFQKQCGVNSTYPSSELTIFYWDYKNVTYNAPLEL

YBR181C\_YPL090C\_homolog 1635bp public: 1..938, PathoSeq:  
939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632  
(SEQ ID NO 305)

ATATATATATATTTATGTATTTTTTTTATTGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA  
TAATCTATGAACAAATTAAGAAGCTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA  
TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTGTTGTGCGAATAGTTAGCGTAATAATC  
TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTTCTCTTCGCACATATTTTATTAGAGCTTAC  
AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTCGCACGC  
TGTGGAAGGAGAACTTACACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA  
AAAAATTATCAAATTTTCAACCTTGAGAGAAAAAAGTGGAAGAAAAAACTTCTTCTTACATTT  
AGTTAATTTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT  
ATCAGTGATTATAATTAGAGTCTTTATTTGGATATTGCAATAATTGGATAATAAGAAAGAGCATA  
AGAGTAGGAGTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTTTATCGTCGTGATTA  
TAACAAATACAAAGAAATTAAGCAATGAAGTGATATAAGCAAAATGAAGGACTAGTTTATTAGGGGT  
GACATTTTATAGACTACGTAAAAGTACTTTTCGATTCAAGGAAAACCAATTTTAGTATCTATCAACA  
AATAACAAATCAATTTAGTTAACTTCAATAATGACAATAATTTTAACTACTGAAAACAATAAACAT  
GCAAAACAAGCAAAACTAGTCAAGCTTTACGAATCAGTCAATACTAACAATACTTTTTTTTTTGTTC  
TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA  
AAATTACGTGTTTCTACGGAAGAAAGAAATGGGTCAAGAAGTTGAAGGTGACTCAGTTGGAGATGAA  
TTCAAAGGTTACATCTTCAAATCACTGGTGGTAACGATAAAACAAGGTGTCCCAATGAAACAAGGT  
GTTATGCACCCAACCAGAGTTAGATTATTATTATCTAAAGGTCACCTTGTGTTACAGACCAAGAAGA  
ACTGGTGAAAGAAAAAGAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTGTGCTAGTTTGGCT  
TTGTCTATTGTTAAACAAGGTGACAATGAAATGAAGGATTAAGTACACCACTGTTTCCAAAAAGA  
TTAGGTCCAAAGAGAGCTAACCACATTAGAAAATTTCTTTGGTTTAACTAAAGAAGATGATGTTAGA  
GATTCGTTGTTAGAAAGAGAAGTTACTAAAGGTGACAAAACCTTACACCAAGCTCCAAAGATTCAA  
AGATTAGTTACTCCACAAACTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAAGTCAAGAATGCT  
CAACAACAAAGAGATGCTGCTGCTGAATACGCTCAATTTGTTGGCTAAGAGATTGCATGAAAGAAAA  
GAAGAAAGAGCTGAAATTAAGAAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C\_YPL090C\_homolog 236aa (SEQ ID NO 306)  
MKLNISYPANGTQKSMIDDDTKLRVSTEKRMQVEGEDSVGDEFKGYIFKITGGNDKQGVPMKQG  
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCIQAQDLVLALSIVKQGDNEIEGLTDTTPVKR  
LGPKRANHIRKFFGLTKEDDVRDFVVRREVTKGDKTYTKAPKIQRLVTPQTLQRKRALKAKKVKNA  
QQORDAAAEYAQLLAKRLHERKEERAIEIKKKRAESLKN

YCL016C\_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;  
CDS 501..1517 (SEQ ID NO 307)

GTGACGAGAACTTCTGTCATCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAACAAT  
GATAACGGAGGAGGATTATCCCATACAAACAGAAATAGTTGTTGGTGTAGTTGTTGGGGTTGGTGGT  
TCTATATTAATTGGTTTGGTGGCCGTTTTATTTTACTTGAGAAAGAGAAACAACCGTGATTATGAA  
GGTGGATGGACTTTCTGGAGAAAGAAATGAGAAATGGGAAGTGATGAGTTCTTCAATGGTGAATTG  
GGTGTGACAGACAGAAATATTAATCAAGGATCAAATTTTAAACAAGGCTTATTTTGGATGAGGGT  
GGTTTTTTTTTATAAGTATTTTGTAGTTGAATTTAAAATTTTGTACCTTAAAGTCTTTTAAATTAAT  
TTTAATAAAAAGTGGTGATTGTCGAACTTCAAGAGTATATTTGGTGAAAAAATTTTG  
GAACTGAACGCGTCTAACATCTTATACCTCTAAGCAAAATGTCAGAGTACTCTGTGTATCAACAGT  
TGAATGAAGATACAAACGCAACTAAATATACTTATAAATTACTACAGCTACCATCAAGATACTAA  
ATCAACTTGAATCCAAGTCAACTAAGTATATAAATCTGATATCAATTTCCCTAGCATTAATGCA  
CTGATTTCAGAACTTTCAAGTTACGACAAATGAACCATTTCCAATACAGTCTTGCTATTGAACAAAG

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AACCTGACAACAAGTTAATTGGGTTTCAGAAAACCAGTTATGAATATGAGTTGACAGAAATCAAAG  
GTTTCGATCGATACGTCCGATATCCCTATTTTCAACGGACAAACAGCACAGCAACCTATTGATTGGA  
TAGCATTGGAAGATAAATTCGATTTGTTCACATCAAGAGTTTTTATCGAATTGGTATGAGTTGGGAG  
GTTGTGAAATTGATAATGGAGCATATATAATGAGTGCAGATATTATTACTGAACATTATATATCTAT  
TAATCACCAAATTGATGAGTTTACAAGTGCACGAGTTTTCTCCGGAAGATGTTTCATCCATCATCA  
CGCCCCCTTATAATGACTCAATGGTAACATCAATCATACACAAATTTTGCACATATAGAAAAGTGAGA  
AATATCAATTGAATGATTTAAAAAATTACACAGTGGTTTGGCATTGTTGAGATGTCAAAAATCAATC  
ATAAAATGACCGATATTTTCAGAGTCTTATTGAATTGGAAAACCTAGTTTGCCGTCATTCTATAACC  
CTCCATTGGACATCAGTCAATTGGCAGGCTATTACTGCTCCCAATCGAAAACAAAATATTGTATG  
TCGACCCAGAATCTTTATCAGAAAATTTGAGTCAACGATTCAAAGAATTGTTTGAATTGGATAAAA  
GTTGGAACATATGATGAGTTTATTCCATTCAATTAAGTTTGTTCCTGCCGGTAAAAAGGTCGACT  
CAATTATTTTAAAGTATGGCAAGAAGAAGAAAGTTGGTAGAGATAGATTTATAGTCTGTCTAGAT  
AA

YCL016C\_homolog 339aa (SEQ ID NO 308)

MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLRQMNH  
SNTVLLLNKEPDNKLIGFQKTSY EYELTEIKGSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE  
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLMSLQVHEFSPEDVSSIITPPYNDMSVTSII  
HKFCTIESEKYQLNDLKITQWFGIVEMSKINHMTDISEFLLNWKTSLSFYNPPLDISQLAGYYC  
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG  
RDRFIVCPR

YCR073WA\_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

GGTGGGGTTCCCATTTTAATTTAAAAAAATTTTACCATCCAAAGGATTTTATTTACCCAAAGAC  
CAAAAAATTATTATTTGAAATGGGGATTAAATGGGGATAATTTTATTTTGCCTGATGAAAAGATT  
AGTACCCGTTTGAAAGTCTTGATTCAAATTATGGTCAAGCTAAAAGAGAAATATTTGATTTAATTA  
CTGGTGATAAAAAACCAAGAATTTTCCATGTTGATGAATCATTAATTGATGATCTCAAGAAGCTG  
CTGATGAATATGAAAAACAATTGATTAATAATTTTGCTAAAAAAGATTCCGGTGAAATTACCTTTAT  
TTGATTTATTTTATTAGGTTGTGCACCGGATGGTCATATTGCTTCATTATTTCCTAATCATGGTG  
AACAATTGAGAGAAAAATTAGCTTGGGTTTTTACCAGTATCAAAATGCTCCTCTGGGACCAGAAAAA  
GAATAACTTTATCTATCCCAGTTATATGTCATTCCGCAAGAGTGACATTTGTTGTTGAAGGGTTAA  
CTAAGGCACCAATTATTAAAACCATTATGGAAAGACCAGAAAAAGGTTTACCAAGTTCAATTGTTA  
ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTTTGTTGATGATGATGCATTGAATGATTTGTTTGATA  
TAATAAAAAGAAATACAAATATTTATCTATACCTGAACCAAGTCATTAA

YCR073WA\_homolog 131aa (SEQ ID NO 310)

VKLPLFDLFLGCPDGHIASLFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICH SARVTF  
VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALNDLFDITKKKYKLSIPEPSH

YDL010W\_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TGTTACAAAACATTCTGTTGGAGAGATAATTGAATTCAAATTAACGTGTTGAAATCCAACATTGAA  
CAATGAATACACGTCCAAGAAAAATTTGACATGATTAGAATCGCGGTCAATTACATTCCCGGAACG  
TCTTGGACTACTTGGATACAACAATGGAAAATGAGGAAAATGAGGAAAATGAGGAAAACGAGGAAA  
ACGAGGAAAATATTTACCGAAGAGTAATTATATTACAAGCATTGAAAGAGGAGAAGTGAACGCCCC  
AAACAGAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAAATTTTTTGGTCAGAA  
CACAACTTTGGAAGAAAGAAAAAACCGGAAAAAGAAATTCATCTAAAACACATACACAATATAT  
ATATATATATATAAATATATATCCATATACATATGCTTTAATTTAACCTTCCCGCCTTTCTTCTC  
TTTTTGAATTATATCGATTTTAAAAACTACACTTCATCATGGCTGGAGTTAGACAAATTAAGAATAA  
TAGCATTAACGGCCTTTGTCTTGGTTTAAATTTTACTTTACATAAAGTTGGATCCAACGCTGCAT  
CCTTGGTTCATGCACAAGCATCAGACCAACAACCAACAACATAACACCAAAAAGTACTACATATA  
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTGATTCTAAAAATGATCCTCAAACCTGATGACA  
AAATAAATCAAAAAATATCACAAAGATCAAGATGAAGCCATCAATGGTAATAAAGACACTAATAAAG  
ACACCACCAAAAGTCAAACCAGATAATGGTGAATATGATCCAATATCTGATTTGATAAAAAATTAGAT  
CATTATCACCAATGACAAATTTTCAGTAAATCATATTGTCCATATTCAAAAAAGATTAAACAATTGT

TATTAGAAAAATATGATATAACACCAGCACCAAATGTTGTTGAATTAGATCGATATGAATATGGAG  
CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAGAACTGTGCCAAACGTATTGGTTGGTA  
AATCATTTGAAAGTAGGGGTGGTTGTTGATGAATTTGAAAAACTTCATAAAGATAATGATTTGATTA  
AATTGTTAGTTGAATGGGGGTCTGGTCGTTTACAAGTTGCAAAGAAGAATACCCCATCAAATGCCT  
AA

YDL010W\_homolog 229aa (SEQ ID NO 312)

MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQQPNKHNTKSTTYTATNDESVANLID  
SKNDPQTDDKINQKISQDQDEAINGNKDTNKDTTKVKPDNGEYDPIISDLIKIRSLSPMTIFSKEYC  
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTVPNVLVGKSFESESRGGCDEFE  
KLHKDNDLIKLLVEWGSRLQVAKNTPSNA

YDL083C\_YMR143W\_homolog 1256bp PathoSeq: 1..1256; exon 1:

501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313).

AGTGGTTGTTCAATAATGGTAAGTCTTTGGAAATAGCCATTGTTGCTTTCTGGTGGTTAGACTTGT  
AGGAAGTAGAACTGTTTCCAATGAAAAGTAGTTTTAATTAGAAAAATTTTCAAAGTGCGTGAAGC  
CCAGTCTGAATGTGCGAGGAAGCCCAGTCAGTTAGTAGTGTCTTCCCTCCACTGTCTGTAATACA  
AAATTTCCCTTTAGTGAAAATGCGAAATATATCTGTACTGGGAACCCCCCGGAAAAAAGAACTTA  
TGCTCAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAACTT  
TAAGTATGGTGCGAAGAGCGTTTCCAATTTTTTTTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC  
TGTTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTTCAGAACAGGAAAATTTTGAAT  
CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA  
AACGAATTGAAATAAAGAGATAGAGAGATGTTTATTTATCAAAATACGAAAGGAAAGGCAATTAA  
AAAGGAAATCAAAAAGTCCCAACCTTGCAGTAGAAGAATTGAGGTATATGAATTTGATAGATAGCC  
AGAACGGTGTTTACATAAATGGGATATAGAACAAAACCTATACGAGGAGTTTGTTTCAACGATCATTC  
AATAACCAGAAAACGATAATATTTTAGCGACCATTAATGACACTTGAAGGCTCACTGGGCCAATA  
GAATATCTCCATATACACTTTTGAAGTATTTACTAACAATTTACTTTTGTCTTAGACTTTTGGTA  
AAAAGAAGACTGCCACTGCCGTTGCTCATGTTAAAGCCGGTAAAGGTTTAAATTAATAACGGTT  
CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTTACGAACCATGACTTTGGTTG  
GTTTAGATAAAATTCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG  
TCTACGCCATCAGACAAGCTATTGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG  
CTTCTAAGAACGAATTAAAGAAAATTTTCGCTTCTTACGATAAGACCTTGTAGTTGCCGACTCAA  
GAAGAATGGAACCAAGAAATTCGGTGGTCTGTTGCCAGAGCAAGATTCCAAAATCTTACCGTT  
AA

YDL083C\_YMR143W\_homolog 142aa (SEQ ID NO 314)

MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVEPLTLVGLDKFQGIDIRV  
KVTGGGHVSQVYAIRQAIKGLVAYHQYVDEASKNELKKIFASYDKTLLVADSRMEPKKFGGRG  
ARARFQKSYR

YDL125C\_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGGTAAGATATAGAAAGCTTACCACCTTTGACAAGTTTGAAATAGGATGGGTGAAAATTTGGACAT  
CTTGAATACTTAAAATTCTGAAGTTGATCACCAGATCCTTTCTTTTACATAATTAGATATGATGG  
ATAGGTTAGAATCGTCTTTAAAGAGAAGGTATAATATCTAACTGATTTGGCGAGGTGTTGGAAAAG  
TCACTCCACTGTATATATTCTCGGAGTTTAAACGTACTACAGTTCAAGTGGGGTGAATACCTAAATAG  
GGGGGTAGAATACGAACTCCTACAAATTTTAAAGGAGACTATGACCCGAAAAGAGAAGAAAATTTA  
TTACTCTAAGAAGTTTATATACCTCCACAAGTCACTTTTCTTTAGTTTCATTCTGCTTTTTTTTT  
CTTACACATCTTAAAGGTCAAACAATTTAACTTATTAAGTCTGTGAAAATCTCACTTCAAGTT  
CTCTTTCAATTGACATTATAGTATTTCCCAATTCAATTATGGCTTCTCATGCTTCTGTATATTTCT  
GTAAAATTATCAAAGGTGAAATTCCTTCTTTCAAGTTAATTGAAAGTCAAGACTTATTCCTTCT  
TGGACATTCAACCAATTGCTGAAGCCACGTTTAAATATCCCTAAACACCATGGGGCAAAGTTGC  
ACAACATTCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA  
AATTGGACGAAAATAATACTCCAGAAGGTGAAGGTTATAACGTTTACAGAACACGGAAGAATTG  
CTCATCAAGTTGTTGATCACGTTCACTTCCATTTGATTCCCTAAAAGGATGAGGCTACAGGTTTAG



GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGTATAAATTAGGAAAATTGCATGAGAAATTAAAGG  
AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C\_homolog 152aa (SEQ ID NO 316)  
MASHASCIFCKIIKGEIPSFKLIETAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNIIPDDYLSLILP  
VVKKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKKDEATGLGVGWPAEATDFDK  
LGKLHEKLKEELAKVDNEKL

YDL133CA\_YDL184C\_homolog 297bp PathoSeq: 1..297; CDS: 220..294  
(SEQ ID NO 317)  
CATAATTATTACATATAAACTCGCACTATAATTTTTTTTTTTTCTATTCTGTGTGTGTGTGTGTGT  
GAGAGCCAGAGAAACCAAAGTACTGAGTGATCGTCTCTCAACAATTTATTTCTCCTCGTCTTATT  
TTTTTCTTTCTTTCTTTTCTCTTCTTCTTCTTCTTCTTTTCTTCTTCTTTTCTTCTTTTCTTCTTTA  
CCAAAACACTAGTATTTCAACATGAGAGATAAGTGGAGAAAAAAGAGAGTTAGAAGATTAAAGAGA  
AAGAGACGGAAGGTTAGAGCTAGATCCAAGTAA

YDL133CA\_YDL184C\_homolog 25aa (SEQ ID NO 318)  
MRDKWRKKRVRLKRRKRRKVRARSK

YDL136W\_YDL191W\_homolog 1303bp PathoSeq: 1..1303; exon 1:  
501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)  
TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAACTTATATTTGAAAGTAAATTTCTA  
TATTTTCTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCTATTGTTGTGTGGAA  
TAAATTTAAAATCCTTCTTATTGGTGTCTAGACTTTTGCTTTTGTGGTGATTAGGGCTTTAGCCCT  
ATCACGTGAAATACTGTATATAAAAAATTCTTTATAGCGCGATAAAACATATTTTTTTTCCGTATT  
AACAAATATGTGTGAAGTTTTGTCTGGTGTCTTCTCACTGTTTTTCTTTTCTGGTAGTAT  
CAATTAACGCTTAGATCCAATACAGTTTTTGGTAACTTGTACACGAACAAAATCTCAAATTTGTTAC  
TGTGTGAACCAACAAGGAAGAGAAAAAAAACCCATACAAAAATTTTTTCAGTATCAAGGAATTAGA  
AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTTAAATATCGATATTATCCA  
TAGATGTACATGTATCCTAATGGGTTTCATTTATTTGGAAGTTATGTTTATGGGAGTTCTATTAT  
TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC  
CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA  
ATGAAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTGTTGGGTTTAGATTACTA  
TATTTTACAAGAAACATATTATATGAAATGATACCCAATCCACAGCGACTTTTCAGATAGCCAAAT  
AACTAAGCAACTCAAGATAACATAGGATCATGCATCAATCAACAATGAAACATTAATACTAATACTAA  
CTTTTTTTTATTATTAGGCCGGTGTGTTAAACTTTGCAATTAAGAATAAATCTAAGGAACAATT  
AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTTAAAAGTTCAAAAATACAAAGACC  
AAGTTTACCAAGAATTCACACTGTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAAGTTGAA  
TCAAAGAGAAAATGTTTCGTGCCTTTTACGCTGGTAAAAAATACATTCCAAAAGATTAAAGAGCTAA  
AAAGACTAGAGCTTTAAGAAGAAAAATTGACTAAATTTGAAGCTTCTCAAGAAACTGAAAAAGCTAG  
AAAACAAAGAATTGCTTTTCCACAAAGAAAAATTGCTATTAAAGCTTAA

YDL136W\_YDL191W\_homolog 120aa (SEQ ID NO 320)  
MAGVKTFELRTKSKEQLESQLEVELKQELATLKVQKLQRPSPRIHTVRKNIARVLTVINLNQRENV  
RAFYAGKKYIPKDLRAKKTRALRRKLTKFEASQETEKARKQRIAFPQRKFAIKA

YDL167C\_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:  
501..2687 (SEQ ID NO 321)  
CTCTGTGTAAATTGATGAAATCCACACAATAAAAAATTTTCTTTCTTCTTTTAAAGAACCTAAAAACA  
GAATCAACATTATTTGCCCCATACATATCCAAGAATTAAATACTTATTAGTTCTAAGTGGAATAGA  
AGAGAATCAAACTTAACATTACTGTTACGCAACGTCAAGAGGGCATTTTTTTTTAGTTTTAATTTGT  
TTCATTTCAATTGAATCTTTAAGAATCACCGAGTATACATACTTTCTTTTGTATTTTATCAGGGAA  
GCCACATCCAACCACCAGTTACATCCCACAAAATCCCTTAATCTTGTTCCTTAGTTGTATTATTAAT  
CTATTGAATTTAAGTTTGATATGCGAGAGAATATTGTGGATTGTATAAGTTTGAAGTTGACTGGACTTGA  
ATACTTTGAGGGCTTAATCATATATTTATACCTTATACCCCTACTCGCGGTGTTGCTTACCACACTG  
ACTAGTATGATCTTTCTGAGATTTCTAGCCAATAAATTTATGAGTGATATTTATATTATTATTCATA

110/161

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCACTAAGGATTCTTCCGAGTTAATTGAATTTG  
CTTGGGAAACAGTCGATAGTGTCACTTTTGGAACTTTTATACAAAGGATCAAACCTTGGTTCGTCCAA  
CCAACACACCTATCACACCTTACTGCTCGAAGATTCATAGAATAACATGGGACAATGTCAAAAATG  
CTGGGTTCGTTCAAAGACGCCATCACAACTTTGATCAATACGTACAAGAACACATAATTTCCAAGA  
AAAAGGAGTTTTCAATTTGTGATGTTTGACATTTCCAAATTTGAGAGTTTCAGTTGGTTCGTGAAGCTA  
GAGACAAATCCGTGGTTTTTACCCCTCGTATCTACAACATCCAAGGATTTTGTATTTACCAAGAGAAT  
ATTTAAATTTGGCAATCTAGCCACCTGAAACATTATCATACCCCCCACTTCTTTAACTAATATTA  
TTACTGCATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTCGACTTGCCAACTTTTCTTCCA  
CACCATCACCATCAAAGCTTCAGCAACAACGACGACGACAACCTGCAAATGTCACAGCCATTGACG  
TCCTTTCCAGTGAAACAGAACCAATGGTAAAGTCATTGCAAATTTGCACGCCAAAATTGCCAAAC  
AATTGATCAAAAAATCCATCCCTGTTGAGAATCACCCTAATGTATTTACAAGACCTTTTGATTTCGG  
CTCAAGATATCACTGCTTTTACATCAGAAAGATCAAAGTACTCTATCTTTTCCAACCTTGCCAAACG  
ACACCACACAATCAGAGTTGGAATCATGGTTCACTCAGTATGGTGGGAAGACCAGGTGGGTTTTGGA  
CTTTTAAGTCTGCAGATGATAACAATAATAACAACAACAATAGCAATGGCGGGAAAGGATATC  
AGAATGCGAGAAAATATGGTATTTTCAGGGTTTGTGGCCTTTAACTACTCATGAGGAAGCAGTTGATT  
GTTTAGCTTTGAATGGGAGAGTGTGAATGATCGTCCTATTGAAGTTCAAGCGTCTTCTAGTAAAG  
TGTTTTGATATGGCCATGGATAAATTTGTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC  
CCGGGGATTGGACTTGTATCTTGTGGGTTTCCAATTTCCAGAGAAGAACACACTGTTTCAGGT  
GCTCTTTTGGCGCAGTGGCGTTTTCAGGATGTTTTTAACAGTAATACAGGCAATGCCAACGGTAATG  
GCAATGTTAGCGGCAACCACAACCACAACCAATAGTGGAGCTCGCCGTGGCATGAATTTACAGC  
CTGCTCAAGCTAATGAGAAAATTGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCAATCA  
AGGGTCCAACAGGTAATGTCACCTAATCACCTCAACAATTCTGAGACCAATTTACTGAACAACACTA  
ATCTTAACAACAACAATCATCATAGTAATAATATCACATAAATACTACCATCACCACAACAACAATA  
ATAACAATCATGGGAATAGCAATGGTAACACCATACTATCGTTCGTTCCATTATAACAATAGTGTTC  
CATTTAGAGCAGGTGACTGGAAATGTGAAAATTGCATGTATCACAATTTTCGCCAAAATTTGTGTT  
GTTTTAAATGTGGTGTGCGCCAAACCTGCTATTTAAACAATCAACAAAATAATACAATTCATTCGGTGA  
ATTCAACGGCCGCTGCCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTAACTTGAATAATAATG  
CATTTTTGAACCTTCAGCAACAACAGTCTCAGTCACAACCCCAAGGTCAGCACCATTACAACCAAC  
ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCCAAGAATCAGT  
ATTACAATAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC  
AAAATCAAATTTTGATGTATTACAACAATTTGCAACAACAACAGCAACAACAACAGCAACAACAGC  
AACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACATGATTTAA  
ATGGAAGTAGCTCTTCCCATCAACTGAACTTCAATTGAATAATACTTGA

YDL167C\_homolog 729aa (SEQ ID NO 322)

MSDIYIIIIHISTTCDDSPFTVKDSSELIEFAWETVDSVTLETLYKGSNLVLRPTNTPTIPYCSKIH  
RITWDNVKNAGSFKDAITNFDQYVQEHIIISKKKEFSIVMFDISKLRVQLVREARDKSVVLPSYLQH  
PRIFDLPREYLNWQSSHPETLSYPPTSLTNIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT  
TTANVTAIDVLSSETEPNGKVIANLHAKIAKQLIKKSIPVENHPNVFTRPFDQAQDITAFTSERSK  
VLYLSNLPNDTTQSELESWFTQYGGRPGGFWTFKSADDNNNNNNNNNSNGGKGYQNARKYGISGFVA  
FNTHHEAVDCLALNGRVLNDRPIEVQASSSKVFDMAAMDKLLLSFPLSKNRPRPGDWTCLSCGFSN  
FQRRTHCFRCSFAAVAFQDVFNSTGNANGNGNVSGNHNHNHNSGARRGMNLQPAQANEKIGTGNI  
SIPSYNDPIKGPTGNVTNHLNNSSETNLSNNTNLNNNNHNSNNYHNNYHHNNNNNNHNSNGNTIH  
GRSHYNNVFPFRAGDWKCENCMYHNFAKNLCLCKCGVAKPAINNQQNNTIHSVNSTAAAIAAATAS  
GQPLNLNNAFLNLQQQQSQSQPQGQHHYNQHSRNNNASGASKFNNGYNPKNQYYNNNSKNLSNNF  
GLNGMHQQNQNQILMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDNLGSSSSHQSKLQL  
NNT

YDR238C\_homolog 3359bp public: 1..1467/1469..3040/3042..3359,  
PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

AATAGCATTGAACAAGAAGAAGAGGACAACGATAGACCAAGGTTGGTTTTAGCCAATCCTGATTAT  
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AGGACTTGTTTTTTTTTAGTAAGTAGTGATCTCTTTTCTGGGTGTACATTTCCGATAGCCAACCA  
GGTTATATTTTAGCAGTTTATAGACAGTGTATTCGATGGGTAATATAAATAAAAGCTCATTTGAATA  
CTATCTAGTGAAAAGTCGTGTGTAAATCGATTGTGAAAAATATAAAACCATAACGTAAGTAAATG  
TGTGTGAAAGTACAACCAACAACGAAAAAGAACAAAAAAAATGTTGTCCGCCAAAAAAAAG

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTTGTCACCATAACTATCAATTGTTCA  
CCTCTTGAACCAACATCAAATTGAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT  
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG  
ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAATGGAGACCCCTTACCTG  
ACTTGTTGATGCATATAATCAGATTTGTCATGCCTTCCAGAAAATAAGAATTGAAAAAGTTGTTGT  
ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAAATGAGACATGAAATGATTCTTG  
TGTGTAATGCCATCCAACGTGATTTACAGCATCCAAATGAATATATTTCGAGGCAATACTTTGAGAT  
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ATCATTTAGCTCCTGATGCTGACGAGTTAATTTACAGATTTTGTATGAGGAAAACGATTCTGTTT  
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ATAATATTTTCAGTTATTGAGACTTTGGATCCATTGATACAAATTGGCTTTTATTGAGTTTATCAAAA  
AGGACTCTATTTCAAAATCCAGCTTTAAAGCAACAATATGCCCAATTAATGACAGAAATTATTGAAA  
GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT  
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TTATCACTTTAGAGAGAATAAATCAATTACACAAGCAACATCCTGGTGTGTTACAAGACTTGTCAT  
TAGAAATTTTACGAGGTTTATCTTCCCAAGATTTGGATGTTAAAAAGAAAGCTCTTGATGTTACTT  
TACAATTTATCACCACCAGAAATGTTGAAGATGTTGTTAAGTTATTGAAGAAAGAATTGCAGTCTA  
CAGCTTTTATCCAATGATGACAAGAATGCAGATTATAGACAGTTGTTAATTAATGCCATCCATCAAT  
TGGCTATTAAATTTGTGGAGGTTGCTGCCAATGTCATTGATTTATTGTTGGATTCTATAGCCGATT  
TGAATACCACTGCCGCCTACGAGGTTATCACATTTGTTAAAGAAGTTGTTGAGAAATTCCCAGATT  
TAAGGGACGCTATTTTGAAGAAGATTGATTTTGGCTTTTGCACATGTGAAAAGTGGTAAAGTTTTC  
GTGGTGCAATTATGGGTTATTTGGTGAGTATGCCTTAGAGGAATCATTAATACAAGAATCTTGAAAT  
ATATTAGAGGAAGTATTGGTGAAGTACCAATTATTGCTAGTGAATTGAAACTGAAAAGCGTGATG  
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TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTGACAAGCGAAACAACGACTCTTTGAAA  
GTGACAGCAAGACTCCTATCAGAAAGCAAATTCCTGCTGGTGATTTCTACTTAGGTGCTGTATTAG  
CATCAACTTTTGGTGAAATTGATTCTCCGATTGCAAAGTTTGAAACAACTCAAGAAAAAATTTTGA  
ACGGATTAAAAGCAGAAGCATTGTTGATTATGGTTTCGATTTTAAGAGTTGGGGAATCTAGCTTGG  
TTTCTAAGAAAATTGATGAGGATTCTGCTGACAGAATTTTGTCTTACATCAAGATTTTGAACGATG  
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TTAATAATGCTGAATTGAAGAAAGCAGAAGCATTGGCTAAGGATTGTCATGATAACGCTGAACAAA  
TTGACGATGCAATTGTTTTTACAGAGTTGGATAAAGATAACAAAAGAGTAAAGCTTCTGTGGATG  
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TTGCTACATTTGGGTGATTTGAAAGTGGTTGATAAACCACAACTACCGCAAAATATTGGACCTCATGGT  
TCTACAAAGTTTCAAACAACATAAAGTTACTTCCGCTGATACTGGTGTGTCATCTTGGTAACATAG  
TGTATGACGGTCAACACTCGGACGATTACGTATAGTTATTTTGAATGACGTTACGTTGACATTA  
TGGATTACATTAAGCCAGCCACTTGTTCAGAAAGTCAATTCCGTAAAATGTGGAACGAATTTGAAT  
GGGAGAATAAGATAACCATTAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA  
AGGGTACAAATATGCAATGCTTGACACCGGGTGCGTAATTGGAGAAGAATGTCATTTTATCAG  
CAAACCTTGTACTCAAGGTCAAGCTTTGGTGGAAGATGCATTGGCTAATTTATGTATAGAGAAACAGA  
GTGATGGACCAATAATTGGTCATGTCAGAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTCAATTGG  
GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTAA

YDR238C\_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSVNEFKNLLEKKGDDVKVDTMKKILITILNGDPLPDLMLHIIRFVMP  
RNKELKLLYHYWEVCPKMDESGKMRHEMILVNCNAIQRDLOHPNEYIRGNLRLYTKLKEPELLET  
LVPNVRQCLEHRRHAYVRKNAVFALWSIHKVLSDHLAPDADELIYRFLYEENDSVCKRNAFVCLGDLN  
REAAALQYIQDNISVIETLDPLIQLAFIEFIKKDSIQNPALKQOYAQLMTEIIESSSNVVMYEAANT  
LTVLTSNPQSILLAGNKFVELATRESNNVKIITLERINQLHKQHPGVLQDLSLEILRGLSSQDLD  
VKKKALDVTLQFITTRNVEDVVKLLKKELQSTALSNDKNADYRQLLINAIHQLAIKFVEVAANVI  
DLLLDSIADLNTTAAVEVITFVKEVVEKFPDLRDAILRRLILALPHVKSQKVFGRGALWVIGEYALE  
ESLIQESWKYIRGSIGEVPIIASSELKSKRRDDTEESQEEETEYDGKPRRKGPVLPDGTYATESAL  
TSETTDSLESDSKTPIRKQILAGDFYLGAVLASTLVKLIILRLQSLKQTQEKILNGLKAEALLIMVS

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAELALA  
KDLHDNAEQIDDAIVFRQLDKDNKSKASVDDVAAASGSNELKKENLSSRLNKIIQLTGFSDPIYA  
EAFVKVHQYDVVLDVLLVNQTTTTLRLNLSVEFATLGLDKVVDKPTTANIGPHGFYKVQTTIKVTS  
DTGVIFGNIVYDQGHSDDSRIVILNDVHVDIMDYIKPATCSSESQFRKMWNFEFEWENKIKSPIET  
LKEYLDELKMGKTNMQCLTPGAVIGEECQFLSANLYSRSSFGEDALANLCIEKQSDGPIIGHVIRRS  
KGQGLALSGLDRVASISRKGKKATIARV

YDR294C\_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;  
CDS: 501..2267 (SEQ ID NO 325)

GTTTGTATCACATGTGTTGTGAACACTCGGGTAATACAAAATAGTGAGAGAGAAGAAGGGGAAAAAA  
AAAAGCAGAACACAAAACATGGAATTTGAAAACAATTTTGTAATTCATCGATCCGAGACTTCCAT  
AGCAAAGTTAACAAGCACAAATTGTCAATTTTAACTTAATTGGTGGATTAATCGGGATCAATCTGAAT  
TGTTTTCCCGTATTGTTTAAAACCAAAGAAAAAGGATAATCAAACTAAATCTTTCATATTAACT  
ACCATTTTGTAGTGGTCAGTTTATATAATTATCCACTGTTCTCTTCACAATTAACAAAAA  
AAAGAAAAAAGAAAGCTCTCTCTCCCCCAAAGAAAAAGCAAAGGTAATTCCTTCATACACACCTT  
TGATATCTTTCCTCTTAGACTTTTCTTTTAATACTTGCATCAATTGGAATATTACTTGTTCATACT  
GGAGTTTTCATTGAACTAAATATTATTAATATATTATATGCTTGAATTGAATTCATTAACGATTC  
CTCGGAATTTCACTGAATTTCAACTCACAGCATTAAAGATCTACTATCAACTTAAGATTTTATTTTC  
TTGCCACATACTGTGCTCAAGGATCAATTTGGCTTGAACGGTTCAGTCTGTGTTAGCAAGAGATATTT  
TTGTTGGCTATGTTGTATACACTCAATTTATTAAGCTTTATCGAGTATTAAGAGGGTACGGTATTG  
TAGATTCTATTTCGAAGGTTATACCTATATGTTAGTCTACGGTGTCACTCTCAATCTTTTCACTAC  
CATTTATTAATCCAAAATTGACAAGGAATTGCAAGCGACTATTGGCAAAGTAGAAGAAGAGATTA  
TGAAAAACGATCCACAGTTATTACAGTTTCCCGAATTGCCAGAACAGGGTATTGACGCTGACAATG  
TTTCCTTGGAGTTGGATAAATTACAAAACCTGAAACATTTCTGACTGGATCAATGGAAGAGTCAGTG  
GAGCAGTTTATCATGGAGGTGAGAATCTATTGTCATTACAAGTTGAAGCTTACAAGAAATACGCTCGG  
TGGCCAATCAATTGCATCCCGATGTTTCCAGGTGTGCGTAAGATGGAGGCCGAAGTAGTTTCATA  
TGTTTGGATATCTTTAATGCTCCGAGTGACGGGTGTGGATCGACAACCTTCGGGAGGTACTGAGT  
CGTTATTGTTAGCCGGGTGTGTCAGCTAGAGAATATGGGAAGAAATATCGTGGAATAACTGAGCCTG  
AAGTCATTGCCCCCGTGACAATACATGCGGGAATTGAAAAAGCCTGTTTTTATTTTGAATGAAAT  
TACATAAAGTTGACTTAGATCCGGTTACCTTTCAAGTTGACGTTAAGAAAGTAGAAGATTGATCA  
ATAGTAATACAGTTTAACTCTGTGGATCAGCCCCAAATTATCCTCATGGAATAATTGATGATATAG  
AGTCCTTATCCAAGTTGGCAGTCAAGTATAATATCCCGTTGCACGTTGATGCATGTTTGGGGTCAT  
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GATTACCAGGTGTCACGTCAATCTCATGTGATACTCACAATATGGGTTTGTCTCCAAGGGGTTCAT  
CAATAATTATGTACCGTTCCGCAAAATTACGTGAGTGTCAATACTATATTGCAAGTGATTGGACGG  
GTGGAATGTATGGTTCTCCAACCTTTGGCTGGTTCTAGGCCAGGTGCTCTTGTAGTTGGATGCTGGG  
CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTGTGTACGATATTGTGCTGGCGTCAA  
TGAAAGTTAAACGAGCAATTGAAACTGACCCGATACATCCAAACATTTACAAATTATTTGGTGATC  
CAATTGGGTTCGTTAATTTTCGTTTCAACTTGCACTCAGCAATCGGGAATTTAAGTATTTACGAGA  
TTAGTGATTTGTTGACCAAAAAAGGTTGGCATTTTGCAACTTTACAAAACCCATCAGCATTACATT  
TTGCATTTACAAGATTGACTGTCCCGGTGGTCGATGAATTGATTGCAGATTTGGTTGAAGCTACAA  
AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAAGAATGGAGTGACCAAGCTCCAGGTGATACTG  
CTGCGTTATATGGTATAGCTGGCAGGTACATACAGCAGGGTTGGCTGATAGATTAATTGTTGCAT  
TTTTAGATACCTTATACAAAATTTGA

YDR294C\_homolog 589aa (SEQ ID NO 326)

MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGYVVYTQLLKL  
YRVLRGYGIIVDSIRRLYLVSSTVSSQIFSLPFIKSKIDKELQATIGKVEEIEIMKNDPQLLQFPEL  
PEQGIDADNVSLDKLQNLKHSWDWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVPV  
RKMEAEEVHMLDIFNAPSDGCGSTTSGGTESLLLAGLSAREYGKKYRGITEPEVIANPVTIHAGIE  
KACFYFGMKLHKVDLPVTFQVDVKKVERLANSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP  
LHVDACLGSFIVSFLEKSKVHGDRKLPIFDRLPGVTSISCDTHKYGFAPKGSSIIMYRSPKLREC  
QYYIASDWTGMYGSPTLAGSRPGALVVGWATLINIGKQGYTKFCYDIVSASMVKRAIETDPIL  
SKHLQIIGDPIGSVISFQLAPQQSGNLSIYEISDLLTKKGWHFATLQNPALHFAFTRLTPVPVDE  
LIADLVEATKEAVAIAEEHKKNGVTKAPGDTAALYGIAGSVHTAGLADRLIVAFDLTLYKI

YDR430C\_homolog 3605bp PathoSeq: 1..330/1927, public:  
331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327)

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AATTTATAAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATCTACAATGAAATGA  
TTCACATGAAATATGTTACAATTCCACACTTGCTGCTAAAAAGCAACAGTTTGTGCAATAGAGAAAA  
GCATGATATACTATCGATAAATATCTTTCGATAAGAACTTAAATGTAGCAACGTTGAATTTTAAAAAT  
AAAACCTCCCTTTTCTGCTGATATAATTTTGACTTTGAAGCATAAAGAAGACAGAGCTAAAAAAA  
CTACTCTCTAGACAAAATCAAAACCTCGAATATATTTTTTGGTGTTCTTTTTTTTTTTTTTGCCT  
CTCGTTGAAATCATCTCCATTCTTCTTTTCCACGTCTTTGTTGAAAACCTTTGCAACCTAAAAAAT  
AAGAATCACTCCAACAAGTTTAAACTACATTATCAATTATGTTGAAAACCTAGATTAAACCAAAGCA  
GGGCCATAAGTCGGGTGTGAAGAAGATATGCATGCTCACACCCCATTTCTCCCAATCTTGATAAGT  
ACCCAGTTGGTCTAAAAATTGCATGGTTACGAAGTTACCCAAACATCACCTATCCAGAATTTTCCC  
TCACTGCTGTATCATTAATAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCCTAATG  
ACAGTAATAATGTATTTCTGATTGCCTTCAAAACAAATCCTCCAGATAATACTGGGGTTCCCCATA  
TTTTAGAACATACAACTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTATAAATGA  
CCAACAGTTCGTTGAGTAACTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG  
CTACCACCAATTCAAAGGATTTTGAAAACCTAATGGATGTGTATTTATCGTCAGTGTTTGAACCGC  
AATTAAACCATACCGATTTCTTGCAAGAAGGATGGAGAATAGAAAATCAAAATGTTTCATGACATAT  
CGTCCAAGCTTGAATTCAGGGAGTTGTATATAATGAAATGAAGGGCCAGTATTCGAACCTGTCAT  
ACTACTTTTATATCAAGTTCCTTGAGAGTATATATCCATCCTTGAATAATTCAGGGGGTGATCCCA  
AGAAAATTGTTGATTTGCTGTACGAGGGTTTACTAGAGTTTCACCTGAAAAATTATCATCCATCAA  
ATGCAAAAACATTTACTTATGGAATAATACCATTGGAAGACAGTTTAAGTAAAAATAAGCAAATACT  
ATGAATCATTCGAAAAAAGGTGTCTTCAGTTGACGTCAAACAACCTATATTTTACAGATAAAT  
CAGAAATCTTTGATGTCACCATCCCGGGTCCAGTTGATACAATGAATGGTAAAGAGATTCAGAAC  
AGTATGCACATCTATCACCTGGAACCTGGGTAAATGCCATTTGGATCCAAACATGCAGTATGATATTT  
TTAAATGGAAAATATTGAGCTCATTATTGTTTGATGGACACAACCTCTCCTTTCTATCAAGAGTTAA  
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CGTTTACTGTTGGTCTCAACTACTTAACCAAGCAAAAAGTTGATAATTTTAATGAAAAAGTTATGG  
AAATCATTAATAATAAAATCATTCCCGAATTAAGTAACGAAGAGTCCTCTCATATCATGGTAGAA  
TTGATGCTATATTGCATCAAATAGAAATAGGATTCAAAAGACACAAGCCCCGATTTTGGATTGGGAT  
TATTGAGCTCTATTGTTCGTCATGGGTGAATGGAGTTGATCCAATTGACACCTTGCAAGTGGAAA  
AGATATTGTTCGATTTTAAAGAAGATTATAAACAAAATGGTTTAAAGGATCTTTAAAGAATTATTAG  
AAAAGACATTTGTGTAACCCTCATTCGCAAAAATTTAAATTCACCATGGAGCCAAGAGAAGATTTTA  
CCAAACAATTGGTAAAAGATGAGAAATTTGATGATCGAGAAAAGAGTAAGTGAACCTCACAGAAGATA  
ACAAGAAGGCAATCTATGAGCAAAAACCTTGAATTAGCTAAATTACAATTGGAGGATCAAAATACAG  
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GCCAAGTAAATAAGAAAGTTGTACATGAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG  
CTTTAAAGATATTTCCCTATTTACCCACCAAACTTTACAAGTACCTTCCATTGTTTAAACAACGT  
TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAAACTAAAATACAAATGTTAA  
CTGGCGGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC  
AGTATGTGTTAAGTGGAAATGGCTTTGAAAGAAAAGTCATCCTCAGTTTATGATTTATGGTTGGAGA  
TTTTAACTACTACCAAATTCGACACCAGTGATGAGGTATTAGAAAAGTTGTCAGTTTGTATTAAAA  
ACATGGGACAAAACCAAATCAATAATATTGCTGATCGCGGTCATTCTTATGCGGCTGCTGTGAGCT  
CACTGAAATTGACACCGCTGAAAATACATCAGTGACATCGTTTCAGGTTTGAGTCAAGTTCAATTTG  
TAATGGAGTTGAACCTCAAATTAGAATCAGAAGGGAAAGAGTACTTGGCCAAAGAGATTATTCGGA  
TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAAATCAAG  
AGATTATTGTTGAAAACGAAAAGCTTATTGAGAAATTTGATAAGGATATTTCTTCGAACAGACCAA  
CTTTATCGTTAACAGTAACAGATGGTTTACTGGCATTGTTGAACCTCATTCAATTACAATCATACAA  
GTGAAAATGTCTTAGTTAACTTACCATTCAAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT  
CGTATTTCATCAAAAGGATGGTGCTTCTTTACAAATATTATCTCAGTTATATTCCTTTAAAAATCTAC  
ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGACATATGATGGGTGAACGGGA  
CATTAAACTTTTATTCGTATCGTGATCCTAATCCTGTTAAGTCGATTCAAACCTTTAGAGATTCTT  
TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTC  
AAAGCGTCGATGCTCCAATTAATATCTCTTCTCAGGGTGCTAGTGCCTTCTTTGAAAATATAGATG  
ATTACTTGAGACAGGAAAGAAGAGAAAACCTTTTGGGTACCACTTTAAAGGATCTCAGAGATGTGA

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CTGAAAAGTATCTTGTGATAACCAAAACAACCTTGTCACCTGTTATTGGTGACAATGAAATTTTAA  
ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C\_homolog 1034aa (SEQ ID NO 328)

MLKTRLKQSR AISRVVRRYACSHPI SPNL DKYPVGLKLHGYEVTQTSP IPEFSLTAVSLKHTESGA  
THLHLDSPND SNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT  
GHDYTFYFPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE  
MKGQYSNSAYFYIKFLES IYPSLNNSGGDPKKIVDLSEGLLEFHSKNYHPSNAKTFTY GKLPLE  
DLSKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCT SITWNLGNP  
LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNLYLTKQK  
VDNFNEKVMEIINNKI IPELSNEESSSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIVPSWVNGV  
DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTL CNPHSQKFKFTMEPREDFTKQLVKDENLMIE  
KRVSELTEDNKKAIYEQNLELAKLQLEDQNT EVLPTLTIDDI PKRGDFY AIDL GQVNKKVHERVV  
DTNGLVYANALKDISYLP TKLYKYLPLFN NCLTNLAGTENTP ITELETKIQMLTGGITFSSKISTD  
PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILT'TTKFDTSDDEVLEKLSVLIKNMGQNQ INNIADR  
GHSYAAA VSSSKLTPSKYISDIVSGLSQVQFVMELNSKLESEGKEYLAKEIIPILQEI QKYVLQGE  
FRYRLVGNQEIIIVENEK LIEKFDKDISSNRPTLSLT VTDGLSALLNSFNYNHTSENVLVNL PFQVG  
YSSLGKIGSSYSSKDGASLQILSQLYSFKNLH SKIRESNGAYGGGLTYDGLNGTLNFYSYRDPNPV  
KSIQTFRDSL SYGLDANWNDKDLQEAKLRVFSVDAPINISSQGASAFFENIDYLRQERRENFLG  
TTLKDLRDVTEKYLVDNQN NLVTVIGDNEILNVDNKWQIRNFQV

YDR450W\_YML026C\_homolog 1366bp public: 1..1366; exon 1: 501..548,  
intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)

TTAAGAACTAGCAGATGTAAAATGTTTATGTCATTATATAATTTGTTAATACATGTATATAGATT  
TTTTAATGAATGTATTCCTTAAATAGAACAGAATTATGATGCTGTTACAGCAAAAACCTGGTTTGAG  
TATTGGAGAATGTTATAAACTGAAATTTGATTTACAACCAAAACCCGTGTCACGTGTAAGTAATTA  
GGGCTTTTAGGGCTTTCTATATACAGGCACCAGAATTTTTTTTTTATGGGCGATAGAAATAATGTAT  
GCGCGCGATTCTTCCTGCTAGAGGTTTTTCTTTTGTATGTCTGTAACAGTGCGACTCACATAGTT  
AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCCCTAATCACATAGTTAATTC'TCAAA  
CTT'TCTCTCTTTCTCTCTTTTGCTTTTCTCTCCTAAGGAAAAAAAAAATTTATTTCAATTTGTTGAAAAT  
TTTTGTATAGTTCAGTTTAAACAACACCAGTAATCAAACATGCCATTAGTTGTCCAAGAACAGGTT  
CATTCACAACACATTTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGGTT  
AAGGAAGGAAAGAAATTATCCAAC TACTGTTTTGGGAAAGATTAATCAGAAATTTGAATGCAATGA  
AAAAACT'TTTTCAAGAGATGGATATGGAACAAGATTTCGATTGTTATCAACAAATATAAAGAAAAGC  
AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATACTACTATTTACTTTGG  
AGTAATATGTTT'CAATATTATCAGAGACTTATCAAAATTTATGAGTTTAT'TATTATTGAAGTTCA  
ATACCATCAAGCCTTT'TTTTAAACCATCACTCTATTCAACAATCATTTAAATATTAAAGACTCTTTT  
TTTCCCT'GTTTAAAGTATTTCGATTTACTAACATTATGAATTA'TTATTATAGTTTGT'TAAACACCAA  
CATTGATGGTAGAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC  
CAACTTGGTTTGTA AAAAAGCCGATGTTGAATTAACCAAAAAGAGCTGGTGAATTGACCCAAGAAGA  
ATTGGAAAGAATTGTCACCATTATGCAAAACCCAACCAACTATAAAATCCCAGCTTGGTTCTTGAA  
CAGACAAAAGATCAAGTTGATGGTAAAGATTACCATGTTT'TAGCTAACAACTTGGAATCTAAATT  
GAGAGATGATT'TGGAAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT  
GAAAGTTAGAGGTCAACATACTAAAAC TACTTCTCGTGGTCGTTAA

YDR450W\_YML026C\_homolog 145aa (SEQ ID NO 330)

MPLVVQEQGSFQHILRLNLTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL  
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDHYVLANNLESKLRDDLERLKKIRSHRGIRHFVGLK  
VRGQHTKTTSRGR

YDR471W\_YHR010W\_homolog 1327bp PathoSeq: 1..1327; exon 1:

501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)

ATAGTTATTACAATATAATAAAGCAAATAAATAAAAGAAATGATAAAGAACCATATTAACAAAGTT  
TGAACGTGCTGTAAGTAAATCTTGTATACGAGAATATTCATCTTGGAATATTTCTAAACGATACTG  
GTAATACCTAAT'TCTATTTGGTGTGGTGCATCACGTGCTAGGGCTATAGCCCTAATAGTATATGCA  
GTCGCATACATTAATTGGTCATCTCATAAGTAAATTATATAATGTATAGTGTGCGCGCACTGTAAT

TTTTACACTAAGTTAAGGAGAGTGCAGAAAAATTTAGTACTAACAAAAATTGTATTGTGTTGTGTGT  
GGCTATTGGGCAGAGCGAAAAATTTACCCCTACTGAGAGGAACTGTGAGGGAGAGAGATACACAC  
AAACTCTGTGCGCAAGAAGAAAGACAAAAAATTTTTTTGAAAAAAGAGACAACCAACCTT  
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TTGGTATGTAAAAATGAGTACCTATATGGGTAGACAATGATAGATTTATTGGCCAACTATGAATGG  
GATAGATATATATGATATGGGAGAGAATTTTGAAGGATTGAAATATTTTATATAAAAGAGAGAAGC  
AAAGAGAAAATGAACAATTGAAAAGAAGATACAAATACTGTTAATTAAACTAGAATATGCCATT  
GAAGATTTAAATGATTACCATCGTAATAAATTTATTGGAAATTTGGGAGATTCTTTTGGAGTTAAGA  
AAAAAGCAAGTGATTGATCAATCACTATGGAGCCGTCACAAGACATCAACGAATCCCACAACATTT  
TTATTTATTTCATATCCATCATATGGCAGTAACAATCATGAATCTACAAATTACATTTAAAAAAGC  
ATTATACTAACTAAATTTTGTAGCTATTGTTGTAAGAGGTCGTTACGCTGGTAAAAAAGTAGTCAT  
TGTGAAACCACATGATGAAGGTACCAAATCTCACCCATTTCCCATGCCATTGTTGCTGGTATTGA  
AAGAGCTCCATTGAAGGTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAGAAGTAAAGTCAA  
GCCATTTGTTAAATTAGTAAACTACAACCATTTAATGCCAAGTACCTAGTACTCATTAGATGTTGAATC  
ATTCAAATCTGCTGTCACTTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT  
TGTCAGAAGGCTTTTGAAGAAAAACATCAAGCTGGTAAGAACAAATGGTTCTTCCAAAAATTACA  
CTTTTAA

YDR471W\_YHR010W\_homolog 136aa (SEQ ID NO 332)  
MAKFIKSGKVAIVVRGRYAGKKVVIVKPHDEGTSHPFPHAIVAGIERAPLKVTKKMDAKKVTKRT  
KVKPFVKLVNYNHLMPTRYSLDVESFKSAVTSEALEEPSQREEAKKVVKKAFFEEKHQAGKNKWFQ  
KLHF

YDR486C\_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)  
TTCCAGTCATTCCGAAATGCATAAGCAAGACGTTAGTTGTATTGTGGTTGTTTAGTCTAATCCAAA  
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ATTCTTTTTTCAGCATCATTCGTATCTTTAAGCACAGGGAATAGCAATGGATCATGTAACAAATTCA  
CTTTCGTGATTTCGAAAGCCCAAAATGTTTCGTTTAAACAACGCACACACATGTGAAACCTAAACCG  
AGTTAGTCGTCAAGAAAATAATTCAGTGTAAAGTCTGTACCTTAAGCGTCAAACGTAACCTCTGCA  
ACCTCTGGCATTGAGTGTAATTTAAATATTCATGATAATCTGGAAGTACAGCTACGAAAAAAGCA  
GAAAAAGAAAAATAGTACGAGTTCTTGGTGAGATAAATAATGGAGAACACTTTTTTTTCTCTTTT  
GGAGGTTTTAGAAAGGCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAAGCA  
CTGCGCCCAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG  
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GACCCGGAAGTCCGCACTAAAACAAAAGCAATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG  
CTCAAAAGGATCAGTTAGAGAATCAATCTTGGAAATATGACACAAGCTTCCATGACAACAGATAACT  
TACAAAATACCATGGTCACAATAAATGCAATGAAAACGCCAATAAACTGTTGAAACAACTTATG  
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ATGAACACAGAGAGGCCTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG  
ATGCTGAATTAGAAGCTCTTGGCGAAGAAATGATTTTGAAAATGAAATGGCAGAGAGTGGGATAG  
GTGCACCTAGTTACTTAAATGATACAGAACCCTACAGCAGCAGATAAATGCCTACATTTATTGACG  
ACAACCAAGAAGCTCAAAAAATCGCAAACTAG

YDR486C\_homolog 218aa (SEQ ID NO 334)  
MNRLFGTKSTAPKPSLNDIAIKGIDERVGSLDVKLSKINSELSTYQQKISRMRDGPGRSALKQKAIK  
LLRQRKQIEAQKDQLENQSWNMTQASMTDNLQNTMTINAMKTANKSLKQTYGKINIDELEDLQD  
EMLDLIDKSNELQELSTSYDVPDDISESELDAELEALGEEIDFENEMAESGIGAPSYLNDTEPTA  
ADKLPTFIDEQPEEAQKIAN

YDR507C\_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS:  
501..4547 (SEQ ID NO 335)  
GAATGAGATTTTTTTTTTTTACTAAGGGTGCCTACTACTAGTTATTTGTTTTGTTGTTGACGATCA  
TTAAAGAAAAAATTTACAGTATACACAAAACACTTTACTTCTGCTGTTTTTTTTTTTATTTTAGTTT  
TTGGTTTCATAAATTATTTAAAGAAAGCAAATAATTATTGAAATAAATTTTATATTTTGGTTTTT  
TTTTCTTTGGTTTCTTTGAATTTTGCAAACCAATCCAAATTTTTTTTGAAAATTTTCCTTCTTCT



TCATTTGTTGACTTTTGAAGTTTATTCATCCATATTCTTCAAGTTAAAATAGTGTTCATATCT  
GTCCAACCAAGAAGAAAACCAATAAACCAACATCAATTCCAACTTTGTTFACATCAAACAGAAACAA  
AAAACAGATAATTTATAGACACCTTCATTCATTCTGTTATTTTTTCCAAGTACTACACGTCTTTAT  
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CGTCATCGATTATGTCCCAATCAAATCATAATCATCCACAGAAGATCGGACCTTGGAAATTAGGTA  
AAACTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATTAGCTACTCATCAAACCTACTGGTCAAAAAG  
CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT  
TACCATATGGTATAGAAAGAGAAATTATTATAATGAAATTATTAACATCATCCTAATGTTTGTAGAT  
TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTTGTCTAGAATACGTTGAAGGTGGAGAAT  
TATTTGATTTATTGGTGGAAACGTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAAA  
TCATATTGGGTACGGCTTATTGTCTATGCTCTTGGTATATGTACAGAGATTAAAAACAGAGAATT  
TGTTACTAGATTCTCAATTGAATGTAAAAATTAGCCGATTTTGGAAATGGCAGCTTTAGAAAGTAACG  
GCAATTATTAGAGACTTCTTGTGGTTCACCTCATTATGCTGCTCCAGAAATCGTTAGTGGATTGA  
AATATCATGGAGCTGCTTCTGATGTTTGGTCTTGTGGGTTATATTATTTGCCTTGTGACAGGTA  
GATTACCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA  
TGCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAATGTTAGAGGTTGATCCTA  
TGAGAAGAATATCTACTGAAAAAATCTTAAGACACCCATTGTTAACCAATACCCAAATGTCAAACG  
AAGATTTAATCAGTGAAAAATCATTACCACATCCACATACTGGTTACAAATCTTTAGGGTCAGTTA  
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ACAAGCATAATCAAGACGATAACACTAATAACAATTCACCAAAGAAATCAACGAGTTTCAATAATA  
AAGTGGTACGCAGTGGGTCCAAATACAGTCTTAATGGAACCCCTAGAAGAAAAAGAGCCAGTCACA  
TAAGTGTGTCAAGACCAACATCTTTCCAATACAAGTCTAATCCTGGCGCTGGTGCAACAGCAAATA  
GAAACTCCGTTGCCAGACATTCTGTGGCTTCCTCGGCCAACAATTCCTCGTAAATCACCATAACA  
AGTCACCATACAGATCACCTTATAGATCACCATAAAATCGCCTTCTAAGAGATATTCAATAATC  
AATCCCCAACTAAATCTCCTTACGGAAGAAGATCAAAATTCACAAAGACAATTTGAAAATGAACCAT  
TAAAGGCAAAGCCAAAGAAATATTTACAATGAGATTGTTGATGCACAAAGCAACTTTTCTCTACCTC  
CATCGCTTCCACCTTCCTTACCTTCAAAGATTCTCGTTATATGATCGATGAACCCAATCAACCCC  
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ATTCCATAACCATGAAATTGTATCTACTTATGCTAAATTATCAGGTGATGACGACTGGGAATACA  
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GGTTAATGGAATTGGAAGAAAAGAAACATGAAGCTGAGTTGAAAGCTAGAAGAGAATTAGAAAAGA  
AGAAAAGAAGACAAAAGAGACGTTCCATTTTGAAGTTCTAAGAAATTAAGTATTATTGTCAAGAATG  
ATGCTGATCCAAATAATAGTGAACAAGAGTTGGTTCGATGAAGGTATAAAACAACCAAAACGTCAAT  
CCAAAACTTGACCGCTTTAAGAGCATTATCTGAAGGAATCATGCATCTGAAGAATTGACATTGG  
AAGACGTTGAGAAATTTGAAGAGACGATCAGCATCAGACCGGTTCCAAAAAGAAGACAAACTCCGG  
TTTTGACAAGAGACCTGTATCAAGATTAGATCCATTATGGCAAGCACACGAGAATGAACAGTTAG  
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GTAAAAAAGTCAACAGAGAGTCGATGATATCAGTTATGGATGATATTGTTGAAGAGGACCAAGGCC  
GTGTCAACAGGAGATCAACACGAAACACTTACTATGAAAGGGAAAGAGACTATGAATTACCAGAAC  
CAACTGTGGAAGATTCCAACCTTGACTGATGACTACATGACAGAAATCAGAAAATCAAGACTTTTGA  
ACAGTCAGTTAAATGTTAGGGATCCACTTAATGAAAAAAGAAAATCTGAACCCAAGACTCTTATTA  
GCAATGTTCAAATACCGAGTGTACTAGAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT  
CGGTATTGTCTATGTATTCAACAAAGGAATCATACCGTGATTTGAATTCTATAATTAATCAACCAG  
ATGAAAACCCCGAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAGTATTGCTGATCGTT  
TGGATAAAGCTGGATTGGCTGAACCAGAAATATGAACTGAGACTGATGGTGAAGATAAAGTGTCTG  
TTATTGATTTGGATGATCATTTAGCTGATAGAAGGACTTCCTATTATGATGGATCTGGAAAGAGAG  
CATCTAGAGCTTCAACAACCTAAACGTTACAATGTTTCAATTCAGTTTCAAGAAAAAGACCAAAATCCA  
AAGTTCCTGATTTTGCACAAAGATGATTATGATGACACATTTGTGAGTAATAGTGAAGTTCATA  
AGCGTCAGTATAAATCGATGGTTTCTGATGAGTCTAGTGCATCTGATGATGTATTTGATAAGATTA  
AATTACCAGATGGTAAATCAACTAAATCTTCCATTGATGAATTTGGCTAACGGCACGCTTACAAGTG  
GTCATAGAAAACCAAGATAAGACATTCTCAACCGGGCCAGAAATGTTGATTCTTCATTTGAATG  
GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTCGTGGTAACAATTCAGTGGTCATGATGATA



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GTGTTCCACCACCACCGCCAGCTCACAAGGTGAATAAAAAACCATTTGGATGATAAGACGAATTTCC  
 CTCCACCAGAAGTGGATCCAAAAAGAAAAGGTTTCATTTTTTTAGAAAACTTTCTTGGGGATCCAAAA  
 AAACCATTTGAAAATAATACAAACGCCGCCACTAATACCACGACTCAACAACAATTACCAAGTCCTG  
 CTGAATCAAAAAGAGGAGAAACCAAAAAGTTCATTTTTTTCAGATGGTTTTTCGTCATCTAATACTCCAT  
 CTGCTGCTGAAATTAGAAAATTTCAACACCATTTTACCTAAACATGAAATGTCTACTGCTTTATTTG  
 CTTTATTGAATTCCTTGGTCTAATTTTGGTTTGAAGATTTACGGAATGATCAAGTTGGATATTATA  
 TTACTGGTGCTATTTCTAAACATAATTTCTTTTAATTTAAAGAGTTGTAAATTTAGAATTAAGATTA  
 ATCAAAGAGATTTTAATCAAAAATCAGAAATTTGTTTGTGTTTAGAGTGAAAGGATCTAAAGTTACAA  
 CTGATACTTTATTTTGTGAAATTGAAAAGGTCTTACTCAAAGAAGGTGGTTTAGATAAATAA

YDR507C\_homolog 1349aa (SEQ ID NO 336)

MPHSRQPSISSSIMSQSNHNHPQKIGPWKLKTLGRGATGRVLLATHQT TGQKAAVKVSVKSELQD  
 EETEKNGDGLPYGIEREIIIMKLLTHPNVLRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE  
 VEAIKYFRQIILGTAYCHALGICHRDLKPENLLDLSQNLVKLADFGMAALESNGKLLTSCGSPHY  
 AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDENIRNLLLKVQAGNFEMPVDEVSRARDL  
 IARMLEVDPMRRISTEKILRHPLLTKYPMSEDLI SEKSLPHPHGTGYKSLGSVRNIDKQILSNLTI  
 LWNDRPEEEIVDCLLKDGSNPEKTFYALLMRYKHNQDDNTNNNSPKKSTSFNNKVVRSGSKYSLNG  
 TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYRSPYK  
 SPSKRYSYNQSPTKSPYGRSNSQRQFENEPLKAKPRNIYNEIVDAQSNFSLPSPSLPSPSKDSR  
 YMIDEPNQPLQOPALSQVPENPIVDESPDLMSAKISSGKRNSIIGKNNNNNSNSNKRMSKRKSIR  
 ASMTTGLKRNSITMKLLSTYAKLSGDDDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP  
 EEKEAKEYERLMELERKKHEAELKARRELEKKRRQKRSILSSKKLSIIVKNDADPNNSEQELVD  
 EGIKQPKRQSKNLTALRALSEGNHASEELTLEDVENLKRRSASQVPKRRQTPVLTRRPVSRDLPL  
 WQAHENEQLDRAKDALEQEWDRSQKRSSTVSRKKVNRESMISVMDDIVEEDQGRVNRSTRNTYYE  
 RERDYELPEPTVEDSNLTDYMTAIRKSRLNLSQNLVRDPLNEKRKSEPKTLISNVQIPSVTRKSR  
 NFTTSNKRSLSVLSMYSTKESYRDLNSIINSPDENPEQHONMKNPALRTSIADRLDKAGLAEPEYET  
 ETDGEDKVSVIDLDDHLADRRTSYDGSQKRASRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT  
 FVSNSDEVHVRQYKSMVSESSASDDVDFDIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG  
 PEMLIPLHNGGIESSQPMKSVRGNNSSGHDDSVPPPPPAHKVNKKPLDDKTNFPPEVDPKRKGSF  
 FRKLSWGSKKT IENNTNAATNTTTTQQQLPSPAESKEEKPKSSFFRWFSSSNTPSAAEIRKFNTILP  
 KHEMS'ALFALLNSWSNFGKDLRNDQVGYITGAISKHNSFNLKSKCFRIKINQDFNQKSEIVC  
 VRVKGSKVTTDTLFCIEIKVLLKEGGLDK

YER102W\_YBL072W\_homolog 1121bp public: 1..1121; CDS: 501..1118  
 (SEQ ID NO 337)

ACAATACTAGGCACGTGTTGAGTGAGTGAGCATTTTTTCTGTTTCTCACTCAGTTAACAAAAATAAAA  
 AAAATTTTTCATAATTTAGAAGTTTCATTTACAGTCTTTTTTCAATTAACAGTGATAACAAGATGTA  
 TGTAAGACAACATGTACTAGCAACTATAATATGATTTACCAATGATTGGGATCACAATAAATGTG  
 TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA  
 TGGTATACAACTAAAATGGAATTATTTTCAAATATGCAACTATCATTATGACTACTACGACAACAA  
 TTTTAATCGAGAGAAGATCATTAGATCAAGAGTTGGGAAACTAATACCAAGGAAATATCATTAAGA  
 ATTAATAGCTTTGCAAAAATTGGTTTTACTCATATTATTTGTTTTAGTTGGAAAGCGATTACATCA  
 TGGAACAAAGTTTACTAACAACATTTGTTATAGGTAAAAATGGGTATTTCTAGAGATTCACGTCA  
 AAAGATCCGCCACTGGTGCCAAAAGAGCCCAATTCAGAAAGAAGAGAAAGTTTGAATTAGGTAGAC  
 AACCAGCCAACACCAAGATTGGTCCAAAAGAATTCACCTGTGTCAGAACCAAGAGGTGGTAACCAAA  
 AATTGAGAGCTTTGAGAGTTGAAACCGGTAACCTCTCTTGGGGTTCCGAAGGTGTTCCAGAAAAA  
 CCAGAATTGCTGGTGTCTGTTTACCATCCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA  
 AATCTGCTGTTGTTCAAATTGATGCTACTCCATTGAGACAATGGTACGAAAACCACTACGGTGCTA  
 CTTTAGGTAAAAAGAAGGGTGGTGCTCATGCTGCTCAGCTGCTGAAGTTGCCGATGCCAAGAGAT  
 CAAGAAAAGTCGAAAGAAAATTGGCTGCTAGATCTGGTGTCTGCTGCCATTGAATCCGCTGTTGACT  
 CTAATTCCGTTCTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGATGTG  
 ATGGTTACATCTTGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAATAA

YER102W\_YBL072W\_homolog 206aa (SEQ ID NO 338)

MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGPKRIHSVTRGGNQKFRALRVETGNFS  
 WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTSAVVQIDATPFRQWYENHYGATLGKKKGGGAHAH

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY  
LRRLTAKK

YFL014W\_homolog\_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG  
TACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTCCA  
AATTGAGACCCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAAGG  
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAAAT  
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACAGCACCACAGCAATATAGCAA  
TCATAAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC  
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTTCTTTGAATCTTGTTTTTT  
TCGACATACACCATAAATCCCATAGAAAAGTCAAAATGTCTGACGCCGGAAGAAAAACATTTCT  
ACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAACAA  
GTCACCAAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTCAA  
ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA  
CAAGCAGAGGGCGAACAAGACCCCTTGCTGAAACAGCTCAAGAATATGTTCGAGGTTGCCAAAAGT  
AAATTGGAAGGCTGCTGAATACGTGA

YFL014W\_homolog\_1 106aa (SEQ ID NO 340)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADSVQQGSDN  
AKADLKKQSEQAEGEQRPLSKQLKNMSRLPKSKLERSST

YFL014W\_homolog\_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG  
TGTAATACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTG  
CAAATTGAGACCCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAA  
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA  
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACAGCACCACAGCAATATAGC  
AATCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCT  
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTTCTTTGAATCTTGTTTTT  
TTTCGACAAACACCATAAATCCCATAGAAAAGTCAAAATGTCTGACGCCGGAAGAAAAACATTT  
CTACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAAC  
AAGTCACCAAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTC  
AACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG  
AACAAAGCAGAGGGCGAAGCAAAAGACCCCTTGCTGAAACAGCTCAAGAATATGTTCGAGGTTGCCAAA  
CTGAAATTGGAAGGCTGCTGAATACGTGAGTGGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA  
CCGGCGCTGATAGTACTAAAAAATAG

YFL014W\_homolog\_2 127aa (SEQ ID NO 342)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADNVQQGSDN  
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C\_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTAT  
TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTTTTCTCGAGTCTTGGTATCGGTTGTAAACG  
TATCTGTTTCACTTATCAGTATCGTCATTTATATTAACACTTTTCTCCTATGGTTATATATTGGT  
AAACAAAGAAACAAACAAACAAAAAGAAGTAGTAGTTTGTGAAAATTGTCAATAAAAGAAACAAAG  
AATGAAAGAATGATTGAATGAAAGAAAAAATAATATGAAAGTGAGTGCGACATAATGTAGAAAAA  
TGTCGAATGCTTGAACCTTACCCATTGAGTAGTTGTTGTAGTGTAGGAGGAAGAAACAACAGAA  
AGAAAGAGAGAAAGAAAAATTTGCCACTACAAATATTCAACAAGTTTCATATAGTAATATAATCC  
CAATTGATCATTACTTTATTCACACAATTCATAAACAATGTCCAATTCAGCAGGTTTGTAGTAGAC  
ATATCACTATTTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT  
CAGCAAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATCACAAAAGAAGA

TCCAGATAAGTTATTAGATCCTAAAACCGTGTGCATATATTTTTTAAATCACTCCTAGTATAGGAA  
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG  
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAAGTTTATCAAGAAGAATGGCGAATATAT  
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTTGGGTGTTGCTTTAACTTTTATTCAAGTTG  
ATTTTGCTGATGAAGGTAGAGGTCCACAAATTTTTAAATGTGATCCTGCTGGATATTTCACTGGGG  
TGAAAGCCGTGGCCACTGGTCCAAAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA  
AAACCGATGCTGTTAAAGGAGATTGGCAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCG  
TGATTGGAACGTAATTCAGAAAAAATGATATTGAAATTGGTGTGGCCACTGAAGGAGAATTTAGAA  
TTTTGACACCAGAAGAAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

YGL011C\_homolog 247aa (SEQ ID NO 344)

MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY  
IFKITPSIGMVATGSIADARAQAMRARSEATEFRYKYGYEMPVESLSRRMANISQLYTORAYMRPL  
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQOEAT'TYLEKKFKKTDVAVKGDWQKTV  
EFAIIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C\_YGR148C\_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

CATTGTAGGTACACCTGTTTTTGGCTCAATGTACACACACACGCACCAGCAGTAGGAAAAAACA  
AATTAATGAAAAATCATTTTCGTTCAATATTAAGCTTCTTAAGATAACCAACCAATTAATATGTA  
TGTGACATACCATATAAATAAAGCTACAAATGGGGATAACTATGTATTTAATGATAAATGAATGGA  
AGACCAGAAATGTATAATGTTATAAGATAGTGATTTATATTGAAAACACCCTTAAAAAATCAACCA  
CCCATCTAACCGTCGAATTGGAAATGTCAATTTAGTTAGCATCGAAAATCAACAAAGACATGGGGA  
ATCATTTACATATAAAATAATGAGAGAGAATTACAAACTGCTACGTTATGTTTTGTTTCATTATGTC  
TTGTTCAATTATGTCTTGTTCATTATGTCAAAAAATCTATAGTTACCTACCTACATCAATTTATG  
GTCTGAAATACTAACATTTTTTTTATTATTATAGTGA AAAATGAAGATTGAAGTTGACTCCTTTTCAG  
GTTCTAAAATCTACCCAGGTAGAGGTACTTTATTTGTGAGAGGTGACTCTAAAATTTTATGATTCC  
AATCCTCAAAATCTGCTTCTTTATTTCCAACAAAGAAAGAACC CAAGAAGAATTTCTTGACTGTTTT  
TGTACAGAAGACACCACAAAAAGGTATTTCTGAAGAAGCTGCTAAAAAGAGAACCAGAAAGACCG  
TCAAGCACCAAGAGCTATTGTGCGGTGCTTCTTTGGAATTGATCAAAAGAAAGAAGTCAAAAAC  
CATCTGACAGAAAAGCTGCTAGAGACTCTAAATTAGCTAAAGACAAAGAAGCTAAAAAGCTGCTA  
AAGCTGCCAGAAAAGCTGAAAAGGCTAAGGCTGTTGCTTCTGGTGCTTCTGTTGTTTCTAAACAAC  
AAGCTAAAGGTTCTTTCCA AAAAGTTAAAGCTACCTCCCGTTAA

YGL031C\_YGR148C\_homolog 155aa (SEQ ID NO 346)

MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE  
AAKKRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKA AAKAARKAEKAKAVA  
SGASVVSQKQAKGSFQVKATSR

YGL043W\_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

AATCTACCATTAGGCAATGTCAATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT  
CCATAATTTATAATGGCATAACCTTTTGGATTTACCTGTTAATTCATCAAATAATAACTTCACATCT  
AATACTGGTCCAACGTATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA  
CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCTCTGATTCTT  
GGTAACAAAAAATATAATTATTTAACAAATTATCGATAGAATCTCTTCCAAAGTACAACCAATTT  
CGATACATTTTTTTCTATGAGATGTTTTTTTCCCTTTGTCTTTAACTAATGTATTTGGGTACACT  
ACCTGAACCTACCAGTTCAGTTCAGTCTAAAAAATTTTTTATTTATTGTGTTTGTGTTTATACTACCC  
TTTGCATATATTACTAATATTTATCTTACCCTTTTCATCATGGATACAAAGGAATAAGATCTACCG  
TATCTAATCTTGAAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG  
GGGTTAAACCATCCGAAAAAATCTTTGAGAGAAACCAAGTAGGTGTAGCTGTCAACAAATTCAGAA  
GTCACGACAGTGCCGAAATCAACGGTTTAGTTAAAAAATGATCAGAAATTGGAGAGATGCCGTGC  
AAGCCGAAAAGAACAACAAAAAGAGTTAGCAATAGCAGCTGGAACAGGAACAGGAACACCTTCAA  
GCTCAGCAATTTGCCCATCATCATCGGGTCTGGAAGTACAACACCAAAACCATCAGAGTCAACCA  
CACCATCGGCTGCCCGTAAAGGTCCAAGAAATCCAAAACTGACGGTGTAATACTCAATTATACG  
AAAATGATACCAGAAATGCATCGGTTAGTGCTTTATACACGTCGTTAGCAGTTGATCGTGACGATT

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CACCAAAACACATTTTGGAGAATAGCTATTGAAATCGAGGCTGAAGTATACAAGAGCGAATACCTGA  
AAGTAAGTGACAGTTATAGAAATAGGTAAAGAAGCTTTACCATGAATCTTCGAAATAAGAAAAACC  
CAGAATTAAGAGAAAGAATCTTATCGAAACAAATTTTACCTGCTGCGTTCATTAATGACCCCTA  
ATGAAATGGCTCCTGAGGCATTGAAAAAGGAAATTGAAAAATTGCACAAACAAAACCTTGTGTTGATG  
CTCAAGGTGCTACTGAAAAGAGAGCAGTGACCGATAGATTCACTTGTGGCAAGTGTAAAGCACAAGA  
AGGTCAAGTTATTATCAAAATGCAAACCAGATCAGCGGATGAGCCTTTAACTACATTTTGTACTTGTG  
AAAATTGTGGCAATAGATGGAAGTTTTCATAA

YGL043W\_homolog 305aa (SEQ ID NO 348)

MDTKEIRSTVSNLEKAVDDTTILKLLNLDGVPSEKLLRETKVGVAVNKFRRSHDSAEINGLVKK  
MIRNWRDAVQAEKNNKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK  
TDGVNTQLYENDTRNASVSALYTS LAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNLRSF  
TMNLRNKKNPRLRERILSKQILPAAFIKMTPNEMAPEALKKEIEKLHKQNLFDAQGATEKRAVTD  
FTCGKCKHKVSYQQMQRSADEPLTTFCTCENCGNRWKF

YGL103W\_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon  
1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)  
ACATTTATTGTTGGCTATACCTTCCAGTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT  
TTTACTGTAATGTGTTGTGCCAGTGTATGGTTTATCAAGACTAAAGTTCCCTGAGACAAAGGTAAG  
CATTCGTACCAGGAAGTCTGGAATTAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT  
TTGTGTTCTAAAGTTGCGTTAGGGCTAAAGCCCTAATCAATAGTAGTGTACTTTGTTTGAATAAAT  
AATACATGCAAAATACTGCATATTAGAATTATAAGGGAATGAAAATGAAAAAAGAAATAATTT  
TGTAAGATCGCATAGTGTGAGCGCGCACACACACAACTTTGTAGTGCTACAGTTTCTCTCTTTC  
CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCCTT  
TTGAGTTTTCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAACTAAAACCAGAA  
AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTAAACGGATGAAAGAGTATTGA  
ATGTTCAAGGACATATGGAGATTTAGAGAAAAACA'TGGAAAACTAATCGAAAATGAATAATGAATGG  
AAAATTTTTTAACTGAATATCAGAATAGACACAACACAACAGATCCAGAGTCATTATCACATTGA  
TCATACAACCAAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTTCAGAA  
CAATCAAGTTTATCATTTACAGAAGACAGTTCCATCAATATGTCCAAAATACTCTTTGAAGTCAAT  
TAAAGTCAAATGAACGAATTACTAATTATTTTCTTTAGCCGGTAAGGGTAGAATTGGTAAAC  
ACAGAAAGCACCCGGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCAACTGGGATA  
AATACCATCCAGGTACTTCCGTAAGGTTGGTATGAGATACTTCCACAAAACAACAAAACCACTTCT  
GGAGACCAGAAATCAACTTGGACAAATTGTGGACTTTGGTTGATTCTGAAAAGAAAGACGAATACT  
TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT  
TGGGTAAAGGTAGATTACCAGAAAGTTCCAGTCAATTGTCAAAGCCAGATTTGTTTCTAAATTAGCTG  
AAGAAAAAATCAGAGCTGTTGGTGGTGTGTCGAATTAGTTGCTTAA

YGL103W\_homolog 149aa (SEQ ID NO 350)

MPTRLTKTRKHRGNVSAGKGRIGKHKHPGGRGKAGGQHHHRTNLDKYHPGYFGKVMRYFHKQQN  
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLEPVPVIVKARFVSK  
LAEEKIRAVGGVVELVA

YGL147C\_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO  
351)

GCTATCAAAATCACTGTTTCACAATGGTGACAGAAAACACGTTGCTGCTTTAAGAACTGTCAAATCT  
TTGATTGCTAACTTGATCACTGGTGTCACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCG  
CATTTCCCAATTAACGTTAACATTATTAAGAAAGATGGTCAAGATTACGTTGAAATTAGAAATTTT  
TTGGGTGAAAAAAGAGTTAGAGAAGTTAAATCCATGAAGGTGTCACCATGGAAATTTCTTCTACT  
CAAAAGGATGAATTGATTGTTTCTGGTAACCTTGGAGCTGTTTCTCAAAATCTGCTGATATT  
CAACAAATCTGTGTCAGAAACAAGGATATCCGTAAATTTCTTGGATGGTATTTATGTTTCTGAA  
AGAGGTACCATTTGTTGAAGAAATCTAA

YGL147C\_homolog 140aa (SEQ ID NO 352)

AIKITVHNGDRKHVAALRTVKSILIANLITGVTKGYKYKMRVYAHFPINVNIIKKDGQDYVEIRNF  
LGEKRVREVKIHEGVTMEISSQKDELIVSGNSLEAVSQNAADIQQICRVNRKDIRKFLDGIYVSE  
RGTIVEEI

YGL213C\_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353)

GATGATCGCTAACAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC  
AACCTTAAATAGCTTGTAGTTTTTATGATTGGGACTAAATGTGCAGCATCGAACAATATTGCCAGT  
TGCATAGAATAAATCGGTATTATTACGGCATACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA  
TTCTGGGGTTGTTGCATTTCAGTCCATAAACGTTGAAACACAAATTTGCTGTGTAAATTTGGTGAAT  
GAATTGATCAGATGATCCTATGGGTGGCATTGTTAAGGTTGTTTCGCTACGATGTATTTCTAGGATA  
ATGAAGGTAAGTACGAACCTTATGAGTTTTGATTTCTTCCTGATGTTTTTTTTCTTTGTTTTCTT  
TTGTGCTGTGTAGCAAGAAGAAAAAAGTGTCTTCAACAAGCTTTGGACTCAATTTTCACCCCT  
CCACAAACTCAATTTCAATTAACATCAATAATCCAATATGGGTAAACAGTATATCTACCGTCA  
GTGCATCTCAGGCTCATAAGCTGGATATTCTTGGTGTAGCTATTACCAATAAGTTCAGTGTATCCG  
TGTCTAGTGATGGATATGCGAAATTTTGGGACAACAAGCAAGACGAAGTTCATCTGCCTAAAGAAT  
TTGTCCAACCTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGCGTGTACGAAAATGTTTTGC  
CAAGCTCTACATTGAAAGTGACATTATTAGCATTTGCATGTTTCAATGGATCTATCATCTTCAGAT  
ATTATATCAATGATGACTTTTCAACTATCGAAAGCTAACTGATGATATAAAATCATTTGAAAGCA  
ATTGTTGGACCCCTGGCTTTTTATCGCGATCCAGAATCCAAACAAGACTATTTATTACAACCAAGA  
CCAATGGCACTACAGAGGTTTCATTTATTGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT  
TTGAAAAGTTTGGGCAATTTAAAGGAACTCTTCTTTTCCCAAATTTCTTTGGCTATATGTCCAA  
CAGAGAATAAAAAATGTGCTGTGGGGTACATCAATGGTGATGTCTTGTATATGACTTTGTTAGCT  
TGAAATTGATATACACATTTTCGTTTCGAGTGATTTGGTGACCAGTAGAAATTTCCCAATCGACGTCTA  
TACCTAGGGTGTGGCATTTTCCCCTGGTGGAACCTTTGTTGGCTGTGGCAAGAGACAATCAAGCTG  
CTGGGTCAATTACATTATACGACGTTGAGCATGTGAGAATGTGGGGTCTTTGGCCACACCCCTCAC  
ACTCGGCCAAATCTGTGTTGGTGGGTTTGACATCAAGGCTGGATTTTGGGGTTGAGTTTGTATG  
AGGAAGGTAAGCACTTGGCTAGTTGTGGATTTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA  
GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG  
ACGAGAGTGTGCTTCTGGTGTGCTTTTATTAAAAAGGGGGTTAGAGGTGGCTCTGGTGGTGACA  
GCAATGAAGGATTATGTGTCTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA  
TATAG

YGL213C\_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFVSVSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH  
AVAAYENVLPSSTLKVTLALFACFNLSIIIFRYIINDDFSTIESLTDIISFESNCWTPGFRDPES  
KQDYFITTKTNGTTEVHLLNIVDENEKAVITFEKFGQLKGNSSSFNPNSLAICPTENKKCAVGYING  
DVLLYDFVSLKLIYTFRSSDLVTSRNSQSTSIPRVLAFSPGGTLLAVARDNQAAGSITLYDVEHGE  
NVGSLATPSHSAKSVVGGFAHQGWILGLSFDEEGKHLASCGFDKCI RVWNLET SEREATISISISD  
LDDTTHNDQDESVASGVAFIKKGVRGGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C\_YPR102C\_homolog 1418bp public: 1..1418; exon 1: 501..503,  
intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATTCTGGTGGTTCAGTTAAATTTATATCATGTCACTGAACAAGGTTGGACTTATC  
ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTGTAAATG  
TAGATGGATAAAAGTAAGTTGATTGTATAAAAAAGAATGGATTCAATTAATATAAAATTTACAAATCT  
GATAATAAACTACAGTAACTATTATGCAACAATTGAAAGTATCCTGTGTACAGTGATTAGGGCTCA  
AAAGCCCTAACAGGTTGCACGTGATGTTGATTTATTTATCCC TGACACATTTGAGTTTTTTTTCTA  
TGGTGAAAATTATTAGTGAGACGATGTTGTTTCGATTTTACCACACACTCTCACACTGAGTGTAGT  
CATACTAACAATCTTCTCACACTATACACAAAAAATCTTTTCGTTTGAAAAGTTTTTGAAAGGTTT  
GTTTTCTCAATAGTATATCCATACATAAATACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGAGATC  
GAAATGTTTTGTATTATTAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG  
AATTAATTGAAAGAGTTTTCTTTTGGGGAAATGGGTCAATAAGATTTTTTCAAGATTGGAATCAAA  
TTATGTCAGATGTGAAGAAGAGTAAATATAACAAGAAGTTCAAATCATTAATAAATTTTATGTAAAT  
ACAACGATTATCAATTACAGTCAACGAATAGAATAAAAACAAAAGCCAGCATATAACAGATACCAGT  
GATTCATCCCAGTGATATAAATAATGATATTCAATTAATAAACAATATTAAGACATTTTATTATTTAT

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GTATCAACAAAATACTAACTTATCTTTCTTTTAAATTAGTCTGACAAATCCCAAAATGTTATGCGTG  
AATTACGTATTGAAAAATTAGTTTTTAAACATTTTGTGTTGGTGAATCCGGTGATAGATTAACCAGAG  
CCGCCAAAGTTTTAGAACAAATTATCTGGTCAAACCCAGTTCAATCTAAAGCTAGATACACTGTCA  
GAACTTTCCGGTATTAGAAGAAATGAAAAAATTGCCGTCCACGTTACTGTCAGAGGTCCAAAAGCTG  
AAGAAATCTTGGAAGAGGTTTTGAAAGTTAAAGAATATCAATTAAGATCTAAAAACTTCTCTGCTA  
CCGGTAACTTTGGTTTTCCGGTATTGATGAACATATTGATTTAGGTATCAAATATGATCCATCTATTG  
GTATTTACGGTATGGATTTCTACGTTGTTATGGGTAGAGCCGGTGCTAGAGTCACCAGAAGAAAGA  
GAGCTAGATCCACTATTGGTAACTCTCACAACCAACAAAGAAGATACCATCCAATGGTTCAAGA  
CCAGATACGATGCTGAAGTTTTTGGATAAATAA

YGR085C\_YPR102C\_homolog 174aa (SEQ ID NO 356)

MSDKSQNVMMRELRIEKLVLNLCVGESGDRLLTRAAKVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA  
VHVTVRGPKAEEILERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGIKYDPSIGIYGMDFYVVMG  
RAGARVTRRRRARSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W\_YPR132W\_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTTGTGTGTATATGCGAGAAATG  
AGTAATTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAATAAAATGTCATATTGACAT  
GATAAGGATTTATCAATACTGTTAGGTCTATAGCCCTAACTTTAATCATTTACACGTGATACAAAA  
AAGTTGTTTGATCCCGCACGACTATGAGTACGCACCTACTAATTATAGCCTGAAAAAAAAAATTTTC  
CACATAGTAAGGGGATTTTGTATGGTGGTGCCTCGCCTAAGACGTCTGCATACATTTTCTAAAGT  
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTTCCACCAAATAACTTTGCGGACACTCT  
CATATACTCAATTTTTTTCTTACAAAAATTTTTTTTCTTCTACTTTTTTCAAGAATCTCTCTTTTA  
CAATTCAACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAAGTCTGCTAGAAAAATTAAG  
AGTTCACAGAAGAAACAACAGATGGGCTGATCAAGCTTATAAAGCTAGATTATTAGGTACCGCTTT  
CAAATCTTCTCCATTTGGTGGTTCATCTCACGCCAAAGGTATCGTTTGGAAAAAATTGGTATTGA  
ATCTAAACAACCAAACCTCTGCTATCAGAAAAATGTGTCAGAGTCCAATTAATCAAAAACGGTAAGAA  
AGTCACTGCTTTTCGTTCCAAACGATGGTTGTTTGAACTTTGTGACGAAAAATGACGAAGTCTTGTT  
GGCTGGTTTCCGTAGAAAGAGGTAAAGCTAAGGGGGATATTCCAGGGGTTAGATTCAAGGTTGTTAA  
AGTTTCCGGTGTCTCTTTATTAGCTTTATGGAAGAAAAGAAAAGAAAAGCCAAGATCATAG

YGR118W\_YPR132W\_homolog 145aa (SEQ ID NO 358)

MGKGKPRGLNSARKLRVHRRNNRWADQAYKARLLGTAFKSSPFGSSSHAKGIVLEKIGIESKQPNS  
AIRKCVRVQLIKNGKKVTAFFVPNDGCLNFVDENDEVLLAGFGRRGKAKGDIPGVRFKVVKVSGVSL  
LALWKEKKEKPRS

YGR277C\_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

AATTCATTTGATCTCTAAGAAGATGAACAGGCCTTGAATGGGAGGGGTTGGTTCCGACTTCCACGAA  
ATGTGGTTGGAAAACTTGAGTCCTCAAAAAGGTTCTCTCGTAAAAGGCCAGAGAAAAAGAAAAACC  
ACCAAACCCCCACCACCAACCTAACCTTTTCCTTCCATCCATTCTCTTTCCTTACTTTGCAAATG  
TTGAATCCAGTTATATTCAATTAAGAATCCTATAAAATACGATTATTACAATTTATTATATCTTTA  
CTCCCGAAATTCATTAATTGTAATCGTATTGATTAGTTATACTTTGTCAAATCACCGAATCAAAT  
CAATTGAATGAAATTTTATGTTTTTATTATCAATTAATTTCGTAATCATAAGAATAATGGAGATACT  
GATGGAGATACCGACAGTTTGCCTATGTTTGATTATCGATTGAAATTAATATATTATTTAATTTA  
TCAACAAAAAATTGAATCAATTATGTTTAAATAATTGGAATCATGGATATATTGCGGAAGGTGAT  
AATGATAACAGTACTAAGTGTCTCTTGGCATTGTCAATAACACAAATATCAAAACATTGAAATTT  
CCAACAATCCAATCAAGAGCAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAAATTACTACT  
AGTCGGCAATATCAACAATTTAAACTACTGCTGTAGGTGGAACATTGATCATTTACATGATGGT  
CATAAAATTTTATTATCAATGGCAATTTTTTAACTTCAAATAAATTAATTATTGGTATAACTGGT  
TCTAATTTTATTAAATAAAAAAATTTAAATCTCAATTACAACTTTTAAATCAAAGACAAAATTTA  
GTTATTCAATTCATAAATTTATTATTATTGAGTGAAACCAGTGTTATTTTTTTTGAATTTTATGAA  
ATTAATGATGTTTGTGGTCCAACCTGGTTATATTAATGATATTGATAATTTAATAATATCTCAAGAA  
ACTAAATCTGGTGGTGAATTTGTTAACAATTTTCGTAAAGATCATGGATTTAAATTTATTAGATATT  
ACAATAATTAAGTGATTGGTGGGAATATTGAAGAAAATTCATGGAAGGTAAATTAAGTTCAA

123/161

CTGATATTAGAGAACAAGAATATAATCGATTATTAAATCAATAA

YGR277C\_homolog 322aa (SEQ ID NO 360)

MLNPVIFIKDPIKYDYSQFIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD  
TDGDTDSLPMFDYRFEINILFNLSTKKLNQLCLNNWNHGYIAEGDNDNSTNLSSPLSITQISNIE  
IPTIQSRANSSSAYNDEDDKITTSRQYQQFKTTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT  
GSNLLINKKFKSQLQTFNQRLVIOFINLLLLSETSVIFFEIEINDVCGPTGYINDIDNLIISQ  
ETKSGGEFVNKFRKDHGFKLLDITIIVIGGNIEENSWKGKLSSTDIREQEYNRLLNQ

YGR284C\_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAAATCTAAATCGTTCCAATGATTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT  
TGGTGGCAGTAGTATTGGTATTAAGTGGGTGGGTGATGGTATTAGAGAGTGGGTGTTATAAAAGAA  
GGTTGTGATTTTTTTTCCACTGGTGGTGGTGGTGCTGATTGTACTGCTGTTCACTTTATTGT'TT  
CGTTTCGTT'TTTCCTTTGT'TTTGTTGACGTTGACATTTTTTTTGTCTGTTGTTGTTGTATGGGAATT  
TTTGTATTAGTTGTTCTTTTTTTGT'TTTTTTTTACTTGTTCAAAGTTTTCATATAATAATAATATTCT  
TGT'TTTCATATTTTTTTTTTTCAGAACAAAGAACAAATACAACCTATATAATTTGATCTTACTCTTAT  
CCCCAGTTTTTTCTATTTGTTTTTTGGGTTTGCCATTCATATATATATATCTATTATTCAAATCAAT  
TTGAGGAGTATCATTAAATTTAAATTATATCAGTTAACAATGTCGTATCGTGGTCCCTAATCAATTTG  
GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCCACATATTGGTCCAATATCTTCCA  
GCAAAAGTCCTTTTGAACAATTTGAAGATGTTGCTAAAAAAGTTGAAGATTGGATCGATGATTATT  
TTAAAGTCTTGAAACCATACGTCCCAGCAATTGGTAGAGCATT'TTTGGTGGCCACTTTCTATGAGG  
ATACTTTAAGAATCTTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACCTATAGACACTATT  
GGCGTTGGTTGACCGTTT'TATTCTTGATCAATAATATGGTGGTTATGACAGTTGCATCCACTTTAG  
TAATTGCCAGAAAAAAGAATAACATTGCTACTATTGCAATTGATCGTTGT'TGTTATTATACAAGGTA  
TTGGGTATGGTTTATTGTTTGTATGCTCAATTTGTTTTTGAAGAACTTGTCCGT'TGTTGGAGGGTTAG  
TATTAGCATT'TTCCGATAGTATTGTTAGAGATAAAAGATCCTTAAACATGCCAGGTTTACCGATGT  
TGAACAATCAAGACAACAAAAAGTATT'TCCTTTTAGCTGGTAGAATTTTGTAGTATTATTATTTT  
TGGGATTCGTCTTTTCTTCTGATTGGTCAATGGGTAGAGTTTTCATTATTATAATCGGGTTAACTT  
CTTGTGCTTCAATTGTTGTTGGTTACAAGACAAAGTTTTCAGCTGCTATCATGCTTATTGTTTTAT  
TCTTATACAATGTGTTCACTAACCAATTCTGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT  
TGAGATATGAATTCTTCCAAGTTTGTCAATTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG  
CTGGTGAATTCTCCATCGATGAAAAGAAAAAGAT'TTATTAA

YGR284C\_homolog 308aa (SEQ ID NO 362)

MSYRGNPQFGNQPPHHGIPSQPQPHIGPISSSKSPLEQFEDVAKKVEDWIDDYFKVLKPYVPAIGR  
AFLVATFYEDTLRIFTQWNEQVYYLHNYRHYWRWLTVLFLINNMVVM'TVASTLVIARKKNNIATIA  
LIVVVIQIGIGYGLLFDAQFVLRNLSVGGVLVAFSDSIVRDKRSLNMPGLPMLNNAQDNKQFFLLA  
GRILLVLLFLGFVFSSDWSLGRVFIIIIIGLTSCASIVVGKYTKFSAAIMLIVLFLYNVFTNQFWAY  
ASQDARRDFLRYEFFQVLSIVGGLLLLVNAGAGEFSIDEKKKIY

YGR285C\_homolog 1876bp PathoSeq: 1..1215, public: 1216..1876; CDS: 501..1781 (SEQ ID NO 363)

AATTATTAGTTGAAAAACAAATCATACCTATTGCCAGAGCTCAAATGAAAGTGAGAATTACGTTAT  
CTAAAAAAGCATACTTAAAGACTTTTCAAGATGAAATAAAACCTGTTATTGATCAAATTTGTGGAGG  
AAGATAACAATGGGAAACAATATGAGATTGTTGGGATTATAGATCCTATAAATTATAGAGTCTTGG  
TCACATTAATTGAAAATACAGATGGAAGCAACAAAGTCGCTAAAGGAGAAGGGTCTATAGAAGTAT  
TAGATATGTCTGCCATAAAAGAATAAAACTAACTAGACAAGTGATAGAATCTTTTTTATTAATA  
GATGCTTATCTTAGTTATGTTCCAGAACAATTCATGTTAGGAGAGAGAGAAACGCAATCACTCAAT  
TTTTGCACAAACAAAAACGAGAAGATGAAGAAGCAAAAAAGAAAAATTTTTTTTCTCAACCATCT  
TAAATCCTCCTACAAATTAATTTTATACCAATTAAGAACATGTCTATTGTATTACCATCAGGAACCTA  
CTGACGGATT'TAAAGCCGTCTCCAAATACTCTGCCCCAGTGGCTCGTCCCAATTGAACCAGTTGGTC  
GTTACTTCTTAGCCCACGCCTCAAGAATTTGCGTGGACACACTTGGTCTGAATTTGAAAAATTGG  
AAGCTGAAAAGAATGTTAAACAAATCGAAGTCAACGAAGATGAGGATT'TGGGAGATGAAGAACAAA  
GTGAAGAGTTATTAGAACACGATCCAAGAGAATGGAAGACTGCCAATTTATATGCTGTTTTAGGTT  
TATCTCATTTGAGAAGTAAAGCCACTGAAGATCAAAATCAGAAGAGCCACAGAAACAGKTTTGA

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAAACGATGGATTTTTCAAAATTATTC  
AAAAAGCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA  
ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG  
AAAGTGAAGCAAGATTTTCTACTAAACAACCAGTTCATTGTTGGGAAATTTAGAAAGCACCAAAG  
AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGAAGACTTTTGAATTCAAAG  
ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAAACGTTATATTGAACGTAAGAATATTG  
CCCAACAGAAAAGAAATTGAAGCAAGAAGATCACAAAGAGATTATCGAATTGGTCGAAAGAGCTCATG  
CTGAAGATCCAAGAATTAAATTGTTCAAAGAAAAAGCCAAGAAAGAAAAGGCTGCTAAGAAATGGG  
AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAGGCTGCTGAAGAGGCCG  
CTGCTAAGAAAAGCCGCCGAAGAAGCCGCCGCTTTGAAAGCCAACCTCTAAAAAAGCTAAAGAAGCTG  
CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG  
GTGACTCAGCTAAATCTGCCGACATTTGATGCTGATGTCGATTTGTTAATCGAAAAATTCGACGATG  
TCAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAGTGAAATCTACTTTTG  
TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCCTATTTGAAATATTTTAACT  
AGATTTTTTTTTTTGTAGGAAAATAATATATATAGAATGTAAACTATCAAAAACAATTATACAGAAG  
CTGAACCTCAACAAGACTAAACAGCAAG

YGR285C\_homolog 427aa (SEQ ID NO 364)

MSIVLPSGTTDGFKAIVSKYSAPVRRPIEPVGRYFLAHASRTLGRHTWSEFEKLEAEKNVKQIEVNE  
DEDLGDEEQSEELLEHDPREWKTANLYAVLGLSHLRSKATEDQIRRAHRKQVLKHHDPDKKSASGGL  
ENDGFFKIIQKA FEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFFEAWGPVFESEARFSTKQVP  
LLGNLESTKEEVDAFYFSWGRFDSWKTFFFKDEDVDDTANRDHKRYIERKNIAQQKEIEARRSQE  
IIELVERAHAEDPRIKLFKEKAKKEKAACKWEKESGRKAAEEAAKKAEEAAKKAEEAAALK  
ANSKKAKEAAKAAKKKNKRNIRAAVKDNVYFGDSAKSADIDADVLLIEKFDDVKLGEVADKVKDA  
DAASVKSTFVEVAKELVGAGSLDASYLKYPN

YHR021C\_homolog 1178bp public: 1..537/917..1178, PathoSeq:

538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175  
(SEQ ID NO 365)

TTTCATTTGTAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAATATATATCCAATAAGTC  
ACATCTCAAATTGGTAGTAGAAGAATTCAACCTTGGGACAGTATTCTCTGCTTAAATGAGTTTAC  
TGATCAAATAAAATATTGGCTCAACCATTGAAAAGCTATTCTTGACACTTTTTGTCAGTTTTAGTTT  
TGGTTGTTTACAAATGAAAAAATAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT  
ATTGCTTTTGAGTGAAAAGTGTACATTTGTACACACACAAACAAAAAATACTAATTCTTCCCCCA  
ATATGCTGCGTATAGTGAGAAATCTTCTTCTCTCTTGCCATACTATCGCATTTTTTTTTTTTGGTAA  
CTCACGAAACCTAATTGGAAAGAAGAAAAGAGAAAAAATAATTTTCAGTTTTCATAGATTTTC  
AGTTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTTCATTAGATTACCATGAG  
TTATGGAGGGATATTCTTGGATGATCAGAAATATCATAATATAGGAGTATACTATTTTACTGGAATC  
AAGATATAATTGAATTGAAATAAAATTTGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAC  
AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT  
TAAAAGAACAGGAAAATGAGAAGAGAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA  
TATACTTTTGGTGTGGATCCATGTGTTATTACTGAAATCATCGAAACGAATATAACCCCTCCTTTTC  
CCACATTGACATAACTCAGACACAATCTTCAAATAAAACATGTAATACTAATACTATTATTTTTTTT  
TCGTATAGGTTTTAGTTCAAGATTTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAAT  
TGAAAACCTTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA  
TCACCACTGTTTTTCAGTCAAGCTCAAACCTGCTGTCACTTGTGACTCTTGTCTACTGTTTTGTGTA  
CCCCAACTGGTGGTAAAGCTAAATTGACTGAAGGTTGTTTCATTTCAGAAGAAAGTAA

YHR021C\_homolog 82aa (SEQ ID NO 366)

MVLVQDLLHPSATEAKQHKLKTLVQQPRSFMDVKCQGCLNITTVFSHAQTAVTCDSCSTVLCTP  
TGGKAKLTEGCSFRK



125/161

YHR141C\_YNL162W\_homolog 1179bp PathoSeq: 1..1179; exon 1:  
501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)  
TTTATATTGTTTTTTTGTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTCATGTAATT  
GTGATGTATTTTTTTTGTGGTCTTCTTTGTGTTTTTGATATTTTGCAGCTGGTCGGATCATACAA  
ATTTGGAAGGAGCTACCAAAGCAGAAATGATAGCAAAAAAACAGGAGACTTTTGGAAATTTCTTG  
GTTTAGGGCTCTAGCCCTAATGCCTGTATATAATTGATTGATGCTTTAAAATTTGTGCGGTGAAAA  
ACAGAAGCGAAAAAAAAGAGCTGGAAAAGTGTGATTAACAACAACGAGGGAAGAAAAAAACTTAA  
TTAGGTGAACAAAAATTAATGTGTGAGCGTGTACATGCACAATTTTCAATTGGTTATTCTCACGCA  
CTAACAACTCAACCTCCATTGTGAGAAAAGAGATTTTTCTTTGAAAAAAATTTACATACATATC  
TTAGTTCACTAGTAACTTTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC  
AACAATGAGATACAAGATATTCTTCCAATACAAAGAGATTAATGGTGTTTTTTGATAGAGTGTAAG  
CCATGTGTTTAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGGAAATTGTCCAAACAACAT  
TGAAACGAATTTTCTGGGATAGCGTTCAAACAATCAAACCTATCCAGGTTTCTTATGACAATTAAG  
AAAACAAGTCAATATTATCAAAAGATGGAGTTTATAAGGAGAGATATTGAAACATCAAAATTTGTTGA  
AAGAAATAGCCAACTATTTGGCACCATTTCCTGTGATCATAGAAATACTAACAATCCTCTTGTGTT  
ATAGTTAACGTTCCAAAACTAGAAAGACCTACTGTAAAGGTAAAGAATGCCGTAAACATACCCAA  
CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTCGCTCAAGGTAAAGAAGATATGAC  
AGAAAACAATCCGGTTATGGTGGTCAAACCAAAACAATTTCCACAAGAAAGCCAAGACTACCAAA  
AAAGTTGTTTTGAGATTGGAATGTGTTGTCTGTAAAACCAAGGCTCAATTACCATTGAAAAGATGT  
AAACATTTCTGAATTGGGTGGTGACAAAAACAAAAAGGTCAAGCTTTACAATTTTAA

YHR141C\_YNL162W\_homolog 106aa (SEQ ID NO 368)  
MVNVPKTRKTYCKGKECRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK  
KVVLRLCEVVCCKTKAQLPLKRCKHFELGGDKKQKGQALQF

YIL112W\_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID  
NO 369)  
GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT  
TTCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGTTTTGAACGTGTTTGATTTCAGAGGAGA  
TGACGGTGCAAAAAGATCTACCACCAAGAAGCACATAATTTTTTGAATGATTTCACGAAAGAGTTC  
CATTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTTCCCGTAATGTTTACGGGAAAGCAG  
CAGGCGAAGTTCAATAATAAAAAATTGATCATCATACTAATGTGGACGTGTCAACGAAACCGGAAAA  
TATAAATAGCAGAGATAACAAAACCTGAGAAGAATATGACTTTGAGTTTCAGAGTCAACCAAAACCGAG  
TGTCGAAGAAGTTAGTAAATCTTTGAAACCAACAATTACCAAGAAAACCTTCATTCACTGATTACTT  
AAAATCTGCCAAAACCTAAGGCTAAAGAAGAAAAGGTAACAATCGAAAAAAGTGACAAAACGATTAA  
TTCAGAAGAACGAAAAACGGAACCAATTCAACAAAGCGAGCAACTTTTAACGGACAAAAAGGATAA  
TAACTGGAACCCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG  
CTGTGCCCTAGGACCTGATAAGAATACTGGAAAAAACGATTCAGATAAAATCAGAAACGACTCAACC  
AAAACCTGCCCCGCTCAGAATCATTTGCCGATACATCATTTATGTTCTCCAGTTAATGAAAGTGATAC  
TGATTTCAATTTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTCAAGTTGTGGCAGCAAA  
TGTGCTGGAGAACATTGATGAGAATGAAAATATTTTCAGAAGCTGAAACTGTTATAGCAGATGACCT  
TCCACGTCTCGATGAAGGAAAAGAACTTTTACGTGAACAAACAGCAGATGTAAAGAGACATAAAT  
GAAGAAAACAAAATTGAATACTATTTTTAGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACCAGA  
TTTCAAACCTCCAAGAACCAGAAAAACCTACCAGAAGATGACCAACATCCTGATTTTCAAAATTTCAA  
AGCAACAACAGAAATCAGTAACGATAAAAACAGAAGTAAATAAGCCAGAAGTGAAAGAGGTTGGCGA  
GAAAGAGAGAAATCACCAACTAGAAGATAGATTACCAATTAAGAAAGAGAAAATGCGGTTCGGAGAA  
TGCAAAGACATCTGAAAACGGTGTGAGTTCAAATCAGAATCTAAGATTTCAAAGTCGAAGAAACT  
ACCTTACAAAGTTAAACGTGATTCAAGTGGTCGATCATTTATACAACGAGCTTGCAAGAAGGGTAA  
TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAAATGAAAAGGATTTCTGTGGATT  
CACATGCTTGATGAGGAGCAGATTGGAAGGTCATACACAAATTTGTGAAATATCTCATGAAAAATGG  
TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGATTCCGAGACACCATTGATCGATGCAGCTGA  
AAACAACATCTTGATTGTGTTAAAGTGTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT  
TGATGGATTACCGCTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAT  
TATTCAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTCAAGTTTGT

ATCAGATGCTCCTATTGGTAGTGACCAATCATGGAGGATCCAAATGACAACCTATTTTGCAGAGCT  
 AATTAAAGGTAAGGGAATATATAAATACGCTGCAGAGAATTCAAAGAGAAAACAGCAGAATATTT  
 TGGTGGCTGGTCATAATTTAGAAGGAAAACAGATATTTTAATTTTAGCTGCTAGAAACGGCCACAC  
 AGAACTTGGTTGATATTATACTAGGGCTAAACCCCTACACCTTTTAATATTGATACCGAGTCAAGTTG  
 TGGTGTACTGCATTATTGGCCAGTATTGGACGCGGTCAATTTGAAGTTGTCGATTCCCTTGTGTGTC  
 CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAGATGGGTGAATGCTTTAGAAATTGCACAACA  
 CTCGCCACATTTTGATTACGCGGAAGTTAGTGTAATAATGAAATTCATGGAGAAGAAGAGTGGAAC  
 CAAAATTTTGTCTGGTATTCCGTCAAGGGTAGTATCTCGTGCAACATCTCGTGCACCTTCTGTTCC  
 CGTATCATCAGACGAAGATGACGTAGTGGAAGAAAAAGAAATTACAGCACACACAGAAAAATAAAG  
 TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTCAGCAATCGGAAACC  
 CCACGAGTCTACAGGTCGAAAACCTGAAAAGACTCATAGCAATGAGGAAAAGAAAGCGGAAACGTGA  
 ATGGTCAGACGATGAACCTAAAGAACCACATCTTTTGAAGAAGTCAAAGTCTGATTTGAAATTGAA  
 ATCACTACATAGAGAAATCACTTCTGATGATCACCACACCCAGTGAAGCCATTTCAGATTCCTTTGC  
 AGAAAAAAGAAAAACATTTATCGGCAACGCCACCTGCTCCTCCGCCACCACCACCACCACCTTC  
 TCAAGCAGTTATCAAGGCACAAGAAGAACAAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA  
 AGAAAAGGTGAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAGAGAAAGA  
 GCAGAAACGGAAAGAAGAAGAAGATTGCGAGCACAAAGAAAGAAACGAAATGCCCCAAAGCAAAACA  
 GGAAGAACAGGAGAGACTTGCTAGAGAAGCAGAAGAGAAATCGAAAGAACTAGAAGAAAAGAAAGT  
 GGGGTTCGACACAGTTGACATTAGATCATTATCCGGTTGGATTGCGTTATTGCAAGTTTGATGG  
 AAACCCAAATATCTCGGCTGTTGATAAAATTTTGCCTTTCTATGTATTTGTAATCGACGATAAAAA  
 GTATGCTGTTGATTGCAAGTCTCCTTGATCACGTCAACGGTTGTCAGCAAGGTTATCAATACTGT  
 ACAACCTCATCAGAAGAGAGAAAAATAATGCAACTGAAAAAAGCAAATTGTGGAAGCTCTTTTTCAA  
 GTTTATTGGTATTGATCCTAGGAATCCAAATTGTGATCAAAGAAGCTCAATAACAAATGGTCAAAA  
 ACAGTTTCAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTAAAGGAATT  
 TCCAGAAGTACACTCAAAGCAAAAAGATAACCAAATTGATGTTAGTTTAGAGTCTTTGAGTGGGTT  
 TTCTGATTGCGTCAAGGATGATATAATAGTTGATGGAAATCTTGAAATTGATATTGATTCGAAGAA  
 AATCGAAAAGTTTATTCCTCCTCATTTGAATAC'TAGGAAAGACATTATTAGGACTGTCAGTACTTT  
 AGCACACCCACTATGGTGA

YIL112W\_homolog 1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKKTSFTDYLKSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ  
 SEQLLTDKKDNKSEPNSEVNLKDNNDISKATAGCALGPDKNKTGKNDSKSETTQPKLARSESFADT  
 SLLSPVNESDTHDFNFELAEIPEAKDGSVVAANVSENIDENENISEAETVIADDLPRLEDEGKKLLR  
 EQTADVRRHKLKKTCLNTIFSSDEEEEEIEQPDFKLQEPKLPEDDQHPDFQNSKATTEISNDKTE  
 VNKPEVKEVGEKERNHQLEDRLPIKKEKMRSENAKTSSENGVSSKSESKISKSKLPYKVKRDSGR  
 SLLQRACKKGNFADVQDYIERGASANEDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG  
 DSETPLIDAAENKHLDCVKVLLENDADPTIFNIDGFTALTAKIYNEHEGEEGYDEIIQVLEEATANY  
 NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKGIKYAAENSKEKTAIEYFVAGHNLEGGPD  
 ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVVDLSLSKGADPFKTRKK  
 DGLNALEIAQHSPhfDSREVSVMKFMKKSGTKILSGIPSRVVSRASTRAPSPVPVSSDEDDVVEE  
 KEITAHTENKSAEKKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDPEKPHL  
 LKKSksDLKLKSLHREFTSDDHHTSESHSDSFAEKRKHLSATPPAPPPPPPPPPPSQAVIKAQEEQK  
 IKDAEEARLWQEKVEAKKRARREMLKSEKEKEQKRKEEEEELRAQEEKRIAKAKQEEQERLAREAE  
 EKSKELEEKVGLRQQLTLDHYVPGLRYCKFDGNPNISAVDKFLPFYVFVIDDKKYAVDLQVSLIT  
 STVSKVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCQRRSSITNGQKQFQNLHLHFVE  
 VDLAEEFLKEFPEVHSAKDNQIDVSLSLSGFSDCVKDDIIVDGNLEIDIDSKKIEKFIPPHLNT  
 RKDIIRTVSTLAHPLW

YIL148W\_YKR094C\_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCCTCACTCATGATTGATGTATTTGCCCACTAAAAAGAAAACCAAT  
 GAAACAATAAGATTGATTGATAGATTTGGTTGTAATTAATCTGATGCTTTCAACATTTGTTTTTGT  
 TCGTGTCTCGGTCAATTGAGGTTGGGTAAATTGTTTTTCTTTTGAAGATTGTGAGCATGCAATGTG  
 CATGCAATATGATGTCGCTCAATTGCGACATACTACTTAGGGCTATAGACCTATTGCACGTGCGT

TAGTTTTAAACCTAAAAAACAATTTTGTGCGAGTCGTGCACCATTTCGTTCTATTTTTCTACTGTGA  
TTGACGTACAAACCTTCACAGTTCACGACACTTTTGTGCGATTCTCAAACCTCTCTCACAGGCTTG  
GTAGGAATGAAAAAATTTTGGTAAAGGCGAAAAAATAAACTTGAATATTTTGGAAATC  
CCCTTTTTGATTACTACAATAGATTAAAGTAACTAAAGATGATTGAACCATCCTTGAAAGCTTTAG  
CTTCAAATAACAACCTGTGAAAAATCCATTTGTGCGTAAATGTTACGCTAGATTGCCACCAAGAGCCA  
CCAACCTGTCGTAAGAGAAAGTGTGGTCACACCAATCAATTGAGACCAAAGAAGAAATTGAAGTAG

YIL148W\_YKR094C\_homolog 52aa (SEQ ID NO 372)  
MIEPSLKALASKYNCEKSICRKYARLP PRATNCRKRKCGHTNQLRPKKKLK

YIL150C\_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:  
501..2294 (SEQ ID NO 373)  
ACTCAGCCTTTTGAAATTCACCTTTTGGTAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT  
CTAACTCCATATTGTTGTTCCCTACCCTCTTGCATAGAGACTTTGATCGTGACATTTTGTAAAGTGG  
TAGAGGTATGGGTAAAGATTATTTTCACCACCGTTTTCCTTTAGCAAATAGTCTAAAGCATTTTCTG  
AATTGTTGAGTTTCGGTACATCATTAGCTATCTTTGTGACAATTGATTTGCTTCTACCTCTAGTCA  
TGGAATAACAAGTTAACAGCGTGTTTTGTGTTGGTTTGTGGAACAAATAAATTTGTGGTGTGTAAT  
GTGTGTGTTTGTTTTTTTTTTTTACCAGCATTTTGTCTTGTTCATAAAATGAAACAGCGCAATGAT  
TCTTTTCATAGTTTTTTTTTTTCCATACATAACTTCTGACGCGTGCACTATATCTGCTAACATACTC  
GGCAACAACAAAGAAAGAGAATTTGAACCTAATCCGAAGATGAACGACCCAGAGATGAACAAATTG  
ACTCCGATGATGTATTAAACAGAAGATTCTATCTGATGAATTGAAGGACTTGGTGCAGGAGTTGAAT  
TGAAATATGCAGAATTAAAGAAGAACAAGCCTTGAAAAACGTCGTTACAGTCACCACTGGAAG  
ACATGCTGAATAAACAGAAACCCCATCAACCGGAGGTCCCAGAACCCAGAAAAAGCTAAAGTCC  
ATTTGGATAAGGTAGTAGAAGAACCAGCAAGAAATTTTACCAAGAAGGAGCCTCGGGATTTCCA  
AGATAAAAGAATCAAACCTTCTTAAACAACCTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG  
CCCATAAAATAGATTTTCAGTAAAGAAGGTTTGAGTTTCAATTGGATAAGTATACCTTTACGCCAA  
AAGACGTTGTTGATGATTTAGAACCGATATCCAAGCTTTACTTGCGCAGAAAGATACCTTGCCCAAC  
TGCAAATTGCCGACATTATTGCCGAACTGATAGCAACATGAAATTCCTTAAATTTGACAAGTTTT  
TAGCGAAAACCCATAAATCAAACAACCTATGCTGAACCCAAGTATTGTAATTGGTGTCTTGTTCCT  
TTGTGGTGCAGCAAGGACCCAGTGCAAGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGTTG  
GAAATTTTATGAATTCCTGTAGACTTGATGCTTTTTGATAAGGCTTTTCAGAAAAACGGGAAATCC  
AACCGGGTGATTTATTATTTCATTTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG  
GCCAGTTTCAGTCTGGGTTCAATTTGAAAGTAGAAAAACACCAATGTGTCAAGTATTTTAGAGATAG  
GATCGTTAAGAGATTTTGGGTTTGGCAAGTTTACTAGAAAGCTAGATAATAGCAGATGCAAAAGGG  
CCATCAACACAAGGACGCAAGAATTCTGCGATATACATTTGGATATGAAGTTTAAGTCTAGTACAA  
GAATGGAATTAAATGGAAGTGTTCGATTAGATCCCCGCAAAAAACAAGAAAAAGATGTACATGA  
ATAAAATGGGTCTGGCTTTATTAAGCAATATAACGAGGAGAGTACTGTTATAGGAACAAGCTACG  
GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAATCAAGCGGCGCA  
AACTAATAGACGACAAGGCAAAGGAGATGCTTGAACAAAAGCTATCGAAACTAGGTTCCGGCTTCAT  
TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCGAGTGATCGTCTGAAGA  
GCAAAGGATTCACCAACACAATGATTTACATATTGGGTTTGATCCAACAGGTACATCTTTGAACC  
AAAATAGTACCTTGCTTGGCAGCAAGCTGATGGAAAAATCTCGAGCACGGGAATTGCATGATTTGA  
GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA  
AATGGAACACGAATATCAGAACTTTACAAAATTACGATCGACGAGTTGCCAGCCACTCCTTGAGTA  
CCTCTCGTTCGGTTACAGAATCTTGTAGGAAAGCAACACACGCTACACTAGTAGATAAAAGGAAAA  
GAGTGGTTGTCTCAGATGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT  
TTGACGACGAAAAGTCTAAGATGTCTACATGAAAATGACTGGAGCCAGGTAA

YIL150C\_homolog 598aa (SEQ ID NO 374)  
MNDPRDEQIDSDVLTEDSSDELKDLVQEFELKYAELKKNKALKKKRRSQSPSEDMSNKQKPHQPEV  
PRTPEKAKVHLDKVVVEPKQRIFTKKEPRDSKIKESNFLNKLYETSNKHDKEDAHKIDFSKRREFE  
QLDKYFTTPKDVVDDLEPISKLYLRRRYLAQSQIADI I AETDSNMKFLKIDKFLAKTHKSNNYAEP  
KYCNWCLVAFVVRKDPVQVAANNSKYIKLVGNFMNSVDLMLFDKAFQKNGKIQPGDLLFILNPLI  
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGCKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFKSSTRMELNGSVSIRSPOKNKKKMYMNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK  
VLQNQIKRRKLIDDKAKEMLEQKLSKLGSASLLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG  
FDPTGTSLNQNSTSLGSKSMEKSRARELHDLVSVETSGHKSLSSSKQDRQSKVAKWNTNIRTLQNYD  
RRVASHSLSTRRLQNLVKGQTHATLVDKRKRVVVSDDEQPGMEEDEEDIEIQFDDEKSKMSYMKM  
TGAR

YIL167W\_YIL168W\_homolog 1499bp public: 1..1499; CDS: 501..1496  
(SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTGGTTTCGTTTAGGTG  
GCATCAAGGTAAAGGAGGGAGTTTGGTATAGTTAGGTTTTTGACTTATTTCCTTTTTGTAGTAGA  
TATAACAGAACTACCAAAAGTGAGCCACATCTGTTAATCTTGAAAAGCAAAATTGAGAAAACCAT  
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GTAGCCGACGTGGGTGAANAATATATATTTAAGTATATAAGATCAGGTCAATATAAAATGTTTGA  
AATATAACAAAATGTTCAATGTAAACTGATGGTTAAGGGATTATAAATCAAACAGTAGTGCTT  
TTGTTCCATAAAAACCCATCGTGGTGGTAACGTCAGGAGACCGGACATCAAATGGAATTCACACA  
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AGCAGCCCTCCGGCAGTGTCAAATTAAGAGGCATGGGACACTTGGTTGGCCAGTCTATAGATGTGG  
CCAGAAAACCTTGGCAAATCGAACGTAGCAGTTTTTTCGTCATCTGGTGGTAATGCAGGATTAGCAG  
CTGCTTATGCCAGCCAGTTTTTTTGGAGTATCGTGCACCTGTGGTGTTCCTGAAAGTTGGAAGCCAA  
CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG  
CCGATAACTATTTAACTGATTTTTGTTATTAATAAATCTTGACAAAACAGTCTATCCGGTCTATTGTC  
ACCCTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAAATCATCGATCAAA  
AGCAATTACCCAACCTTGATAAAGTTAAGGGGGTCATTTGTTCCGGTAGGAGGGGGTGGCTTATACA  
ACGGAATAGTTGAAGGTTTGGAAAATCATAAGGAGATACCAGTGTGGCAATTGAAACTAAACAAG  
CGGCCACGTTTACGAGGCGGTCAAAGAAGGTAAAGTTGTTTCAATTTACAAAAGTGCAAACTTTGG  
CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAATATATTGAGCGTCTTACAG  
TTCTTGCTGAAATTGATGACTTGGACGCTGTTAAAGGTGTTGTTGATGTATACGACCATTTCGGAT  
ATATGGTTGAGCCTGCATGTGGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA  
AATTTGGTACATTAAGTCCAGATGATATTATCATTTGTTGTCATATGTGGTGGATCGGCTATCAACA  
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAGACTCTTGA

YIL167W\_YIL168W\_homolog 332aa (SEQ ID NO 376)  
MKEPSITTTTVEVTDKLPKPPCRVFFKNEYEQPSGSVKLRGMHVLVGQSIDVARKLGKSNVAVFS  
SSGGNAGLAAAYASQFFGVSVTVLPSSSKPTVIEKLKSLGADVIIHGKHWEADNYLTDFVIKNL  
DKTVYPVYCHPFDDPLLWEGHSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI  
PVLAIETKQAATFHEAVKEGKVVHLQKVQTLATSLASPYLSSKALANYIERPTVLAIEDDLDAVKG  
VVDVYDHFHYMVEPACGASVASVMHRQDLLNKFGLTSPDDIIIVVICGGSAINKYIIDEYRSLEK  
DS

YJL034W\_homolog 2564bp PathoSeq: 1..806/1401/2504, public:  
807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)  
TTTTTGAAACAGAGAATGAATGAACAATTGATGACCATAGAAATGAAGTGAGAACACATAAATCT  
GCGACACTTCACGTGATAACAACAAAGTGACATGAACAACAAATGTCGTTTGATATAATTTGCGACA  
TTTGTGTTCAAGCCAAAAAAGAAAGACAGAAACAGAAAAAAGAAAAATCTCAAAGTTGCCACGT  
AAGCACAATTAATCTTTTATGGTTGTAACATTTCTAGTATATTCTACGTAATAGGTGAGGTCCCT  
ATATGCAGTACACACAGGTTTTTTTCACAGATGTTGACACAGTGTGAAAATTATTCACGTTGATT  
TATAAATATACAACCTTACCTTCCACGGTTTTTTTTTTGATTTTTTGATTTTTTGAATTCCTTTCT  
TTTTTTTGTCAATTTATTTATTAACAACTTCTCTGTAATACTTTATTTGATAAATTTTACAAGATT  
TAATTAGATCAATTAGATTATAGAATCATTTCAATATAATGAGATCATCACAACTCTCTTGGTTAC  
CACGTATTGGTTTATTATATGTGGCGTTAGTTATACTTATACCATTTTGGTTTTCACCGAAGCACG  
CATTTGCGGTTGCTGCAGTGAGCGATGATGAATCCTCGACAGATAATTATGGTACAGTCATTGGTA  
TAGATTTGGGTACCACTTATTCCTGTGTGGTGTATGAAAACGGTAAGGTTGAAATTTTGGCCA  
ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

ACGCTGCCAAGAATCAAGCTTCCTCTAATGTCAACAACACTGTTTTCGATATTAAAAAGATTGATTG  
GTTTGAAATATAATGATGACACTGTGCAAAAGGAACCTTAAACATTTGCCTTACAAAATTGAAAATA  
AGGGTAACAAACCAGTTGTAAAGTTGAATACCAAGGTGAAGAAAAAACTTCTCCCCTGAAGAAA  
TTTCATCTATGGTTTTGGGTAAAATGAAGAGTATTGCTGAAGATTACCTTGGCAAAAAGTTACTC  
ATGCCGTTGTCACCTGTTCCAGCTTATTTCAACGATGCTCAAAGACAAGCTACTAAAGATGCCGGTA  
CTATTGCTGGTTTTGAACGTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCCTATGGAT  
TAGACAAAAGGCGACCAAGAAAAACAATTATTGTTTACGATTTGGGTGGTGGTACTTTTGATGTTTT  
CTTTATTGTCCATTGAAGGTGGTGTTCGAAGTCTTGGCTACTGCTGGTGATACTCACTTGGGTG  
GTGAAGATTTTGATTTCAAGATTGTCAGATACTTGGCCAAACAATTCAAGAAGAAGCACAATATTG  
ATATCACTGCCAATTCTAAAGCCATTTCCAAATTGAAGAGAGAAGCCGAAAAGGCCAAGAGAAGCTT  
TATCTTCTCAAATGAGTACTAGAGTTGAAATCGACTCCTTTGTTGATGGTATTGACTTTTCTGAAA  
CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTGCTGCTTTCAGAAAGACTTTGAAACCAGTTG  
AACAAGTGTGAAGGATGGTGGTGTCAAGAAATCCGATATTGATGATATTGTTTTGGTTGGTGGTT  
CCACCAGAATTCCAAAAGTTCAAGAAATTATTGGAAGGATTCTTTGATGGTAAAAAGGCTTCTAAAG  
GTATTAACCCAGATGAAGCTGTTGCTTATGGTGCCGCTGTTCAAGCAGGTGTTTTGAGTGGTGAAG  
AAGGTGTTGATGACATTGTTTTGTTGGATGTTAACCATTGACTTTAGGTATTGAAACTTCTGGTG  
GGGTTATGACCCTTTGATCAAGAGAAACACTGCCATCCCAACCAAGAAATCTCAAATCTTCTCAA  
CTGCTGCTGATAACCAACCAACTGTTTTGATCCAAGTCTATGAAGGTGAAAGAACCATGGCTAAAG  
ACAACAACAGATTGGGCAAATTTCGAATTGACTGGTATTCCACCAGCTCCAAGAGGTGCCACAAA  
TTGAAGTCACTTTCTCATTGGATGCCAATGGTATCTTGAAAGTTGAAGCTGCTGATAAGGGAAGT  
GTAAATCTGAATCCATTACTATCACCAACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA  
TGGTTGAAGAAGCTGAAAAATACGCTCAACAAGATCAAGAATTGAAAGAAAAGATTGAAGCTAGAA  
ACTCATTAGAAAATATGCTCATGTCTTGAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTTAG  
GTTCTAAATTTGGATGACGATGACAAGGAACTTTGGATGACGCTATCAAGGAACTTTAGAATTTA  
TTGAAGATAACTTTGATACTGCTACTGCTGAAGAATTGGAAGAACAAAAACAAAATTAATTGACG  
TTGCAATCCCAATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG  
ATGCCAAATTCGGGTGATGATGATTCAGATGATGAATTCGATCACGATGAATTGTAG

YJL034W\_homolog 687aa (SEQ ID NO 378)

MRSSQSSWLPRIGLLYVALVILIPFLVSPKHAFAVAASVDDDESSTDNYGTVIGIDLGTTSVGVGM  
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAAKNQASSNVNNTVFDIKRLIGLKYNDDTVQKEL  
KHLPYKIENKGNKPVVKVEYQGEKTFSP EISSMVLGKMKSI AEDYLGKKVTHAVVTVPAYFNDA  
QRQATKDAGTTIAGLNLVRIVNEPTAAAIAYGLDKGDQEKQIIIVYDLGGGTFDVSLLSIEGGVFEVL  
ATAGDTHLGGEDFDFKIVRYLAKQFKKKHNIDITANSKAI SKLKREAEKAKRTLSSQMSTRVEIDS  
FVDGIDFSETLSRAKFEELNIAAFRKTLPVEQVLKDGGVKKSDIDDIVLVGGSTRIPKVQELLE  
FFDGKKASKGINPDEAVAYGAAGVQAGVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI  
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNRLGKFELTGIPPAPRGVPQIEVTFSLDANGIL  
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEAKEYAQDQELKEKIEARNSLENYAHVLRGQ  
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFDATAEEFEEQKQKLIDVANPITAKLYGGA  
AGEGAGGAGDAKFGDDDSDEFDHDEL

YJL035C\_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:  
501..1343 (SEQ ID NO 379)

GCCCCATGGTGACAGAAAAGTATTGATCCAGGTTTCTTTGAAGGTTTGTAATACGTTTAAACTTG  
TGACCTAACTCATTTTCATAAAATTCTTGTATAAAATTGGTTTCTTTGAATTGTTTGTAATCTCTT  
AAGATTGTCTCGTCTTCAGTGTTCAGTGGAGCTGCTATTGCCAGTCGGCGGCATAACAGCAGGT  
TCTGGTATGTCTATCTTCTACTAAGCCGGACAATCCCAAAGCCGCTCTTTGTTCTTTTATTCTT  
CTAAGGAATGCTTTATGTAGTTCTGACATTCTTGCGTAAAAGGAAGTACAGTATTAAAGCTCGAAA  
CTCAATTGCAACAAAAGTCTTAATTTTTCTTCTATAAGTAATTGATCTTGGTCCCCCAACAAAA  
AGATACAGAGGAGAAAAGGAGGGCCTTAGGCTGACAGAAAAAAAATTTAGTACCTGGCCACACAG  
TAGCTTCCAAACCATATATGATTTGATGAGTGTGAAGTATGCTGACAGATCTTACTTCACACTTTC  
AGTACATGGCTATAAGCTTGTTCGCGTTACAAAGCCTTACTAAATAATGAGACACCAGTGTCTAT  
GTATAGTCGTGGATTCAAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCACTCTC  
TAAATGGTACACAACACGCAGAATTTATTGCTTTACAACGATTTGGGGAACAAAACTGAGTATTG

130/161

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC  
AGTTGGGCATCAAAAAAGTAATATTTGGTTGTGGGAATGATAGATTTCGGAGGAAATGGTACCATT  
TATCAATACATAGTGACATCACCTTGCCTAACGCAGCTTATTCCAGTATCGGGGGTATATGTAGGA  
CAGAAGGAATCCAACCTATTACGAAATTTTATATTCAACAAAATGAGTCGGCACCAAATCCAAAAA  
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTGTAGCATTTCAAAGG  
ATGAATTTATAGAGTTTACGGAAATGAAAGAGTGCATATTTACGATGGGAAGATTTTGAATCA  
CTCCATTACAAAACAAGGGTTATGATATAAAAGAATTGATATCGTTGGATATGATGCAAAAAAGTTC  
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAATAATTGAATTTCACTATTTT  
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAACCAATAGGCAATATAACAGTAAAAAGA  
GACACTTTGCAAACGATGAAGAATAG

YJL035C\_homolog 281aa (SEQ ID NO 380)  
MSTDLTSHFQYMAISLFVGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ  
RFGEQKSSIDYNDLILYVTVEPCIMCASYLRLGLIKKVIIFGCGNDRFGNGTILSIHSDITLPNAA  
YSSIGGICRTEGIQLLRNFYIQNESAPNPKIKKNTDIESKEYPENQFCSISKDEFIEFYGNERNVH  
IYDGKIFEITPLQNKGYDIKELISLDMMQVPFLEDELGQITDEQIIIEFHNLFNINDDGTVNYKK  
PIGKYNSKKRHFANDEE

YJL180C\_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;  
CDS: 501..>1502 (SEQ ID NO 381)  
CTTTATCTAATTGATTTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCACAACCTTGCC  
AAACTTTTTCATTTGATTGGGTATTACATATTTTATTTAATTTAGCATTTGTAGTATCAATTATTG  
TTAAATTTGTCATGGCTCGATCAAGTTGTAAATTACCCATGGATAATTCTGCTTGAGATTTATTTA  
ATTGATTATCCATTTCAAGTAGGACTTTTTTGTAAATGCTTCTTGATTCATGATTAATGAGACGAGT  
GTGTGTGTATGGGCGATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG  
AAAAATATACAATCTATAATCAGTATGTTTGGAGAAAAAATAATTGAACAGAAAGATTCATCCTTTTGA  
TCAAACGAAATATATCTTACCATCCCCCCCCCTCCAAATGCTTAGATTTACTAGGACTACTGCTT  
GGAAATTAAGATCTATTCCAATTGCCACTATTCAATATAGACAATTTACTTATTCCACTATATGTT  
ATCAATTAAAAACCCTTACTCCATCTTTAGGAATAAATAATACCAATTGAATCCAATATACCTTCAG  
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AATTACCAATCAATAAAAAACAATTGGCATATTTAATTGCTCATGAATGGACTCATTTACCTGATA  
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AAATGTTAAGATATCTTGATACTGATACTTGTCTTATATTTGCTACCAACAAAGAATGTGATGGTA  
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ATCAATTACCAATTTATGATTTAATTGCCTTGGAGAAAAACAATCTTAACTACTAAATCATTTTTTAT  
GTGGAATTACTTTATTAAGATCAAATGTTAATGATATTGAAACTTTAAAAGAATTATATCAATTTA  
ATAAAAATTCATTGATGAAGATTATTATCATAAACTTTAGAAGAATTAGTTGAATTAGGAAAT  
TAGAACTATTTATCAAACTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C\_homolog 334aa (SEQ ID NO 382)  
MLRFTRTTAWKLRSIPIATIYQRYQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW  
KKGEVKNFNNETQKYEIQLDGKTLRTPPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSLTPLTAL  
ATRAIDLSQQHLSDMKTEKAEEMLALEDIKLQMLRYLDTDCLIFATNKECDGKLKRQEEIYRPL  
INEFNEFFTIIYAHNKNLI PRQKSIELKYLDCE TDGLRGNKQDETTQLVLDWLNQLPIYDLIALEK  
TILTTKSFLCGITLLRSNVNDIETLKLKYQFNKNSIDEDYYHKTLEELVELGNLETIYQTEEWGEV  
EDTH

YJL187C\_homolog 3689bp public: 1..452/3414..3689, PathoSeq:  
453..3413; CDS: 501..3686 (SEQ ID NO 383)  
TATTTATATATAATCTAACAACAAGTACTATCCCTTAACCTATTAGCTCAATGTCATTCTTCATTA  
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TAACTGTATTGTTGGGCTGACAGTAGAGTATTGCGGTCATTTTATAGGAGTGATTATAATTCTCTGT  
GAGAAACGCAAGCAACAAAAAAGAACAAGGAAACACAATCATGATTAATTATATTAATAGTAGA  
AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAACAATCATCCAAAGTTTAAA  
CAAAGTATTTCTTTTTTTTTTCAATTTTACAACCAAAGATAAAATACTACACAACACCCAACATTA  
CAGCCAAAACCACATATCTGTGCAATATTTACGCTCCAATGGATTCAAACCCGTGTCAAGACGTAT  
CGGGTGATACCAGTAGCACACCAATGGCCAACAATAATCCCCTAATGACAGCACAAATCTCCTCTC  
AGAACCATTCTAAAACTGGCTTGAGAAAACACCAACAACAACACTACCACCAACACCTGCACCTGC  
AAATGCATTCTCATTACAGCAGTCACCTTATATTAATCAATTGGAATACTTTACCAATAACCAGT  
TTTCACGCTCTTTCAATAGTTTAATTTTGGAGGATGCCAATGATGCCAACACCAACAATAGTTCAA  
CAACAACCTTAAATAAGAAAACCATTAACAAGTCACCACCATTCATATCAAGCAGGACTTATTAA  
ACGATAGTATCGACACGTTTCTTGATAACTCCAACACGGAAACGATAGAAGATGGAGACGTCACAA  
CAACAGACGACGATCACGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGCAGTACACCC  
CAACTTTGAATATCTTGAAATCCAAAAAAGTCGATAGCTTCAATATTATATCTAGCAAGCATAGAA  
AGAGCAATAGTCAGATTACCTACAATCTGCACGTACGGAAGCCATCCGAAGAAGATACGTCATCAT  
CGATGGCTACAATAAGGTTATCTAACAACCTCACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA  
ATTTATCTATTGATTCCAATTTGAAAACGGTTGATGGAGGTAAAATTCCCAGATGAAATAGATGACA  
TTAGTTTGAACGAAATAGATGTTGCAGTGGCACCTAACGATTTTTCATCACCCTATCAGCAAGAA  
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ACAAGTTGGTTAGTCAATCGCCTTCCCCGTCGTCAAAGAATAAGTTTTCGCATATCATCATCAACCA  
CATCTTCGCCACAGTCTAACTTGCATTACCTTCCAAGTTGGGACTGAAAGGATTCAAATGTTTA  
AAAATGCAAATAGAGACGCGATAATGTGCTCAAGCAGAGTTATGACTCCAGAAAAACCGAAAATGG  
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CAAATCATGCTAGAAAATCTAGTAATCCAATACCATACCCTCCGACCGAACCCTACCGACAAATA  
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GTCCCTTATTTGATGATAAAGAGAATAAAGCTTCTTATCAGTTTGTAAACCATTGCAAACAGCTT  
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TCAATAACACAAGTTATATCAAAATTTTCCCTTCTTCCGAATTGAAAAAGGAGCAGGTGCTTCAGC  
GACCACAAGAAGATTTAGAATTAGTTTTCATTTCTGACATTGAACTAGATGATAACATAATACCAG  
AAACACCAACAAAGAACTGCTACTACCGAATCAGCACCATCAACATCACTTACCCCTTACACGC  
AATCCAAGAGTCCATTGTTGAAGTTTGACACTGAGAAAGATGGAAGAAGGAATTTGTCAAATAGTCT  
TAGATAAATCAAATGCAACTAAACGAGAAATTAGCGAACCACCTTCAACACCAATCAATATGTCAT  
TTGCAAAGAATAGTTTAAAGAAACCTATGAATAATGCTGAAAGAGGTGATGACCCTGATAGTATAA  
TTGCTCAACGCATAGATATTATGCCATCGTTAGATGAAGTTGACTCAGTGTCTGTTTATCCTTCAA  
AGATAGATGAACATTTAATTGAAAAGTTTGGAAATGAAGAATATCAAGTATATTGGATCGGGAGCAT  
TTTCCATTGCTTTTGAATGTTTATTTAATAACGAAAAGTTTGCTATCAAAAGAACTAAAAAACCAC  
TTATTGGAAAATTGGAGAAAACAAACTATAAAACGAGAAATTGAAGCATTGAGAGTGTTGACAAGCA  
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TTGAGGCCCTGGGATTTTAAATAATTACTACTATATAATGACAGAATTCTGTGAAGGTGGTACATTAT  
TTGATTTCTTAGAGGAAAATAAACATTACAAAATTGATGAATTTAGAATTTGGAAGATCCTAATTG  
AAATTCATAATGGGTTAAAATTTATTCATCTGAAAAATTATTTACATTTGGATTTAAAACCAGCAA  
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GATTATCAAGTGATAATATTTCAATGTTTTTACAACACAATCCAAATACCAATAGCAATATCAGTG  
CGAGTGAAGTAGAAGTGGTAGTGGCAGTACAGGAGGCAATGGTAGTGCTGGTGATTGA

MDSNPCQDVSGDTSSTPMANNPTNDSTISSQNHSKTGLRKHQQQHYHQHSHSQMHSQSQQSPYIN  
 QLEYFTNNQFSRSFNSLILEDANDANTNNSSTTTLNKKTINKSPFFNIKQDLLNDSIDTFLDNSNT  
 ETIEDGDVTTTDDDDHDFDEDEDIEDPEAVQYPTTLNILKSKKVD SFNIISSKHKRSNSQITYNSHVR  
 KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSDSNLKTVDGKIPDEIDDISLNEIDVAVAPN  
 DFSSPLSARKPDIFAAITAANGNSNNQFKRPHKLVSQSPSPSSKNKFRISSTTSSPQSNLHSPSK  
 LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVS KIFGKS AKIRRAYTPHTSTPMAVSSLNPPSSS  
 TSNSTTAAITSTSPAAD EHYDIDNDCDSPSKNRKSSNISASSIIYQDENHIKSNHARKSSNPIPY  
 PPTLEPLTNISASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS  
 GSSDRKLPPETPIKRNPLMILNTNKVVPYSSGFAEGKDVMDQHDYSHIPCQNRFPQSVNPNT  
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 IELDDNIIPETPTKKSLLPNQHHQHHLPLYTQSKSPLLKFDTEKDGRRLNSIVLDKSNATKREISE  
 PPSTPINMSFAKNSFKKPMNNAERGDDPDSIIAQRIDIMPSLDEVDSVSVYPSKIDEHLIEKFGMK  
 NIKYIGSGAFSIAFECLEFNNEKFAIKRTKKPLIGKLEKQTIKREIEALRVLTSIKED EATNMQEQE  
 EGKEYLVYFIEAWDFNNYYYIMTEFCEGGTLFDFLEENKHYKIDEFRIWKILIEILNGLKFIH SKN  
 YLHLDLKPANIFITFEGLKIGDFGLATKLP ILEKDFDLEGDRNYIAPELINDKIYTPFADIFSLG  
 LIILEIAANIILPDNGTPWRKLRSGDLS DAGRLSSDNISMFLQHNPNNTNSNISGSGSRSGSGSTGG  
 NGSAGD

YJL189W\_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:  
 501..506; intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)

AGTCAAGAATTTTATGATGACTTTGGAGGATGGTCTGATTAAGACTTGTCTTTTACCAGTTTTTTC  
 AGCATTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGTTGAATTGTCTGT  
 TGATAAAAAGAAACCGTGAAAAGGAAGTATTGTGAAAAATCGATTGATATTTTTTTTTTTCCTCCT  
 TCCTCACTGTAAACAGTAGTAAACACACTAGTTACAACATGATGACCTGCATATTATAAATCTTTCTG  
 AAAAAATTTTTTCCCTGTATTTTGTAAATCTTTTCGCTCTTTCTCACTCACTACACTTATTAAT  
 GAATGAAAGGTTTGGTGTCTACAACTCCACTAACAAAATCTCACTCCTGTGCCTAAACACACACA  
 GACCCACACGCAAACCTTTCTCTCAGAAACAGAAAAAAAATTTCAAGCAAAAATTTTTTCCATC  
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 AATGATGTCTTTCACTCTTTTATTGGGTGATTATTATAATAAATGGCAGATGAGAAATATATTGGA  
 TAATAAACCTTGCAATGAAATCAGTTGACCATTTTGAAATAATGGACCATTAGCAATACCCAGAT  
 TGCTGGAACAAAGACGAGAGAACTAGACAACCTCAGATATAATAGAACATCCATACTAAGTTCACTC  
 ATTTCTTATAGTCTCAAAAATCATTCAGAACTAAACAAAAGTTAGCTAAGGCTCAAAAAGCAAAACA  
 GACCATTGCCACAATGGATCAGATTGAGAACTGACAACAAAATCAGATACAATGCTAAAAGAAGAC  
 ACTGGAGAAGAACTAAGTTGGGTATCTAA

YJL189W\_homolog 51aa (SEQ ID NO 386)  
 MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRD NKIRYNAKRRHWRRTKLGI

YJL190C\_YLR367W\_homolog 893bp public: 1..893; CDS: 501..890 (SEQ  
 ID NO 387)

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 AGAGAAAGGTTTGCCTGTGGGTCTGTGTGTGTTTAGGCACAGGAGTGAGATTTTGTAGTGAGGTT  
 TGTAGACACCAAACCTTTTCATTCAATTAATAAGTGTGAGTGAGTGAGAAAGAGCGAAAGAATTACAA  
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 GTTTACTACTGTTACAGTGAGGAAGGAGGAAAAAAAATATCAATCGATTTTTTCACAATACTTC  
 CTTTTACGGTTTCTTTTATCAACAGACAATTCAACCATGACTAGAACCTCCGTCTTAGCTGATG  
 CTTTAAACGCCATCAACAATGCTGAAAAAAGCTGTAAGACAAGTCTTAATCAGACCACCTCTCA  
 AAGTCATCATAAAATCTTGACTGTCATGCAAAACACGGTTACATTGGTGAATTCGAATACATTG  
 ATGATCACAGATCCGGTAAAATTTGTTGTTCAATTAAATGGTAGATTAAACAAATGTGGTGTCAATC  
 AACCAAGATTCAACGTCAAAATCAACGACATTGAAAGATGGACTGACAACTTGTTGCCAGCTAGAC  
 AATTCCGTTTACGTTATCTTAACCACTTCTGCTGGTATCATGGACCACGAAGAAGCTAGAAGAAAGC  
 ACGTTTCTGGTAAAATCTTAGGTTTCTGTTTACTAG

YJL190C\_YLR367W\_homolog 130aa (SEQ ID NO 388)



CAACGACAACAACAATAAGAGAAGAACTCTTTTCCAGATAATTGTAAAAATCCTTTATATTAATGTTTAATA  
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CTTATCCTTTCTGTAATTTCTTGATCTCTGTTTGAATCAACAACGCTTTGTTTTCTCTTTCTGCC  
TCCCTCTGCCACCCCAAGTTTATTTGTTTGCTTGTGCGACGTGCTGCCAAAAAAAAAAATTGAGTTC  
TCTCTCTCTTTTTTACAAACAGAGAAGAGACAAAGAAAAAAAAAAACATCAAAATTAAGATTCAAGC  
TTTTTTTTTAGTTTTTTTAAACAACAAAATGAAATTGAAATTCATCTTTGAATTTTACAACATTCATATTC  
AGCTCTAAATACATAAATTATAACAATAATTAATGAATTATTCTATAAACCAGTATATTTGAT  
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AGAATTTGAATTTTGACAACCCCTTGGGATATCATGGAGATGTTGCCAATGATTTGGTTCACCTT  
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TCAGTAAGAAATGGTATCACACATTTTACAATTGTTGATTTGTCCAATCAAGGCGTTATACCGGAAA  
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GTAATTTCTTGAATGTTCCATCTACTGAGTTGTTTGCTTATGAGATTTTTTCAAATGCAATCTATA  
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TCAACAACACAGAGAGAGTTTATTAATGTTCTCTACACACAACCTACTTTTTAGCGATTTCAAACCTT  
TATCGGACCAATTATCAGAATCAAAACGCAACTATTTATTTTATCTGATTATAAAAAAGATGGATG  
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CGGGGTGAGAAAATAGTAGTAGAGCACTGGAAGAACAAGATGGATTGTTATTAATAAATAAAGAGG  
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GAAATAATACTGGAGTTACATCCCGTCACTCCGATGAAGAAACAGAAAGTGAAGCTAATTTGGGAA  
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CAACATTGATATCGAAGGACACAGTTTTTGTATTGTGATTGGGATAAGGAAATTTATCAAAAATGCT  
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GTTCTGATGTTGCCAATACTGATTTGACACCTGAAGATTGTTTATACGACTTGATTGCCGTTGATA  
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GGTATPATTTTTAATGATAGTCGAGTCACTGAAATTAATAATCCTCAAGAAGTCGTAGCTAATTCTG  
CGTACCTTTTTATTTTACCGTCGAAGAAGTTCGAAAGGAGCTGGTATTTTGGGAGGAGAAAACTTTA  
TCGACTTGCTTCAAAAAGGTTCGAGAGGAATACTCTGAGAGTTTGCAAAAAGAAAAGATTGGTTCTTC  
AAAATGTTGGCCAAATAGTCAATACGTATGCCAAAATTGAACAAGATATAATTGATAAAGAAAACAG  
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AAGAGCCAGTTCAAGAGCCAGATCAAGAACAAGAGCCAGATCAAGAGCCAGATCAAGATCAAGATC  
AAGAGCCAGATCAAGAGCCAGATCAAGATCAAGAGCAGAATGAAACAATAAAAAAATCTAGACCAT  
TCGATGAACTCAAACCATCAACTAGTGAAACAAAATAACCAACAACAACAACACTCAGTTCAACTTTG  
ATGATGAAGATAATGATTACGATTATGAAGCAGAAGTAGAAGATTCCAATATTCGCAAAACAAGAT  
TACTTTCAAAAGAAAAATAACAGCAATAAATTGGTGCATATTAAAAGCAATGGTCGCCAAGAAGTCA  
CTTCATCACCAGTACCAATTGAAACTGATGGTGACACTGATGTAAGTATTCCAATTCAACATAG

YJL197W\_homolog 1372aa (SEQ ID NO 390)

MPDNIEDRSEIPSDAKEIVTTNEIEATDSEHTTNVDNELPQGESNEQTGDDSDNDNLASKRQLINDL  
LHNDHFEEGTERYIIPQNFLHEFLNLPIDNFSDLKDQLGPIDFHSLLNEQGNLYPENEEPVTFFCHV  
SPEVFQHLGEWFGILGQPIIRAIINPDTEKEQIERFPPLFWVHQLGKKTQPTYLRHRHNSNNH  
HHGHHDSPPIVLLSKTSTFHLMDVIRYNVLKAPRKSTKDFRIWFIVPQDKGLQYLISIQTFMFD  
ISKKTIVSPNMLEDALKDGHIVASSYNIMVEAKEKHQTEFPIDQFILSHSNAYEEVSQGGGHLGLS  
NMGNTCYMNSALQCLLHVPEINYYFFYNIYKKELNFDNPLGYHGDVANAFGSLLKQAFDHVKNSSS  
ISPREFKSTIGRYSSMFSGYLQQDSQELLSWLLDALHEDLNRIHQKPYCEKPELKDDDEIDDPQAIT  
KLANTCWNQHKARNDSVIIDLFTGLYQSTLICPDCKKSITFDPFNDLTLPLPISKWKYHTFTIVD  
LSNQGVIPERIMKLEVLNKTSNFDDLLSYLSNFLNVPSTELFAYEIFQNAIYSDFQLDYTKNKF  
PISDIIRDTDVVIVYIVPHNPAVDIIVPVFNAVEDADSSYQMVNFFGIPLFVVMNKEVDVNSFGFI  
RKKLLETVSLLSKIDLVDEYEKIKRSNEDYVEKVFYKKSDFPALSQPLETSDCEKNNNNTSDNDDD  
EDADNDEGYDSEVSLANPYLGANFGFKIMYVHDYSPKLSNLSRNYNHDQTTKFKQTERVINVPTH  
KPTFSDFKPLSDQLSESKRNYFYFYPDYKMDDEMDQLVEEVNQNLAEQXEARSSESSRASEEQ  
DGFVLINKEDTLKQQSTVPAAETVPPPLPVRNNTGVHIPSSDEETSEANLGSFLDSTSNLPLPP  
PSTYSESTKPSNVNPMESNFESSADLNSGTTLISKDTVLLCDWDKEIYQKCFGDKELQAWENIS  
NLPNPELEKNRAHFERQKAKITLSDCLKSFSTPEILGEHDLWYCPRCTEHRKATKTIQLWSTGDI  
LTIHLKRFHSARAFSDKIDVLVDFPIEGLDISSYVANTDLTPEDCLYDLIAVDNHYGGLGGGHYTA  
SVKNFRDDKWYFYFNDSRVTEINNPQEVVANSAYLLFYRRRSSKGAGILGGENFIDLLQKGREEYSE  
SLQKKRLVLQNVGQIVNTYAKIEQDIIDKETEKQKEEQEQEQEQEQEQEQEQEQEQEQEQEPVQEPDQEQEP  
DQEPDQDQDQEPDQEPDQDQEQNETIKSRPFDELKPSTSETNNQQQTTFQNFDDDEDNDYDYEAEV  
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YJL198W\_homolog 2693bp PathoSeq: 1..899/1285..2693, public:  
900..1284; CDS: <3..2690 (SEQ ID NO 391)

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TTACTGGTGAATTAGAATATACTTCAACTTCTTCCAATGGTGAACATGACACCACCACCATGCCA  
CTAACACATGAATTGATATACACAAATTTTGAATTCTAATGATGAATCATATATTAATCTTAAAT  
CATTAACATTTGATCCATTAAAAATTTTCACTAAACAATTAATTGGTGAATTAATTAATAATTAATC  
AATTTTACAATTCAAAAGAATCGGAAATTTTCAAAATTTATAATAATTTAATTCATGATTTACAAA  
ATCAAAATATTAATATTGATGATGTATTTAAATTCACCTCAAGCTTATAATTATTCGATCCAAATA  
TAATAAATACTGATGATCATCATCAATATCATTTAAATCAACTTTATCAAGAACAGTTACTAATG  
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ATAATTATGATTTGGAGAAACAAATAATACATACGATTGCAATTCATGATGATGATGATTGAGAAG  
ACGATGAAGAAGAAGAGGAAGAAGAAATCATAGTCATGATTGATTACTTAATCATACACATT

TTAATGTTAAACAACAATTA AAAATCACATTA AAAACGTAAAGCCATTACATTATTTATAAATCTTT  
CTGAATTAAAATCATTATTTATTGAATTGAATAGAAATTGGATTACAGAAAATTTGTAAAAAATTTGATA  
AAACTTGTGGTATTTCAATTAACAAGATTTTATTAATGAATTTTACCTCAATATTTCTCGAGTAT  
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TATCAAATAAAATTA ACTACTCAATCAACAACATAAAGAAGATTTTGGATAATATAAAAATTTGAATTAA  
GATCTTATTTACGTGATCATATTTGTATTTGAAAGAAATACCGTTTGGAAAGATTTATTTATCATTAG  
AAAAGAAATCTTATAATATTGATTTAGATAATTCTGTGGTTCAAAATAATAAAAATGGGTGATGAAG  
GTCATATAATTAATTC AATGATGAATTTATCCATGAAAAGAATTAATTTACCACAATGCCTTAAAA  
AATTGATTA AATATGATCATATTTGATATTTCCACAATTTTATTA ACTACTCAAATGCTTAAAAATTA  
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GTTGTTTAGCAGTATTAGTTGCTGCTGCCATGCTTTGGGCTTCAGAAAGCATTACCTTTTATACACTA  
CAGCTTTATTAATCCCACTTTTGGTTGTTACTTTGTAAAGTTTGTAAAACCTCCGGGAACCGATGATC  
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TTCTTTCCATGTGGATTTCTAATGTTGCTGCCCCCGTTTATGTTTTCATTAATTC AACCAGTTT  
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ATGTTGCTGGTATGGCTTTCACCAATTGCATCTCCACAAAATGTTATTGCTCTTGAATCAATGAATC  
CTAATCCAGGTTGGGGGAAATGGTTTGTCTGTGGCATTACCTGTGGCAATCATTAGTTTAATTTTAA  
TTTGGGTGGAATTATTCATGACGTTTAAAATCAATAATGTTAAAATCAAACAATTCAAACCAATTA  
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TATTTTTCGGTACCGGTTTATTA AAAAGTTGATGATTTAAATAATTATCCTTGGTCAATTTGTTATGT  
TAGCCATGGGTGGTATTGCATTAGGGGAAAGCGTTACTTCTTCAGGTTTATTGAAAACCTATTGCTT  
TAGCATTACAAAAACGAATTATGCATTATGATGCCATTGTTGTATTAATCATTTTGGAGCATTAA  
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CAGGGGCAATGGGATTAACCAACTTCAGGATTCCCTAATGTGACGGCAATTGGTATGAGAGATGAAG  
TTGGTAAACCTTATTTGACGGTTAATTTATTTATTACTAGAGGGGTTCCGGGCAAGTATAATTGTTT  
ATGTTTGTATTATCACCATTGGTTATGGTATTATGTCATCATTTGAACCTTTTAA

YJL198W\_homolog 896aa (SEQ ID NO 392)

HFLNSNELSSPMPPSFSINYGSEWDLEIIQTSLDNEKESETKSFTGELEYTSTSSNGEHDTTTTAT  
KHELILQQILNSNDESYINPKSLTFDPLKIFTKQLIGELIKINQFYNSKESEIFKIYNNLIHDLQN  
QNINIDDVFKFTQAYNYSDPNIINTDDHHQYHLKSTLSRTVTNASVFD TINHIDNDYDNNNNNQKN  
NYDLEKQNNTTVAIHDDDDSEDDDEEEEEETHSHDSVLLNHTHFNVKQQLKITLKRKAITLFINLS  
ELKSFIELNRIGFTKICKKFKDKTCGYSIKQDFINEFLPQYSRVFENDTIEELDYKLNQIIKIYAFL  
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HIINSMMNLSMKRINLPQCLKKLIKDYDHIDIPOFLTTQMLKIIIIIVIVFIIILLAVKTFNDPVQGR  
CLAVLVAAAMLWASEALPLYTTALLIPLLVVTCKVKCTPGTDDPMDATKASQYIFGTMWNSTIMIL  
IGGFTLAAALSKYNLAKILSSYILALAGTNPRNVLLAIMCVSLFLSMWISNVAAPVLCFSLIQPVL  
RSIPTDSPVAKALVLGIALASDVAGMASPIASPQNVIALESMPNPNPGWGKWFALPVAIIISLILI  
WVELFMFTFKINNVIKIQFKPIKEKLTMTKQWVFVAVTITTTILLWCVMQKIDGTFGESGIITCPIVL  
FFGTGLLKVDDLNNYPWSIVMLAMGGIALGKAVTSSGLLKTIALALQKRIMHYDAIVVLIIFGALI  
LVVATFVSHTVSALIIIPLVKEVGD SLPKPHPLMLIMGVALIASGAMGLPTSGFPNVTAIGMRDEV  
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YJR049C\_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:  
501..2276 (SEQ ID NO 393)

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GAAAGATAGAAAGCAAGCAAGGTGGAAAAAATTTGTTTATATACATTCAATACTTATATCC  
TAAATTGATAAACAATAGAGTAATTGATACTTTCAAGGACAATAAAACGATATATATATATAT  
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136/161

ACAATTAAATCCAAAAAAGAAATCGAATTCCATATGTCGCATAAGACTCAGAGCCAATTAT  
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CAGCAGATATCATTCAACCACCTCATCAACTACTGTAAATAACAACAATTCAACTGTGACGCAAC  
CAGCGCCACAAAGCTCATCGTTTCAACGCCGAAACAATCCACAACGTTTCAATCGGAATCAACTCA  
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CATTGGGCTCATTAGGTTTTTTAACCATTTTGAATTCAGTGCATTTAGAACAGTATTGAGCAAAT  
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TGAGTGCCATTAGTGTTACTCCAATTTGTCTCACACCTTATCGTTCAGACCTATACTATTACCTG  
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CTGAAGATTTTGTATATTAATTATACTGACAATGAACGTGATTCTTCTAGTTCCACTCCTAGTGAAG  
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YJR049C\_homolog 592aa (SEQ ID NO 394)

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SSISSSPKDFFTREPPRIHSLKICEEIASANNRAAKEVL SRLSTDELRSVKSHTELAETANGVRML  
AKNLSRATIQLDVRAIMIITKARDNGLIYLTKEVVEWILDQHPHITIIYADEKLAKSKRFNPESIIA  
NYPNGCKKLKYWNKKLTTKNPEIFDLVLTGGDGT VLFASNL FQKIVPPILSFLSGLSLGFLTNFEF  
SAFRTVL SKCFDSGVKANLRMRFTCRVHTDEGKLICEQVNLNVLVDGRGSPYVTHLELYGDGSL  
TVAQADGLIIATPTGSTAYSLSAGGSLVHPGVSAISVTPICPHTLSFRPILLPDGMFLKVPSSS  
RATAWCSFDGKVRTELKKGYYVTIQASPFPLPTVMSSKTEYIDSVSRNLHWNIREQQKPFSSYLKP  
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YLR048W\_homolog EMBL\_entry 1042bp public: 1..1042; CDS: 28..786  
(SEQ ID NO 395)

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GAAACAATAACAACAATAACAACCAAAATAAAAAAAGGTTTAAATGATGTATATTATCGATAAGGA

GAAAGAAGAGATTTTCTTTTTTAATAATGAGGATGCCATTTTATACAAATCCAAAATTGTAATTAA  
GAAAGATTAATAAATATAAAATATATATATATAAGTAAAAAAAAAAAAAAAAA

YLR048W\_homolog SWISS-PROT\_entry 253aa (SEQ ID NO 396)  
MSLPASFDLTPEDAKLLLAANVHLGAKNVQVHNKPYVYKTRPDGMNIINIGKTWEKIVLAARIIAA  
VPNASDVAVCSSRTFGQRAVLKFAAHTGATAIAGRFTPGNFTNYITRSFKEPRLVVVTDPRTDQA  
IKESSYVNIPVIALTDMQSPSEYVDVAIPCNKKGKHCIGLIWWLLAREVLRRLRGIIPDRTTESWSVM  
PDLYFYRDPEEIEQNAVEEAKTEGVEGAPVAEAEETEWGTGETEDVDWADSGATPSC

YLR088W\_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:  
81..493/777..820; CDS: <1..1332 (SEQ ID NO 397)  
TCGGGGCTACAAATTTTCGTCCATGAAAATTGGGTTTCGCCACCAATACTTTGTATGCGATTATGCAT  
GCTCCACGAGGTGAAAATACCGAGGCAATGGCGTTGGTTGTGCCATGGACTAATTCTGACAACGAG  
TACAATGAAGGTGCTATGAGTTTGGCGGTGGCTTTGGCACGGTACTTTACAAAGATGTCGATCTGG  
TCGAAAAACATTATTTTGTATTTTCCTGAGACGGGCCACAGACCGTTGAGGTCGTGGGTGAGGCA  
TACCATACGGTGTGAGCAGATACTGCGGGGTCGATTGAGGCGGCGATTATTATGGAGTACGGCAAG  
AACGGTGATTATTTTGTAGTATTACGATATGTTCTACGAAGGGTTGAATGGGCAGTTGCCGAATTTG  
GACTTGTGAATACGGCCAATGTAATGACGTATCATGAACAGATCCCCGTGTCATGCAAGGGATG  
TCGGATAGGGTTATCAATTATAGCACCCGGTTGCAGACTTTGTTTAGGGGTATCCTCAAATTGACG  
CTTGTCTGGGTGACTGATGAAGTTTCATGGGTGTTGAAGCATTTTCGGGGTGGCAGATCCAGGCATTT  
ACGATCAAGGTAAGGGGGACTGAAGGGAAAGATGTTACGCAGTTTGGCCGGATTGTGCGATTCTACG  
TTTAGGTCGGTTAACAAATTTGCTTGAAAAGTTTCACCAATCGTTTTCCTTTACTTGATGTTGTGCG  
CCAAAACACTTTGTGTCTATTGGGACGTACTTGCCTGCGCGATTTCGTTGGCAGTATCGTATGCG  
TTGAGCTCTGTCAAGTGGGTGGTGGTTGCCGGTTGATTTCGAAAGCTATATTTGTGGTGGTG  
GTTGAAATTGCGTGTGCTATTTTGGCGTTTGTGCGGTGAACAGGTGATGCTTGTAGCGATTCTG  
GCGGTGGTGTGTTGCCGCGCCAAGCCATCTTTTCCAAGCAGGCGGCGTTTCGCTAATTTCTATT  
GCGTTGTTGGCAGTGGCATTACTTATTACCGCCCTCTTGATTGTACATTTTGCATTGGCGTTTAGT  
ATTGGGATTTTAGCCCTTCCATTGACATTTGTCCCAGCATTAATGAAGAACAAGTCTAGGCTAACA  
GCTTTTGTGTTGGCGGTGTGCAATCCGTTTTTGTGATTTTCGTTGCTGGGAAAGTGCTTGGCCAC  
CCCAGCTATTTGACCGGTTGGTCACTGCCTGGTCCGACATACAGTGTGACATGGGTTTATCGTT  
GTTTTGGGGTGGTTCCAGCGTGGGTGATTATCACACTAAGCTACTGTGGCTACAAGCCAGTTAAG  
GAAAAAAGTGAATAG

YLR088W\_homolog 444aa (SEQ ID NO 398)  
SGLQISSMKIGFATNTLYAIMHAPRGENTEAMALVVPWTNSDNEYNEGAMSLAVALARYFTKMSIW  
SKNIIFVFPETGHRPLRSWVEAYHTVLDDTAGSIEAAIMEYGKNGDYFEYYDMFYEGNLGQLPNL  
DLNLTANVTYHEQIPCAMQGMSDRVINYSTRLTGILKLTGLVGLTDEVHGCFAFSGWQIQAF  
TIKVRGTEGKDVTFGRIVDSTFRSVNNLLEKFHQSFFFYLMSPKHVFSIGTYLPSAILLAVSYA  
LSSVSAVVVAGFDFRKLIFVVEIACAILAFVFNQVMLVAISAVVLLPRQAIFSKQAASFSLISI  
ALLAVALLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH  
PELFDRLVTAWSDIQCWTWFIVVLGWFPWVIITLSYCGYKPVKEKSE

YLR167W\_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO  
399)  
TAGGTCATTTCATAACAATTGATAGATGCAAGCTAATTGGAATGAAAAATCCATCTTGTATCAAAAC  
CCTTTGTTCCCTCATAGTTAATCCGACTAAAGAAGTGTTTTTTTTTCTTTTCTTTTGTCTATATC  
CTAGTTGCCTTAACGACAGTAATAGTTAAAGCGTTGGGAAGTAATGGTGAACCTCGAACCATTGGT  
TGACGCTGACGATTAATAATGTGAATTTCTTTTTCTTTTGGTTGTAGTAATTGCTTTGTTTTGT  
TGCTCTAAATTAGGAAAATGTCGTGACCTTACGTACAGCACACACATACCACTGTCGTGACTGACC  
AACACAATGCGGTGTTAATCGATAACCAAAAGATTATAAATAGGGGGTGAAGGTGCGCACTGTT  
TGAAATGAATCAACACAGTTTTTTTTCTTCTTGTCTTTTCTTTCTATTTTACATTACAAATCTGA  
CAATCGTCAACTAACATATATATACAAATCTACAAGCAATGCAAATTTTCGTTAAACTTTGACTG  
GTAAAACCATTACCTTAGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAG  
ACAAAGAAGGTATTCACCAGACCAACAAAGATTGATTTTCGCCGGTAAACAATTAGAAGATGGCA  
GAACCTTGTCTGACTACAACATCCAAAAAGAATCTACTTTACATTTGGTTTTAAGATTGAGAGGTG  
GTATGCAAATCTTTGTTAAACTTTAACTGGTAAGACTATCACTTTGGAAGTCGAATCTTCTGACA

138/161

CCATCGATAACGTCAAATCCAAGATCCAAGACAAAGAAGGTATTCCACCAGACCAACAAAGATTGA  
TTTTCGCCGGTAAACAATTGGAAGACGGTAGAACCTTGTCTGACTACAACATCCAAAAAGAATCTA  
CTTTACATTTGGT'TTTAAGATTGAGAGGTGGTATGCAAATCTTTGT'TAAAAC'TTAACTGGTAAGA  
CTATCACTTTGGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAGACAAAG  
AAGGTATTCCACCAGATCAACAAAGATTGATTTTTGCTGGTAAACAATTAGAAGATGGCAGAACCT  
TGTCTGACTACAACATCCAAAAAGAATCTACCTTGCAC'TTGGTCTTGAGATTGAGAGGTGGT'TTCT  
AA

YLR167W\_homolog 229aa (SEQ ID NO 400)

MQIFVKLTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYNIQKEST  
LHLVLRRLRGGMQIFVKLTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTL  
SDYNIQKESTLHLVLRRLRGGMQIFVKLTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFA  
GKQLEDGRTLSDYNIQKESTLHLVLRRLRGGF

YLR234W\_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

TCCAGAATAGTAATTAGGGACTTTAATTTTATTAGGAGTGGATTGCATAGAATATGCTATCTAATA  
GATACATCTTATTATATTTCTTATTCATGGGAAAGCACCAGTATATGGAAATGCTGCCAAGGTAGT  
GCACACAACAACTAGTTTACAAAGTAAAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTC'TTATA  
GTAGTTGCTCTACTCTATCAAAAAACCCATAATTTGTCTATATAACGTAAGGATCACTATATGCTGT  
TGAGTAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAAACTTGTTCATCAAACTT  
GCAAAACACTTGGAGACGCGCGCGCTTTCAACACACAATAAACAACACGAAAAATAAGGTAGAAA  
ACAAAAAATAAAGGAAC'TTAAACAAGAAGTAATCCCCATTAAACTTGATCAACACTTTT  
AGGGTTTCCGATTTCCCATTTTCTTGACTAAAAATAATATGAGAATACTATGTGTTGCCGAAAAAC  
CATCGATTTTCAAAGAGGTGGCAAACATTTTGGGAGGAGGGCGAAAAAAGTAAGAACTCACGAG  
AAAAATTCATCAAAAACTACGATTTACCTTCACTTTCAACTCTGAAGATGGGCCATGTCAAGTAA  
CCATGACTTCGGTGGCTGGACATATCACAGGACTTGATTTTGGGTCTGCCTTTTTCGTGGGGAAATT  
GTGTTCCCGGGCGACTATTTGAAGCAGACATCAAGACCATTATCACCAAGAAATCTATTTATGAAA  
ATATTGCAGAAGAGGCAAGAAACGCTGATAAGTTGATGATCTGGACAGATTGTGATAGAGAAGGAG  
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TTTGGCGAGCTAGGTTTTCACATCT'TGAACGAAATCAATTAATTCGAGCAGCAAAAAATCCCGTGA  
ATTTGGATATGAGTGAGTTTCTGCGATTTCTTGTCTGATGGAAATCGATCTTCGAGTGGGTACCA  
GTTTTACACGTTTGTGACTGATCAATTGAGACAAAAGGGGATAATTGAAAAGAATGAAGTAGCTT  
CTTATGGTACATGTCAATTCCCGACATTGGGGTTTGTGTTGATCGATACAAACGAGTCAAGAGTT  
TTACACCGGAACCATTCCTGGTATATTGAGATTGAAACTAGGAAAGAGAATAAAAAAGACAATTTTCA  
ATTGGGTTCGAGGTCAT'TTTTTTCGACAAGATGTATGTGGTTATGCTTTATGATCGATGCTGCAAAA  
GTGGAGAATTTGGAACCATATCAAAAAATAGAATCAAAACCGGAAACCAAAATTTCCGTCCAT'TCCCAT  
TGACAACCGTGGAGTTACAAAAAGATTGTGCTAGATTTTTTAAGATGTCTGCTAAGACGGCGTTGG  
CAGCTGCTGAAAGACTTTATAACCTAGGGTATTTGTCTGATCC'TAGAACTGAAACTGACAGGTTTG  
CCAAAGAAACCGATTTCAAGAGCTTACTAGAGGTGCACAAACAAGATCCGCGATGGGGAAGCTATA  
CAACAAAGCTTTTGAACGAAGGTTTCGAAACTCCTCGAAGCGGT'TCTCATGATGATAAGGCGCATC  
CTCCAATCCATCCTATCAAATATG'TTTCTTTGGACACCCTAAACACCCTCGATGAAAAGAAAGTGT  
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AGGTCAAGTTGTGAGTGGAAATATTGAAAGACGGTAAACAAGTCCACCCAATCATATGACCGAGC  
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ACAAAATAGAGACTAGGCATATATTAATAAATGAAAAAGGGGAAAAATGAATATATTTCTTCTCA  
CTCCTTTTAGGAATGGGGCTTATAGAAGCCCTTGAAAAATGGAATTTGAAGATGTATCTACATCGA  
AACCATTTTGGGAAGTCGTTGGAACGATCACTTGAGGACATAGCAACCGGGTCCCGGCCAAAAG  
TGGATGTTTTGAATACAACAATAGGCGTATATGTTGACGCTTATAGTGT'TTGTCTCATCAGATAC  
TTGTTTTGTGCAATGAATGTAGGAGAATTATACTTGGAATAGCAGTAACAACAACAACAATA  
ATAATAATACGTAA

YLR234W\_homolog 629aa (SEQ ID NO 402)

MRILCVAEKPSISKEVANILGGGRKKVRNSREKFIKNYDFTFTFNSDGPQVMTMTSVAGHITGLD  
FGSAFSWGNVCVPGRLEADIKTIITKKSIIYENIAEEARNADKLMIWTDREGEYIGFEIMNAARK  
YNNRLGLNNIWRARFSLERNHIIIRAAKNPVNLDMSAVSAVSCRMEIDLRVGTSTFRLRLTDQLRQK  
GIIKKNELASYGTCQFPPTLGFVVDYRKRKVSFTPEPFWYIEIETRKENKKTIFNWVRGHFFDKMYV  
VMLYDRCKSGEFGTISKIESKRKPNFRPFPLTTVELQKDCARFFKMSAKTALAAAERLYNLGYLS  
YPRTESTRFAKETDFKSLLEVHKQDPRWGSYTTKLLNEGFETPRSGSHDDKAHPPIHPIKYVSLDT  
LNTLDEKKVYEVVRRFIACCSKDAVGTQTVVTLKWGDEFFTASGLMVHEKNYLEVYTYKKWESSK  
QLPKFTGEQVKLSSGILKDGKTSPPNHMTEPELIALMDANGIGTDATIAEHINKIETRHYINKLK  
KGKNEYILPTPLGMGLIEGLEKMEFEDVLSKPFRLKSLERSLEDIATGSRPKVDVLTNTTIGVYVD  
AYSVCSSHQILVLCNECRRIILGNSSNNNNNNNNNT

YLR241W\_homolog 3098bp public: 1..827/2190..3098, PathoSeq:

828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAATTATGGCTTAGTGCCCTTTATTAACTAAATTAGAGGTTACATTAATACAACCTTAAC  
AAACAAGGAACTAACATCCACGTATAGGGCTTCTTATATTAATATACCTAATTCACCTGATTAT  
ATTGCCTTATATACAGCTTGTAACAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTATCCCC  
CTATTGTAAAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG  
TAACGACAACAACCTACAACAAAAAACAATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG  
CACACGATAAGATTTATCAGTTTCTCTTTCTCGGTTGACCTTAATCTGTTTTTGTATAGACTTTAT  
TTTTTTTGTTTTTGACCACACCCACTTTTTTAATATCACAAAGATATTTAACTGATTATAGAAAAACA  
CAACAATAACCCAAATACGTTAACCACTTTTTATTACATATGATAGACAATATAATCAATAATTGTC  
AAATCATACTACAGCAAAATGATGATAATTTTACATCCCCTCACGACGATGTGATATATCGACCAC  
ATTCTGCTCGTGTAGCACGATATCAAGTAATAATTGCATCTACATTGGGACTCACTGCCCTATTAC  
TATTTTCTATCTTACGATTAAATATCCCAAAATATATGTGGCAAACCTTAATCATTTGAATTTCA  
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TGGAATTTTTTAAAAATGTGCATTCTGAATAATAAGCATATGTTTAGTATTTGCCATTATTTATCATAT  
CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATAGTGACAACG  
ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTACAGCTGGAATTC  
TGGTGGCAAGTAAAAATAACGATGGGAAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA  
CCTATGTATTTACATTTGTTACTGTTTACTTTCTATTCAAACAAACCAATAGGATTATTTCTATGC  
GTCAGAAGTATCTTGGATCGCAAAATTCAGTCAACCGATAGAACGGTAAAAATATCTGGGATACCAG  
GATCATTACGAGATGAAGTGGCACTCGCACGGCACATTGACCGTTTGAATATTGGTGAAGTGGATT  
CTGTGTTGATTGTCAAGGAGTGGCAAAATCTAAACAAACTATTCAAAGAAGGAGAAGAATAGTTC  
GAAAAATTAGAGGAAAGTTGGGTTGAATATTTTGAAGAAATGGGATAACCAATAAGAGCGATTGTA  
TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTTCCAATAGGTATACTGATGATGCAGAAG  
AATCACCAGACTGGGGATCTCAAAATTCGAACCTGACACAAGCTTCAATAATAGATCAAGACTCAG  
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CAAGTCTTCGGAAAGGTTGGTTTCGGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACACCG  
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TGTTGGTTTATCCAGTCAGATTTATGGCTAGTTTAAAAACACTAAAAGCATTCTAAAAATATGGC  
CATCATTGGGGAAAGCTATTGAATCGCATAAATGGGCCGAAACTTTGATTACTGGATTATTTGCCAA  
CTTATTTATTTACAATTTTAAATATTGTGATTCCGTTTTTTTATGTATGGATTCTGAAAAGCAAG  
GTTATTTATCTCATAGTGATGAAGAGTTGTCATCGGTATCCAAGAAGCTTTTCTATATATTTGTGA  
ACTTATTTTTGGTTTTTCAAACTTTTGGTACCGCCTCTTTTGTGATACGACCAAAATTCGATTTG  
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GTATATTTCCCATCAAATTATTATTGGTGGGGAACCTTACTTCGCTTTTGTAGTGAATTCATTATTA  
GGTGCAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT  
TACCACAACCAATATTGATATTTATTATTACGTTGGTATACCTCGGTAATGTCTTCGAAGATATTAA  
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TTCATCCTCCACACTCAACGGGCAAGTTTGGCCAATAATTTTCCGAAGAATCATATTAGGGTTAT  
TTCTTTTTTCAAAATCAAAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT  
TGGCACCATTTGCCGTTTTTGCACACTTTACTTTTGGTGGAGTTTCCATAACAATATATTCCTTGT



CAACATTTCATTGCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTTGGAGCAAA  
TCATTGAAAACAACAATAATAAACTCTTGACGAAAGAAGGGAATTGAACACTAAATACGAATACC  
CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA  
ATCGAGATGGTACAACCTGTACGGAACACCTCAATATTTTCAGTTCAGAATGGGACTATTAA

YLR241W\_homolog 865aa (SEQ ID NO 404)

MIDNIINNLQIILQONDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKII  
VANFNHLNFSLSHSTSRRLPELPSNSLFGWIPTVYKITEQEILEHAGLDAVVFLEFFKMCIRIISI  
CLVFAIIIIISPIRYKFTGRVDEDYPDDSDNDDDDGSNNNGTTIIKHIVSAGISVASKNNDGEQYQ  
QFLWLTYTIFTYVFTFVTVYFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI  
DRINIGEVDVSLIVKEWQNLNKLFRRRRIRVRKLEESWVEYFEKNGITNKSDLISLHPQVGESYRF  
SNRYTDDAEESPDWGSQNSNSAQASIIDQDSESVEGDSSDTLNRLNDESRTSPSLRKGWFLGFGP  
KVDSINYYTDKLEVIDKEITRARTREYPATSTAFITMKTVAEAQMLAQAVLDPKVNLHITNLAPAP  
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSISKIWPSSLGKAIESHKWA  
ETLITGLLPITYLFTILNIVIPFFYVWISEKQGYLSHSDEELSSVSKNFFYIFVNLFLVFTTFTGTAS  
FVDTTKIAFDLARSRLDLSMFYVDLIILQGLGIFPFKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK  
PPVFNFGLQLPQPIILFIITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPPHSTGKVPWI  
IFRRIILGLFLFQITMVGTLALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE  
NINPTDLEQIIENNNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLIVNRDGTTVRKPPQY  
FSSEWDY

YLR321C\_homolog 1559bp public: 1..947/1189..1559, PathoSeq:  
948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT  
TTTGTTTTATCTTGGAGAACCTGTGTTGTTGTTGGCGTTCTATCTCTTTATATATTTTCTCTATTA  
ATTCAATTGAAACATTTGAAGGAAATTTCTTTCTTAAAAGCATCTAGTGACACATGATCTCTAATCT  
CCAGTCTTTTGGATTAAATATTCTTTTGTAGAATATCAGGTGAAGAAGTGTGGTAGTCATAGCTAGTA  
GATACTGTGTGGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCAGTGATATATT  
TTCTTTTGTCAATTCCATCTTTTTTTTTTTCTCTTGAGAAATGTATAACAGAGGATCCATCCATT  
TGCTTGACAGAGAAATACAGAACACTAAACAAACATTTTTTCATTCTCTTTCTTGTTTTGTCTGTT  
ATACCCCAAAAGTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG  
ACATACAAGCTCTTGCAACTAGTTTCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA  
TTAATGTTGCACTCAACTGGTCGACAAGCCAAAAGACATATTCACAGATTAATTACTCCGAAGAGT  
TTGGAGATGACCTTGATTTTGATGAATTCCCATCTTCGACACCCGGTACTAGAAGCTTAAATGAAA  
ATAAAGCTCAAAATAGAAGCACAAAGATATTCCTTGCGAAAAACACACCAACGCCCAAGAGAATCT  
TAGAAAAACCGGTGTATCTGAGTTGGTTGAAAAACCAGTGGTGTCTTATCCTATCAAAATAATGA  
TTACACCAACTGAGTTTGCGGAAATGTTTGCACTGATTTAGATTTACCATTCAGTATGGCTGCAC  
AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTACAACCTACCAA  
ATAAGGGCCCTTACAATGTTACCATTTGATTTATCAGTAAACTTAAATAAACAATTATACCAAGATA  
GATTTGAATGGGATATGAATCAAAATGAAGTTACACCAGAAATTTTTGCTGAAATAGTTGTTGCTG  
ATTTGGGGTTATCGTTAGAATTTAAGAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG  
TGAAAAAGAAGTAATAGATGGTACTTTTGACAATGAAATGCACAACCTGCATCTAGTAAAAGGTA  
TAATGTTTGAAACAAGGAATTAGAATTTTCACTGAAAACAGTGTTCAAAATGGAATGACCGTTGGG  
AACCTTTGGTCGAAGTATTGACTTCTAGTGAAATCGAAAGAAGAGAAAATGAAAGGGTTAGAACT  
TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG  
GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C\_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSFPKRLANDSDNSLLINVAPTGRQAKRHIQQINYSSEFGDDLDLDFDEFPSS  
TPGTRSLNENKAQIEAQRYSLAKNTPTPKRILEKPVLSSELVEKPVVLIPIKIMIENLNTNQKLIDS  
FMWNLNESLITPTEFAEIVCSDLDFPSMAAQIADSINQIEEYSYASNLQLPNKGPYNVTIDLSV  
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIIRVKKEVIDGTFDNE  
MHNHLHLVKGIMFEQGIRIFTENSVQNGNDRWEPLVEVLTSSEIERRENERVRNLRRLKRENMRD  
DDHSRRRQAGKRRYDELEGA



YLR325C\_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAATTTGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA  
TCGCTCCTGACCATTGTTTACTATATTCAACAAAACGAATTTCAACAAGGCAAACGAAAGCTACATG  
AAACTAAGTATCGGCAACGTCGTGGCCAAATGGGGTGGTCAATGTAGGTATTCATGCAAGAAGT  
GCAGCACTGAAAATAACCGGTGCCTCTAACGTCAGTAACATAATGCTAAGCGAGTCTACACGAAGA  
TGGATTATAAGTATAAAGAGGTTGATTAGTTTTAAAGAGAGAGTATATAATAATGCACGTGATTAG  
TTTAGTAATTTTTTGGGAGTTAGGGCTATAGCCCTAAGACATTCACACAATAACAAAAAGGAAGT  
TCTCACGCACATAACGTGTAACCCACATAAAGAAAGAAAAAAATTTTCCTTTGAAAAAATTCACA  
TCACGCTTTAACCACCTCAACCTATAACAACCTCAACCATGGCTAGAGAAATCAAGGATATCAAAG  
AATTCGTCGAATTTGGCTAGAAGATCAGACATCAAATCTGCTATTGTCAAAGTTAACGCCAAGGTCA  
ATGCTAACGGTAAAAAATTCAAACAAACCAATTCAGGTCAAGAGTTCAAGATACCAATACACTT  
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTACAACAATCTTTACCACCAACCTTAAAAATCA  
CCAACCTTGTA

YLR325C\_homolog 78aa (SEQ ID NO 408)

MAREIKDIKEFVELARRSDIKSAIVKVNKVNANGKKFKQTKFKVRGSRYQYTLVVNDASKAKKLO  
QSLPPTLKITNL

YLR344W\_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron  
1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCC CGGGGAGCTAATTATACCCTCATT  
TTTGAACCCACCAAATTTTCTTTTCACATTTATAATGAAATAAGAGTATTCCTTGGCTTCTTTTTTTT  
TTTTTTTTTGGCAATATAGAGAAGACTGTAATAAGTATAGCTCACTAAAAGTCTTTTTTTTTTCTATT  
CGTTTTTATATTTTTTTAAGAAATTTGATGTTGATTGGTAAATGCCAAATTTTAAATGTGTGTAG  
GGCTATAGCCCTAATGTACTGTATATGCAGTATCAGAAATACTTTTGTACGCACAGTTTGTCTTA  
CCAAATACATTATATATATATATTTTTTTTTTTTTTGGAGTAGAGGAGCTACACTAGACCACAGTGGC  
AAAAATTCATCTCTCTATACACTTACTCAATTTGAAGATATTCAAATTTTTTTTCAAAAAAAATTC  
CTTTTGGATCGATACTAGATAGCATATAATCATCAAAAATGGCCAAGATCAGTCAAGGTATGAAAT  
AGATATTCAATTAGATATGGAGAAAGGAAGATAAAAGGAAAAAGAAAAAAGAAAGAAATAA  
AGGAATATATACATTGAAAAGGAGATAGAACATCAAAACAACCAATTAAAGATTAAAGTTTAAATAC  
AGTTTCAATAAAGAGGGTTTTTTTTTCTCAGAACAAACCAATTGACTGAAGTACTACACCAAGAAGGTA  
TAATGATTTACAGATTTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAATAAATA  
CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTTCAAACCTGTTGAATGGAAAA  
CTTGAAAAATCAAATCAAATCAAATCATAACCCCTTCAATATATTCCTTCTCTTACTTTTCTCT  
ATTAAACAAAGACTAAGAAACATTCAGTAAATACTAACAATAATTCATTTATATAGACGTTTC  
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ATCTGCTCCATTATCCAAAGAAATTAAGACAACATACAATGTCAAATCTTTGCCAATTAGACAAAA  
TGATGAAGTTTGTAGTTGTAGAGGTTCTAAAAAAGGTTCTGAAGGTAAAGTTAATTCTGTTTATAG  
ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGCTTCTGTTCCAAT  
CAACATTCATCCATCTAAAGTTGTCTACTAAATTACATTTGGACAAAGATAGAAAAGCTTTGAT  
TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W\_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRKARKAYFTASSVERRVLLSAPLSKELRQQYNVKS LPIRQNDVLLVVRGSKKGS  
EGKVN SVYRLKFAIQVDKLQKEKSN GASVPINIHP SKVVITKLHLDKDRKALIQRKGGKAE

YLR393W\_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;  
CDS: 501..1628 (SEQ ID NO 411)

TTCATCTTTTCAAATCTTCCCTCTTGGAAACGACCAAGAGTTGGATTTCGGTGCCCTTGACTAGCAC  
AACTTTGTTCAAATCTTTATTTGAATAATGCAACACCACGAACCGGTATGGTCGATTTATATTTTCC  
GAATTTAGATAATGCTTCCCTGTGGGTCACCCCATTTCCAAATAAGCGGGCATTTCTCTAAAATCTT  
TGTACTGAACGCTTTCATCTTCATGCTTTGCAAATCGGGATTCAACTGACGAACAAAGTCAGCATA  
AAACCATTTGTGCTTCCCTCAATCTGAAACATTATTCTTTCAATGGAAGATAAATCCTCTTCGGGAAC  
ATTCACCACAAATCTAATAACAAATCTTCCAACACCCGATCTAGAGTTTGATTAGCTAAACCAT  
CGGTAATTGGATCGACATATCTTGTATTTTCTATGATTAATCTTTCTTTTTTCTTTTCTTTTTCAC

TGAATATTTCGTAATTAATAATTGATTCAAAATTGTATTGATGTTTGTATACTGGATAAAACAAC TTGT  
GTGAGATCATTCAATGTATTTGCTGGCGGAGAAGGAGGCAAGGACGAACTTTTTTCTTCTACTACT  
TTTTTTTTTCTCTCTCTCTTTTCTTTCAGTCACATTGTCTGAGTGTTAAAGGCTGGCTTTTCTGTG  
CTGAACCTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAAAGAA TTTTGA  
AAAACCGTGGT TTTGAATTCGACCACAGATTGGTTGGACGACAAAATGCAAAGTGTATT CATCCGGA  
CTTTTGCTACCTCAAGAATAGAGTTCCAGCGGTACCAGCCGCGTTTTGTTAATACCATTAAGAAA  
CGGTCAAATCGGCACAAGAAAAGTCGTACAGTATTACTAGACCATTGGGGTTGTCAAAACAGTTT  
TGTTAAATCATAAATTGTCAGACACATACTCATTTGTCCAATATATACGAGGAGTTGTTTGGTCAAA  
AATCCAAAGAAAGAAGACAGAAACAAC TAGACTACGATTTGAAACACTCGCCAATTTATGAAGTCA  
AGTCATTTGAGAATACAAAGGGGAAAATATTTACTCCTCCTGTTTCGTACTTTCGACAAGACAAAT  
CTTTGTATTTCCCGGATTTTATAGCGAAAACATTGGCAGGTAATCAGAGAAGTTTGTACGACTCAT  
TAGACAATAGATTAAAGCATAGTCAAATTTGTTTCTTCTGTTGCTGGTGAGCAGTGACCCGTTGCT  
ACTTTAAGGTTGAAAACAAAGATTACTATTCCAGGATTATGATACCTTTGTGGAGGAATATCCCC  
ATACCCAGATACTTGATGTGAATATGCCGCAAAGTTGGATCAAGGGGTTTGTGACAAACTTGAGCA  
CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTTATCTTGCCTGGCC  
ACATAATGTCAGCGGAAATTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTATA  
TTGTTGATTTCGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT  
TGATGTGGAAGGTTGTGAAAGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W\_homolog 376aa (SEQ ID NO 412)

MFVYWINNLCEIIQCICWRRRRQGRFTFFPSYFFFSLSLFFQSHCSSVKGWLFC AEPCGSVNARHRV  
IFGETKRILKNRGLNSTTDWLDDKMQS VFIRTFATSRIEFQRYQPRFVNTIKETVKS AQEKSYSIT  
RPLGLSKPVLLNHNKLSDTYSLSNIEELFGQSKERRQKQLDYDLKHSP IYEVKSFENTKGKIFTP  
PVSYFRQDKSLYFPDFIAKTLAGNQ RSLYDSLDRNLSIVKLFSSVAGEQCTR SYFKVENKD YYSQD  
YDTFVEEYPHTQILDVNMPQSWIKGFVTNLSTGNLRKTLKPASRYENYFILPGHIMS AEIREQLYC  
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKL MWKVVKGVQREMTK

YML063W\_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS:  
501..1268 (SEQ ID NO 413)

CCAGTGCGTTTTGTTTGTTCACATCATACACTTCACTGAAACTAAATAAGTTTGTTTACATTTT  
GAGACTTCAGGTACGACCCAGGTTGCGACAAAGTTTAGGTAGTTTGTCGTCGAATGTCGCAACA  
AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGATTGCTGGTGCGCAA  
AAAGATTATGTGTATTTTATGTGCGTTGTTATCCTGCACACTAAAATTGAGCAGTGACACACACA  
CATATTTGGGCTGTATTTTATTCTTGT TTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT  
TGTGTGTGCTGTAATAGTGTGTGTGTTCCAAGTCCCAGCTCTCACAGATACTCACGCACGCCATA  
CTACTGAAAATTTCTTGACTTTCTGTATCTAAAAATTTTACTAGGAATTTTTTTCTTTTACGTT  
TTTCACTTGTTTCATATAATCACCAACTCAAGTACAACATGGCTGTCGGTAAAAACAAGAGATTGT  
CCAAAGGAAAGAAAGGATTAAAAAAGAAGGTCGTTGACCCATTCAACCAGAAAAGATTGGTTTGACA  
TCAAAGCTCCAACCAC TTTTGAAAACAGAAATGTTGGTAAAAC TTTGATCAACAGATCTACCGGTT  
TAAAGAATGCCGCTGATGGCTTGAAAGGTAGAGTTTTCGAAGTTTGT TTGGCCGACTTACAAGGTT  
CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAAACTTGTGTA  
CCAAC TTCCATGGTTTGGATTTCACTTCTGACAAATTAAGATCATTTGGTCAGAAAATGGCAATCAT  
TAGTTGAAGCTAATGTCACGTGTTAAAAC TCCGACGATTACGTTTTTGAGAGTTTTTGCCATTGCTT  
TCACCAAAAAGACAACCAAAACCAATCAAGAAAAC TACTTACGCTCAATCCTCTAAATTGAGAGAAG  
TCAGAAAGAAGATGATTGAAAT TATGCAAAGAGAAGTTTCCAAC TGTACTTTAGCTCAATTAAC TT  
CCAAATTGATTCCAGAAGTCATTGGCCGTGAAATTGAAAAATCCACCCAAACCATT TTTCCATTAC  
AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTCA TTTATTGG  
CTTTGCACGGTGAAGGTTCAACCGAAGAAAAAGGTAAGAAAAGTTTCTTCTGGTTTCAAAGATGTTG  
TTTTAGAATCTGTTTAA

YML063W\_homolog 256aa (SEQ ID NO 414)

MAVGKNKRLSKGKKGLKKKVVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF  
EVCLADLQGSSEHSYRKIKLRVDEVQGNLLTNFHGLDFTSDKLRSLVRKWQSLVEANVTVKTSDD  
YVLRVFIAIAFTKRQPNQIKKTTYAQSSKLREVRKKMIEIMQREVSNC TLAQLTSKLIPEVIGREIE  
KSTQTIFPLQNVHIRKVLLKQPKFDLGSLLALHGE GSTEEKGKKVSSGFKDVVLESV

YML128C\_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)

TGATATGGATTTTTCAAACCTAAGAAACAATACCAACTACAACAACAAGAAACATAAGTGTGGCT  
TAATTCATGACCTCGAGTCATATTTCCCACGTTTAAAGTATGAGTGTTTACGAAGTTGTGGATCC  
TATTTTAAATAAAACAATAATAGTAATAAAAAAAAAAACCTTCTTTGCTTTTTCGAGAATTTGTAAC  
ACATTTGTTTCTTTCTTTCCCACAGCAACCAAATTTTATTTTATTTTCTTTTGGGACTTACCCACA  
GTTGCTCAATTATGTATAACAAGGGTAGAACTCTGTGGGATTCCCTCCTTAAAAATATAGCAATC  
CTTTTCTTTCACAACGATTGCTATATGACCCCCCCCCCTAAGCATTTCATTGCTTTTATATATATTTA  
ATAATGTATTTCTCTTGTTCAGGATAATTATCACTATTTGTGACGTTTAATTTTACATTTCTTCT  
TCTTCTTCTTCTTCTATTTCAACATTAAAGAACAATTAAATATGTATTTCCCAATCATTGTATGGTTAT  
ATGTATCTATCACTTTTGTGGTTGCCAATTATGGTTTTGATCAATGGACAAATGATGATTTAAAA  
AATTTTAAAAGAACGTAAAGTTGCATTCAATGATGCCTTGGAGAATCCAAAATTAATTAGTTTGG  
CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAATAACAATTT  
TGAATCCTCCAGATGATTCATTAAATGATTATTTGAATTTTGAATTACTTATTTGGGAAAAGAAAAG  
AAAATTATTCAATTAAAGAATGGATTTTTGAAAGTTGGCCAGTAACCAGTTTGCAAACTTTTTTTAA  
CTCAAAAATAATATCCAATATAGTGCAAAGGATACCAAAGATGATTTAATCAATAAGGTTAAAGATC  
AATTTGATTCTATTTCTAAGAAAAATCATGGGCTAGTTTTTATCCTGGCAATTGGTTATATGAAT  
CTTGGTCAGAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA  
CAAAGGATCAATTGGTTGAAAAATTAAAAGAATTTAGTTATCAAGCCACTCATTCAATTAGAGATT  
CCAAAGAATCTTTATTTGATTTCATTGGATTATTTGATAAAACCATTTTGTATAAAAAAGGTCAAA  
TTGAAGATGAATTTTCCAAACCTTGGTCATATTTCTCAATTACGTGAATGGCTTTATTTACATGGAT  
TTATTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCCC  
AAAGTTATAAGAAATGTTTGTGAGTGACATTCATACTTGGTTGGCAAACACTGAAAAGAAGTCTC  
AACCTTGGATCACAAAGGGAGAACAAAAGTCTCAGAAAAAGAAGGGTAGTAATTTGATTATGATA  
CATTCTTTGTTGGTATTAATAATTGGTCCAAGGATAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C\_homolog 338aa (SEQ ID NO 416)

MYFPIIVWLYVSITFVVANYGFDQWTNDDLKQFLKERKQVAFNDALENPKLISLANEEAKKLEKGYK  
KVTEELNNLNPDDSLNDYLNFDYLFGRKENYSIKEWIFESWVPVTSLOTFLTQNNIQYSAKDTK  
DDLINKVKDQFDSISKKNHGSSFYPGNWLYESWSENDLKDWLKSYGIEFNPSSTKDQLVEKLKFS  
YQATHSIRDSKESLFDLFDKTIFFDKKGQIEDEFQWTSYSQLREWLYLHGFIDTKPGIYVEDL  
DKEKLVKIAQSYKKCLLSDIHTWLANTTEKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK  
LRELGNLD

YML130C\_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417)

ATGAGTTCATAGATGATCTGTTTCACTTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG  
ATTTTGCCGCCACTTGTACAGATGGATAGAATTGAATGCAAATCTGCATAAAGATTAAAGTGAAA  
AACAAATTTCCGAAAAAAGAAGAAAATCGAACACATTAGAAAAAGAAACGAACAAAAGAAAAAAAT  
TTCAAATTGTAGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACTGATTACTT  
TTTATTTATATCACCTGTCAACAACAAATTTCCAAATAAATACAACCTCAGAAAAAACACTTACTAT  
CTTTTCTTAGTTTGGTTTCTATAATCTTATTAACATCTTGCCTTTTCATCCTTGATTATCATATT  
AGATCTTATCTTTAATTTGTTTGAATAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA  
ACAACAAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTTCACTAC  
TAATCGTACAATTTATCATAAATACCACTGTTGCAGTATCACCTGTGTCAGCAGTTTACCAAAAC  
TGAGTTTTCAGTCCATTTGATTACCCAGAATTTTGTTCACAGATCATAACTCCCCTTGTAAATACAA  
CTTTCACCTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTGCGGAATTAGTCAAGACCC  
TGTATTTCCGTTATTTTAAAGTCAATTTAGATAACAATGTCGTTTTTGGAAATGCTCAACATTTT  
GTGCTAGTGAAAACCTGTGCTGTGAAATATTGGAAGATTTCAAATTGGAGTCAAGTCACCAATGAAA  
GTTTGAAACCTTCAGGATTAGGTAAGATTTTATTACCTGACAAATCATCAATTGATAATTCCATTG  
AAACCGAAGAAGTTCAAACCTGTGAAGATTTAGATTATAGTGAAATAGATGATGACCATCATTGTG  
TTTATGTCAACTTGGTAAATAACCCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTTGTATG  
TTTGGAAGGCTATTTACCTGGAAAATTTGTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG  
CCGACAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTGTTAGTGGTATGCATG  
CTTCAATTGCAGTACATTTATCAAGAGAATATTTGAATCTGAAACTGGTGAATTTTATCTCAATT  
TAAAGGTGTTTATGGAAAGAGTAGGTATGCATAATGACAGATTATCTAATATTTATTTCAATTATG

CCTTAGTGTCCCAAGCTATAGTTAAATTGAGTGAAATTTTACCATTGAGAGAGTTCAATCAACTGG  
GGTATGATGACATTACTCCAGCTCAAAAGCAACATTTATTGGCTAATAATGATGTCGAATCAGTCG  
AAGTTTATGATCGTTTGTGTTGTTAGATGACATTATTCCTAGTTTGGGAAGCAAATGTTGTGTTTAATA  
CTTCCAACCTTGTTTGTATAATAGCAATTTGAGGGATGAATTTAGATCAAGATTTAGAAACATTTCTG  
CCATTATGGATTGTGTTGGTTGTGATAGATGCAGAATGTGGGGGAAAATCCAAACCATTTGGTTATG  
GTACCGCTCTCAAGATTTTATTTGAAGATGACAACTATGATAATCACAAATTTGAAATTTAGAAGAA  
TTGAAATTTGTTGCCTTGATTAATACTTTTGTATCGTTTATCTAAATCTATTGAAAGTATTAATATGT  
TTAAAGAAATGTATTTGCAACACCTTAAAGATATTGCTGAAGGATTAACCCAACCTGGTGTTTACG  
ACAAAATACAAAACAACAAACCAGGTAACGGATTTGCCTTCCCATTTGTTAGTCCATTACCTCAGA  
AAAAACCTGACCAAAACCAACACCCCCAAAAATCAACAACAAAACAACCTCAAGAAACTGACAAAA  
AAAGACTTACATTAGAAGAAATTGCCCACACAAAACCTGAAGATCGAACTTTTATTGAAGACTTCA  
GATTACCTTTGATGAAGTTTGGCAAGCATTAAAGATTTGTTTAACTAGTTATCAAAGATTCCCAG  
CCGTATTGAGTAGATTACATTTGGTTCAATTGAATGAATGGTGAATAAATTGCTTGGTAAACCAA  
CAGTTTATGATTACCAAAGTTCTTTTGATGTTGATGCCCTACAATACAGTCAAGTCCTTGGATAA

YML130C\_homolog 580aa (SEQ ID NO 418)

MKIFRLFSLILVQFIINTTVAVSPVSAVLPKSSFSPFDSPEFCSQIITPTCNTTFTYIDELNKDIR  
PYLSELVKTSYFRYFKVNLQCRFWNAQHFCASENCAVEILEDNFWSQVTNLSLKPGLGKISLP  
DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCYVNLVNNPERFTGYGGNQSFVDVWKAIYSENCFPN  
TNPMSVTNDADNGGEQCIEKNLFYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND  
RLSNIFYFNALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLLANNDVESVEVYDRLLDDIIP  
SLEANVVFNTSNLFDNSNLRDEFRRFRNISAIMDCVGCDCRMWGIQTIGYGTALKILFEDDNY  
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA  
FPFVSPLPQKKPDQNTNPKNQKQKQPDQETDKRLTLEEIAHTKPEDRTFIEDFRLSFDEVWQALRF  
VLTSYQRFPAVLRSFTLVQLNEWWNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W\_homolog 1004bp public: 1..507/668..1004, PathoSeq:  
508..667; CDS: 501..1001 (SEQ ID NO 419):

TGTGAAAAAAATTTGTGGTGTGGATGTTGTTGTCGTTGTTGCGTTGTCCACAACAAAAAACAAGT  
AACAAATTTCAAAGTTGGGCTTGGAGATCGATTTTTTTTTCCCGCTCTGTGTGGCACGAGACAATTG  
AGTCGACCAGTACGTTTTTAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACATTTCCACTT  
ATTCTATATCAATGTAAAGTCATTTTTTTGATAATATCGTAATTTACACATTTTCGTATATCTCGGCA  
ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTATTATCAAATCAGGAGTATAGAA  
TTCCACCCAACAACCTAGATTTTCCGAATGCGAAACGACGAGGACGACACAACAACGACTAAAGAAG  
AAGAAGAAAAAAATATAAATAAATTGATCACGCACACATTAGAAACACAATATTGGATCACTTTT  
TTTGATAATACTACCACCACACAGCTCATTCACCACTCATGCCCGAAGTTCTACTGCTCAAAAGC  
GTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA  
GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATACTCCATATGCAATG  
GAGTATCCCACGAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG  
ATCCACCATTTGTTACATCCAAATATTTATGCTGATGGAACCGTTTGTATTTTCGATTTTACATCCTC  
CTGGTGAAGATCCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAGTATTGAAA  
AGATCTTGTGAGTGTATGCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG  
CTTGTAATATTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT  
CATTAGGATTATGA

YMR022W\_homolog 167aa (SEQ ID NO 420)

MPRSSTAQKRLLETEYQQLSRDPPPGIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAULTFPKDY  
PLSPPTLKFDPPLLHPNIYADGTVCISILHPPGEDPNQYERPEERWSPVQSIEKILLSVMSMLAEP  
NPESGANIDACKLWRDNRAEYDRQIRQHVKESLGL

YMR118C\_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID  
NO 421)

CTACACAAAGCTTCGAGAGTTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT  
CGATTGTCTTTCTTTATGATTGTTCTTTAACGGAATTGTGTTCTTAAACAAAATCAGTTCTGC  
ACGTGATATAATCTCCTATCGCTAGTAGTAAGTTTTTAATTTTTTTGATCAAAAGTACACTCATCAG  
TCTATTGTCTGATGTTTTCGCATACTTGTGATAATATCTGGTGTGTACACTACTTTTTTGGTTTGTGTA

TTGTAAATTACAATTTTCTATTGGTTAAAATGATAATTGTTAACAAGTCTTTTTTTTCCCCGGGA  
TTGAATCCGGAACTACCATTAATTCCTACTCTACTCACCTTACACCTCACTCACTCAA  
ACAATTATATCAACCCAAAAAATCTTCACTACACCAATAACAAAGAACCAATAGTTCAT  
CTAATAAACCATCCTTCCCCCTAGCCTGCCACAACAACATGATTTCTCGTATTGGATTATTGAAAA  
GACCTACCGTGTCCACTTTAAACAACATATGTCAAATTACAATCGACATTAGCCCTTAAAAGATACA  
CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC  
CTACATCACCTCATTTACAAATTTATGAACCACAATTAACCTGGATCATGTCATCATTTCCATAGAA  
TCACTGGTGTGCTATGGCCGGTGCCTTTATGCTTTAACTTGTGGATTGCTGCTACTTCAATTT  
TAAATATTCCATTTGATACTACTACTTTAGTATCTGCATTCACCACATTACCAACATTTGCTCAAT  
ATGGTATCAAAGCTATTTGTGCTTATCCATTTGTTTATCATATTGGTAATGGGATTAGACATTTGG  
TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTTTATAGAAGTGGGTATGCTGTTTGGCTG  
CTACTGCTGTCATTGGAAGTTATTTAGCTTTCTTATGGTAA

YMR118C\_homolog 176aa (SEQ ID NO 422)

MISRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPTSNDQEQEILVAQRKNRPTSPHLQIYEPQL  
TWIMSSFHRITGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPTFAQYGIKAICAYPFVY  
HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W\_homolog 1176bp public: 1..1176; exon 1: 501..551, intron  
1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)

AAAAGCAAGAAGAGAAGGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG  
TTTAGAACTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTAAATAAT  
TATTTAATCAAACCTGGTTGTAACCTTATGATTATGGTAGTGATCTAAGAACACAACCTGCAAAGCA  
ATGGTAGTTTCTTTGATTTTGTGTTTCTATTAGATTCCCTGTTTCTATTAGATTCCCGCTTTTCTT  
TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTTCTTG  
ATTTTTCTACACTACTAGTAAAAAAATTTTCTTCCGCTCACTATTCACACATACACTCTTTTTTCG  
CACAATTACAGTCTACCAACAGGAAAAGAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT  
TGGTTCTTTTAATACTATCAATCAACTAGAGTCACAGCATGTTAATTCCAAAAGAAGACAGAAAGA  
AGATCCACCAATACCTCTTCCAAGGTATGTAATATGAATTATAAACTGGAACAGAATATGGCATT  
TCAAGGGATGCACGATAAGTCAAGAGTTTCAAGAAAAGCAGATTATAACAGTCGTAAAGAAAAA  
TTTCACTACCAACAACAATAAGAAGATATCAAAAGAGATTCAGTAATCACTACTTACAAGAAACATA  
TAACATCATGGAGAGTTTAATTTGAAATACGAATGAATATACAAATGAACTATACCCTTTTATGG  
CCATATCACGTTTCAAGAAATATTTAAACAAAAATAAAATGAAGAATAAACTTGGATATACTAAC  
ACATGTATTATAGAGGGTGTGCTGTTGCTAAGAAAGACTTCAACCAACCAAAGCAGATGAAATT  
GATACTAGAACTTGTTCGTATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT  
CAATCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATTCTTGAGAACCGAA  
TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAAATGCTCCAGCTGAAAGACCAAGA  
CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W\_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKKIHQYLFQEGVVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTQFSWQYYYY  
TLTDEGEVFLRTELNIPEGILPLTRLKNAPAERPRPSRGGPRRGYRGRARD

YNL054W\_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;  
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATTCTGGCACAACAAATACTTACTTTTAGGTTACTAACATTATTTTTCTTCAGCTA  
ACTAATTATCTAGTTTATATCTATATCCATTATTTGTTGAAATCACTATCGTGAGGTAAATAACAAC  
TACAGAGTTGTACAGTATCCAAAAAACTTTGTACCTATCAATACATTTTAAAGCAATAGGTCAT  
TTATTGCTGTAATCAAGTGTTACCAGTATCTAGTTAATGTTGAGTTTATACCTAAAAACATGAAC  
TATATCAACTTTAAATGCCCTAATCACGTGATACAGCACATGGGAATTTGCTGATCTTGCTTCCT  
TGCACGTACACGGCACATGTACACGACTTTTTTTTCTAAATATTTTTTTTTTTTGTGTTGTTGTTA  
TTAAACAATATTATTTTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCTTTGTCATATT  
TTTTTTTTTTTCTTTTCTGCCAAGTTGATCAAATTCGATGCTACATCCTAATAATTCAGTAGTCG  
ATATGTCTAGCACTGGAAACATGAATGAAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAGA  
AAATATCAAAACAGAATTCAACCAAAACCGATTTTTTGTGCTGCACGATTGGCTAGTGCGGTTGACG  
ATATAGAAAGCAGTGATAGTGATGAAACGTTTATATATGAGAATAATGATACTGAACTTGATGATA

ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA  
GTGTAAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGACTGGTCCCTCCCGGAACATCGATAG  
CGTTAGGATCGGGCCCTTCGATCGCCATCCATACTAGAGGGGGAACAGCTTCAATATTTTCATGACC  
CAGTGAGGCAACAACAGTTCAAACCTTCCTTCTACCAAGGCTCCGTCAATTTCCAACCTCCATCAGCA  
GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTTCAG  
TGAATGATAATGACCACCGAAATCTTGTGCTACCAAACTCAACTGAAAGGTTTACTGCTTCACCTT  
CGAACAATATTGGTAATGAAAATATACCTCAATACCAGAAAACCTAGTAGTGTTGCCCACTCAATCA  
ATGAAGGATACAATGATGATACATTTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT  
CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTCGA  
GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACCTACATACTCTGTCTC  
CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACCGCTCTAAAA  
GAAATTACAAAACCTCATCTCCACTTCCTCAAAAATTAAGATCAACTACATCAAAAACCTTTTCGATAAAA  
AAGGGTCACAACCAAGAGATACAGTACCATTCTGTATGATATTGACATTGAAGATTTCGATGATG  
AGCTTATATACTATGACAACACAGCTAGGTTCCCAGCGAACGAATCAACTTCATTACTAAATCAAA  
ACCAAAGAATCCCCCATTATAGATCACTTAATTTGAATTTCCCTCAGGTGAAGCGCCAAAGCAAGC  
GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGTATCGTGGCTCTAACAAAGATGGTACTGATA  
ATGGAAACAACAGTGATCACAATATTAATTCTCCTTTGACTGCTAATAATAATAATAAATACGTCA  
ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACATTGCTAATAATAGAG  
CATTTCCATTTCTTATCAAGATCAACAACATCATTTACTACGACTACGATGATTTTGACCAAG  
AATCACAATCAATGGACCCAATTTTGATTTGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA  
ATTTTAACAACAACAATAACCCCCAAAAGATTTGGCGACAGTCATTTTTTTCTACCAAGAAAGACAG  
ATCAGTATAGTCAAAGAACAAGCTTTCTAAAGTCATGCATTTATACCTTTGTTTGTATATTAATTG  
TGCTTACCATAGGGTTTGTATTTGGGGTTTGTTTTGGCCACAACAAAAGATTTAACTGATGTAAGGTA  
TCACATCCATTGAGAACCCCATTTGTTAGTAAAGATGAGTTAGTTTTCATGTTGTTATTAAGCAT  
TTAATCCAGGGTGGTTTTCGTTGACATCAATGAAGTAGAGTTGGATTTATTGCAAGAAAGTGGCT  
ATCTACCTGATACAGATAATCTGAAAATATCTAACATGGGAGGGTCACAAAAAGTAGAGACGGTTA  
AATTAGGAACGATTTTGAATTTTGAATCGGTTCTCAATTTCAAAGGTGGGTTTCTCTCTCGAGAAC  
CGACAAATTCAAAAGGGAGGAATCCGATTATTATATCTGGCAAAAATGTTACTGCCGAGGCTAAAT  
TGGTTGTAAATATGGCTGATATTAATAAGCTGCCTCCAATAGCATTGCTAAAGAAAGCACTACTA  
GTAATGACACCAACGATAATGACAACCTCAAGAAGTGGGAAATCATATCAAGCAATCCATTTGATT  
TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTCCTCAAGAACCTCAAGATCAGTCGTGGTTA  
GAAAAACTGGGTATATTGATCCTTACCTTATTCGTAATACCACAAGGAGAGAATAATATTTCAATTT  
AG

YNL054W\_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNMNTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY  
ENNDTELDNASNINNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSGLRSPSILE  
GEQLQYFHDVPVRQQQFKLPSTKAPSISNSISSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN  
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDDTFSYNEVEDNLIDEDSTDDGDLTKNTIT  
NNNNPPTTSSQQQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKLR  
STTSKLFDDKKSQPRRYSTIPDDIDIEDFDDLIYYDNTARFPANESTSLLNQNQRI PHYRSLNLN  
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTDNNGNSDHNINSPLTANNNNNNVNHNHDHGDNKKSN  
NNNNIANNRAPFPYQDQHHYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNPKRFGD  
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFLVLTATKDLTDVGITSIENPIVSKDE  
LVFNVVIEAFNPGWFSVDINEVELDLFARSGYLPD TDNSKISNMGGSQKVETVKLGITILNFESVLN  
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVNMDIKIAASNSIAKESTTSNDTNDNDNSKKW  
EIISSNPFDLIITGVLYDLFPFSRTSRSVVVRKTGYIDPTLFVIPQGENNISI

YNL075W\_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;  
CDS: 501..1349 (SEQ ID NO 427)

CCCACAGACCAATAACGTTTACCAACCAAAAACCTCTGATATCAATGATTGCAAAAAGATTCAATTCA  
ACCCCGGTTAGCTGTTTGAGTATTGGATAGCAACACTTTCAATTAGTGCAACACAATCAAATTACC  
AATACTTGTTTACCTTTTCATCTGATTCTAATTGGTTTCATAGCAATATAGTCTCTTCTGTTGTTTGA  
TATTAATATAAAATAAACTTATTTATCACGTTGTTTAGTAGTCTCGCAAATTTGAAACCATGGATG  
AGTAACTTGTTGTGTTAGATGAGCTCAAATATCTGGTGGAACAATTGTGTAGTAGCTCTTTGATA  
AATATCCAAGAACAGTCGTGCAAGTTTCAAAATACCATCGCAAAAATCCTAACAAAAAATAAAT

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TAATAAAGAAAAGAAATAATTCTATAATAGCTCATCACAACAATTCGTCTACACTTCCCACCTGAT  
TTGTTGGTTTTAAATATAATAAGACAAACCTCAGAAGCTATGATAAGAAAACAGGCTAGAGAAAGAA  
GAGAGTATCTTTATAGAAAGGCTTTACAGCTTCAGGAATCTTCCTTAACAGAAAAAGACAACAAT  
TGAAAGCAGCTCTAGCAAGTGGAATCATTATCAAAGGAGCTTGCCGAAGATGAAAAATTACAAC  
GTGATTTTATTTACGATGAAAGTGAACAAATAGAAATTGATGACGAATACAGTCGGTTGTCTGGGAA  
TATCTGATCCAAAAGTTGTTATTACCACATCCCGTGATCCATCTGTCAAGTTGCTACAATTCCTGA  
AAGAAATCAAGTTAATGTTTCCAAATAGCTTGAAGTTGAATCGAGGAACTATATAATCTCAGATTT  
TGGTAAGTACCTGTAATAGAGTGCAAGTTTCCGATATGATTTTATTGCACGAGCATCGTGGTGTCC  
CATCAAGTTTAACTGTAAGCCACTTTCTCATGGCCCAACTGCGATTTTCACGTTACATAATGTCA  
AACTAAGACACGATTTGCCAAACTTTGGGAAACGTCTCAGAGTCCTATCCTCACTTAATATTTGAGA  
ATTTCCAATCCGACTTGGGTAAGCGTGTGGTTAAAATATTGCAACATTTGTTTCTCCAGGTGTCA  
AGAAAGATAGCTCCAGAGTAATAACATTTGTCAATAACGATGACTACATATCGGTGAGACACCATG  
TTTACGTCAAAACTAAGGATTCAGTGGAGTTGAGTGAGATTGGCCACGTTTCGAAATGAGATTGT  
ATGAAATCAGACTAGGATTACCTGACAACAAAGATGCTGATGTCGAGTGGCAGATGAGAAGATTCA  
TAAGAACAGCTAATAGAAAGAATTACTTGTA

YNL075W\_homolog 283aa (SEQ ID NO 428)

MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKSLSKELAEDEKLQDFIYDESEQIEI  
DDEYSRLSGISDPKVVITTSRDPVSKLLQFSKEIKLMFPNSLKLNRGNYYIISDLVSTCNRVQVSDM  
ILLHEHRGVPSLTVSHFPHGPTAIFTLHNVKLRHDLPLNGNVSESYPHLIFENFQSDLGKRUVKI  
LQHLFP PGVKKDSRVITFVNNDYISVRHHVYVKT KDSVELSEIGPRFEMRLYEIRLGLPDNKDA  
DVEWQMRRFIRTANRKNYL

YNL096C\_YOR096W\_homolog 1061bp public: 1..1061; CDS: 501..1058;  
(SEQ ID NO 429)

TCCTTTTGTTTTTATTTTTTGTCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT  
GACTAATATGAGATGATCGTATGTGGGTGGGTGGGGAGGAAGGGACCCGGAATTC TAGGAACAGGA  
AAAATAAAAACGAATAAACAAAAACCCCCCAATCGGCATGCATCGGAATTC TTTTCAGCCCAATTAC  
TTTATTTTTTGCCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTAGCCCTTTATA  
TGCAGTCTATTTTTATTTTTCTCTTTTTTTTTTGGCTGTTGGTAAACTTTTTTTTTTTTCGCAGGTG  
TTGAAAAAAAATCATTTTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTTGTA  
GTGAGAGTTACTCGTTCACAATAGTATACTTTACAGGGGAGTTCTTTTCTTTTGAATAGTCAACC  
AACAGCAAATAGCCAAGGATCAAGCTTCATCATTAATCATGTCTCTAAGATCTTATCAGAAAACC  
CAACTGAATTAGAATTAAGTTGCTCAAGCTTTCTGTTGATTTTGAATCTCAAGCTGATTTAAAAG  
CTGAATTGAGACCATTACAATTCAAATCTATCAAAGAAATTGATGTTAATGGAGGTAAAAAGCTT  
TAGCTGTTTTCTGTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAACCTAGATTAACCTAGAG  
AATTAGAAAAAAAATTTCCAGATAGACATTTGTCTTTTTTTAGCTGAAAGAAGACTTACCAAAAC  
CAGCTAGAAAAGCTAGAAAACAACAAAAAGACCAAGATCAAGAAGCTTTGACTGCTGTTTCATGATA  
AAATTTTGAAGATTTAGTTTTCCTCAACTGAAATCATTGGTAAAAGAGTTAGATACTTGGTTGGTG  
GTAACAAAATCCAAAAAGTCTTGTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT  
CTTTCCAACAATTGTACTCAAAATTTGACTGGTAAACAAGTTGTTTTTTGAAATCCCAGGTGAATCTC  
ATTAG

YNL096C\_YOR096W\_homolog 186aa (SEQ ID NO 430)

MSSKILSENPTLELKVAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY  
RKVQTRLTRELEKKFPDRHVFLAERRILPKPARKARKQQRPRSRTLTAVHDKILEDLVFPTEII  
GKRVRYLVGGNKIQKVLDSKDSSTAVDYKLDSFQQLYSKLTGKQVVF EIPGESH

YNL178W\_homolog 1256bp public: 1..1024, PathoSeq: 1025..1256; CDS:  
501..1253 (SEQ ID NO 431)

TGTTTTGTTTTTGAATCAACATAATAGAAGACCAACAAATAATTTCTATTTTTTTTGTACTCTCC  
CGTAGTTTTACACTTCTAGCCTCTCTTGTAATATACACCTAATTGACAGTACCATTAGGACCCCA  
TCTTATTTGTTAAGGATAATACTTCTTCTTCTTCTTCTTCTTGTTTAATCAAATTTGCAATAAATA  
AAAAAAAAAAAAAAAAACAAAGCCGCACAAGTTTTCTTAAATGACTTATTTTGTGTAACGCATTAC  
GTGATCATAATTTTTTTAAATTCAAAAACCTGAACCAAATTCCTGCATATTGAGGTTGAAAAAAA  
AGAAAAAGAAAATTTTTTCAATCTTGTTTGGAGAGAGAGAGGTGAAAAATTTTTCTCTCTCTCTTT

CTTTCTTTCATTCTCATATACCATAAACTTAAACAACTTCTTTTACTTTTTCTTTCTTTTCCTTT  
CAAACCTCTACAACAGATCCAATTAATTAACAAAAAAATGGTTAACGCTATCTTATCTAAGAAAA  
AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTG  
AACAAGGTTATGCTGGTGTGAAGTTAGAAAACTCCATCTAAATTGGAAGTTATTGTTAAAGCTT  
CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGAATCCATGAATTAACCTCATTGATTGTTA  
AAAGATTCAAATTATCTCCAGAAGGTATTGCCA'TTATGCTGAAAGAGTTGAAGAAAAGAGGTTTAT  
CTGCTGCTGTTCAAGCTGAAGCTTTGAAAGCCAAATTATTGTCTGGTTTACCAATTAGAAGAGCTG  
CTTATGGTGTTTTAAAGATTTGCTATGGGTGCCGGTGCTAAAGGTGTTGAAGTTGTTATCTCTGGTA  
AATTAAGAGCTGCTAGAGCTAAATCTCAAAAAATATGCTGATGGTTTTATGATTCATTCTGGTCAAC  
CAACTAGAGATTTTATTGATATTTGCCATTAGACATGTTTTAATGAGACAAGGTGTTTTGGGTATCA  
AAGTTAAAATTATGAAAGATCCAGCTGCTAATAGATTTGGTCCAAGAGCTTTACCAGATGCTGTTA  
AAATTGCTGAAGCTAAAGATGAAGATGAAGTTAT'TCCAGCTCCAAC'TGTTAAATCTTATAAACAAA  
CTGCTGAAGATGAAACTGAAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT  
AA

YNL178W\_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKKLVDGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLGEQGRRI  
HELTSLIVKRFKLSPEGIAIYAERVEERGLSAAVQAEALKAKLLSGLPIRRAAYGVLRFAMGAGA  
KGVEVVISGKLRARAQKQKYADGFMIHSGQPTRDFIDIAIRHVLMRQGVLGKVKIMKDPANRF  
GPRALPDAVKIAEAKDEDEVIPAPTVKSYKQTAEDETETDAPVEAEAEVEATA

YNL182C\_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:  
501..2102 (SEQ ID NO 433)

AACTTTCTGATTGAATAAAGTGAACCTCAAATCACATTCTTTCGGCATATATCAAACCATTATTAGT  
TTTATCACGTAAATCTTCAATATACTCAGCCACCCATTGATCATTGGTTCTTCTAGTAAGTAATAT  
TAGTTGTGCTCCTCGTTGTCCCAATTCATATGCTATTTGAGCTCCAATACCACTGGTCCCACCACT  
AATCATAAACACTTTCCCATGCATGTCTCGCTCCCACGTATTTGGTGGCACCATTGGAAATAACTT  
GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTCTTTAATTTGGTCCCAATA  
TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATCACTGGCATAATTGGTATATC  
AAGAGTGAAGAAAAATGCTGTATTGGAGGTTGGAATTTGTTTACAAATTTGGTTGCCTTTTATTCT  
TCTTGTCTCTTTTTTTTTTTCAGTGCTAACATAAATTTGGGATGTATGTATTGAAAAAATTTTGT  
TACAATTTCTTGTCTTGTCTCTCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG  
AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATCATATGGATATG  
TTACATCAATCCATTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA  
CTGCCATAACTGGTATTGGCCAGGAGAAAGAATTTTCACTGCTGTTTCTTAACAAGGCATTAATCA  
ATGTATATTCTGGGAAAGAAAGTGTGTGATCAACGTATACCGATACCAGAAGCATTTGACTTGT  
TCACGTTGATAAACCATTCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCGATTATACA  
AATTACCAAAATTACCGAGTTCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTTGTACATTT  
GGGAATTAAGTTCAGGCAATTTATTATGTGTGAGAGACGCCATTATCAGGGGATCACTACCATCA  
AGGGTTCAAGCTGTGGAACATTTTAAATTAATGAGGAGAGGATGCCAGATGTCTTGTATGGAATT  
TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAACCATATTGGCAAATCACTG  
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAATTAT  
ATACAACCTTCAGAAGACAGCACGGTCAGGATTTATGATATAGTCACAAAGAGTTTGTGTAACCACAT  
TTATTTTACCCAGTTCCGCTGAATGTATCACCAAGGATCCAGCTAATAGAGCGTTATATGTCGGGT  
TGAATAACGGTCTTGTGAAGATCAATTCCTTTTATATTCTATAAATAGCCATACATCAGTGTGGA  
GTATTGGCGGCATGAATAAGATAATCACGGTTGATGCTGATCAAAATTTAAAAGAGACATTTGTTG  
CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTGTTACGAAATTGACAATTTCTT  
TTGATGGTACAAGTATAATATCTGGTGATTCTGAAGGCAGAGTGTGTTGTGCTGACATTGTAACGA  
AACAAGTTGTGAAATCATTACACCTTGTAACTCTCCAATAGCTTATATTGCTGTTGAACTATCC  
CTGATGACTTTGTCAATAAATAGTACTAGTACTACCACTAATAAAGCTGACAAGAAACATAGAA  
TGATACCTCAATTTAAACGAGTACTAGCAAGCACCAATTTCTGAAGAACATCAGATATTCTTGGACA  
TTCTTGGTAAAACACCGCAACCACCAACGCAACCGGCAATATTGACTTTGCAACTTGGTTACAAG  
GCAACAATCTGAAGAATTACAATTTCAAAAACCTTTCTGGAATAAATCTATTTGTCAAACAAGTTG  
GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTAA  
GAAACAAACATGAAGAATTAATTAAAGAACATGCCAAATTATTAGATAAATTAGAATAG



YNL182C\_homolog 534aa (SEQ ID NO 434)

MYVLKKKNFVQFLVLVPLLISSLSYKFTNMDEVVFYIAQGD PADKHSQESYGYVTSIHSSKQYASY  
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALTCITLINHPNGSNNN  
SDNDDNQLYKLPNYRVPWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTIGKSSCGTFLITGG  
EDARCLVWNLAELISIDKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSSESTVRIYD  
IVTKSLLTFFILPSSAECITKDPANRALYVGLNNGLVRSIPLYSINSHTSVLESIGGMNKIITVDA  
DQNLKETFFVAHQKTKTGDDKPVVVTKLTISFDGTSIISGDSEGRVFSVDIVTKQVVKSFTPCNSP  
IAYIAVETIPDDFVNNLATSTTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG  
NIDFATWLQKGQSEELQFKNLSGINSIVKQVGNENVSDLEERLQRVSQAYTEL RNKHEELIKEHAK  
LLDKLE

YNL190W\_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

TTTCTGCAAGTATTGCGTGTGCTGCACAAACTTTTTATATCCGAAAATTTTGGCCGGGAACGAAA  
CGGCAAGAAAAAACAGAAACAATACCACCAGCACGGACAAAAAGATTATAAGCTTTGTGTAATAAG  
GTTATGTCATCGGGTATTACAGATTGCAGGGCCATCTTGTCTTCATCAGTTATAGCATTTCAATAA  
AAATAAGCCACATATGTGTACAGCGCTGAGTCTACTCAACATGTGTAATAAGATAAATCAATTGA  
CACAGTCTTTTGAGATCTGTTATTCTGGCCTATAGCGTTTTAGGAAATTGCGGTATTTTCTTGTCT  
GTTTTTCTTTTATCTATTTTCGCACGACTTGGGGTGGTTTGTGTGACTTTTTTAGCAAATTAATTT  
TGTCGGTCTTCGCAGTAAAAATAAAAAATTCAAAAAAACAATTTGACTTTTTTTTTTACTTT  
CTTTCTTTTCTATCAACAATACTAATCACAAGCCAACCATGAAATTCCTACTGTTGCCACTGTTT  
TTGCTATTTCTCTATTAGCTGCCGCTAAAGGTGGTGAAAAAGATCACGGTAAAGCTTCTACTGTCA  
CCAAATATGTCACTGAAACTACCCACAGATACGGTTCGTTTTGACAAAACCAGTAGATCTAAAAAGC  
CAAAGGAAACTGGTACTCACAGATACGGTAAATTCACAAGACTCCACGTCAGTTACCAACAATG  
TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAAGAGATGCTGTGTTGCTAGAGATTCTAAAAACG  
CTTCTTCCAACCTCTACCACCTCTAGTGGTAACAATGGTGTGCCACTGGTGTGAGCTTGGGTCTTG  
CTGGTGTCTTAGCTGTGGTGTGCTGCTTTGGTTCATCTAA

YNL190W\_homolog 131aa (SEQ ID NO 436)

MKFTTVATVFATSSLAALKGGEKDHGKASTVTKYVTETTHRYGRFDKTSRSKKPKETGTHRYGKFN  
KTPRPVTTTVLVKESDLPKKRDAVVARD SKNASSNTTSSGNNGVATGVSLGLAGVLAVGAALVI

YNL208W\_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCTTTTGTTTTTTTTTTTTGGGTGGTGTGCTGTGGTTCGTTGGGTAGTTGGCTCTTG  
TTTCGGTTCTACTTGTTCCTTTTTTTTATTCTCCTCGTTAATCCTAATTTGTGTAACAAATTAAT  
TATAGCGAGTTGGAAAAATTAAAAAGCTTGAAAAAGAAAGAAAGAAATACCAACGTGGAATTTCT  
ATTACGTAAGTCACTATAAATTGCATAGAAATTTCAAGTTTTCAATTTAAGAAAGTATTAATCAAC  
TGAATTAAGCAATTGAAACGAATTGAACCAGCTCAGCATTTATTTTTCGTTTCTTTTTTTTCAA  
GGGGGTGGGTGAAAGAAAAATCTAAAAATATATAAATACTCCACTTATCTCCTCTCTTCTCTCTT  
TCTCTCTCTAACTCAATTTCAATTTTCCCAAACCAAAATTTCCCTTTCTTTCTTTCTTTTATT  
TTTTACTCAATTGAATCAATATTAACAATAAAAGCCATGTCAGCTAACGATTTTTATTATCATCTG  
GTGATCAATCCAATTATGATCCAAAAAGATCCTCGAATCAAGGATCATCATCATCAAAATGATGAAC  
AACAAGACAGAGGGTTATTATCTACTGTGCGCCGGTGGTGTGCTGGTGGTTATGGTGGTTCACAAAT  
TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG  
CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACACGAGCAACAATATGGTG  
GTAGTGGTAAACACGAAGGCGGAAGACATGAAGGTGGTTTTGGTGGTGGTAGACCAGATGATCGTT  
ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG  
GTGGTGGTTACGGTGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTCGGCGGTGGCAGAC  
CAGATGACCGTTTTGGTGGCGGTAGACCAGATGACCGTTTTGGAGGTGACAGAAGAGATGATAGAA  
GAGATGACCGTAGATGGTAA

YNL208W\_homolog 191aa (SEQ ID NO 438)

MSANDFYSSGDQSNYDPKRSSNQSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGLTGLTV  
LGAIGGAIGANKLEDAYEDRKEHKKHEQQYGGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG  
YNDRRDDGYGGGYGGGRPDDRRHEGGFGGGRPDDRFGGGRPDDRFGGDRRDDRRDDRRW

YOL031C\_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTGAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG  
TTTGAGGGGATGTTTCATTAGCAATGTATATAATTATTGTATATTATGACAAAGAAAGAAAAAGAA  
AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAAATT  
TGAAAGACAATCCGAATGTAGTGCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT  
TGAGGAAATTCCAGATAGCTAACGGTTTTCGATTACGAATTTTCGCAACCAAATAAATATGTGACA  
AGGAATACACTACTGATCAAGGTTATTCTTAGTACAATGGAAAAAAGAAAGCAACAAAA  
AAACGAGAAATTAATGAACACGACTTCACTTCTACAACCTACTGGGAAAAAAGGCAGAGAGTTA  
TTGAAAAAGGATCATATCAAGTTCTTATTGTATATTATATGAAGTTTCTGTTTTAGTATTACTTG  
CCAGTTACTTAGTTGGTGTGAATTCTCTGATTGTTGATACCTCAGAGGAATTAATTTGTCCAGATC  
CAGAAAACCTTTAGATTGTTATCCAAAATTGTTTGTTCACAAACGAGTGGCAAACCATTAAC  
CAGGTCAAGATATACCACCTGGGTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA  
AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG  
ATCATTTCGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA  
AACAGGAGCACGCTCATCGTACAAAGGTTAGCCAGGGAGATTTGAGTAATTTTGACGCAGCTTGTC  
TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAAGGTTGCATTTGGCACTAGATACTT  
TAGAGGAATTAAGTCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTCAGA  
GTTTTGTCAACATTGCCAATGGTGTCTCTGATCCAAAATAACCGAAAAGGTATATCGTGTAATGG  
GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG  
TGGATAATTTGTTTGAGCAATTAGCGAATGAAAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA  
TTCAAGCTTTTAGTCCAAAATAGCCATTTTGCAAGACAATATTTTTCATTTGACCACAGTTCCGGGT  
TAAATGATTTAATAGCGATTTTCCCAAACCTGGTCCAAACTCAAAGTCCAGGGCAAGTAACATTT  
TAGAGGATTTACAATTGTTCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT  
CACAGGTTTCAAAATTTATTCAGAATTCCTTTGTTGGAAATAAACTTGACGAGAAGAATTTCAAGT  
CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGCGACCAAGTGGTGACTTTC  
TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAAGAGACGATTATTCACAAG  
AAGACAAAGACTTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT  
TAAGAAAGGCAATTGCCGACGAGTTGTAG

YOL031C\_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASYLVGVNSSIVDTSEELICPDENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVR  
NIDTLEKEAKLMSADEKDEPVQEVVGGELQDHSREAITENLQKLHESKHPEVKQEHHRTKVSQ  
DLSNFDAACSEIESFKPHESDVERLHLALDLEELSHDIEFGVKLTSKAIQSFVNIANGASDPK  
ITEKVYRVMGSSLRNPEAISNLTNFDKSYVDNLFEQLANENDVLQKRILGIIQALVQNSHFARQ  
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRRSLEDQDPESQVSKFSFVG  
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEEVESRKENKKRDDYSQEDKDFDEYMLRAR  
HEVFGNPMGLRKAIADDEL

YOL048C\_homolog 1244bp PathoSeq: 1..27/985..993, public: 28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTTCTCTGATTTTAGAGCTGTTAATTATACCTTTTTTGTTCCTCAAATAAGCGCTAAAAA  
TGATTGAAATTAATAATACTAACTATTCCAGGTCAAAGTAAACACTATAAAACAATATATTTCAAT  
AACAGGAGCAGTAATTAGCTTCAACATCAAGGTACTCTTTTATTTTTCTACCAAAAACACATCTGA  
AGTAGCTCTTATCCATAGATCCAAATATTTTAACCTTTTTTTTTTCTACTCTCATCTACTTTTTT  
TTGCAACACTTACTGCTCACAACGCCAATGACCATACCATTAATTTCAATAATCAAAATCAAGAGCT  
TATTTGTATCCTCTCAAGGTATGTTAATGTATTAACAACACCGATTCTATTTACCAACATAACACG  
ACAGAAAGGGGTGTACTATTTGTAAACACATCCCACCGTTTGGCCCTTTTACATAACCATATTGA  
TACCTCAATTGGTCCTTACACTAGTCACTTACCTGATTTATGTTTTTCATTGTTCTTCCCACCTCAAG  
CTATTGTATATACATTGTTAATGGGACCATTAGGGGTGATTGGTGCGTGATAGTTTGATCCTGC  
AAGCGAGCACATTGTCTATATTTGTTGTACAAATATCCTTAATGCCTCACATACAACGAGTGGCAT  
ATGATGCAATATTGAGTAGAGAGTGTGCAATGATGTGGTACTAATGGGAAAACCTTAGGAGGTATA  
GAAAACCTACCCATTAGAGTAAGGGCCAGAGAATACCTTAAGGCCATTCCAGATTTTTCGATCTTTC  
CCTTCTCTTTGCTCAAGCTACTTGTGTTTTTTCGGTATTACTTCATACCTTTGTAGGTCCAATCA

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TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG  
 GGTTTTCTGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG  
 TGGTTGCGCTTTGGCTCGAGCTGTTTCCATTTATCAATATGTTTTTTATGTTCCACCAATACTTTGG  
 GAGCTGCTTTGTGGGCAGTTGATATTGAACAACAAGAGAAGGCCGTCACAGAGAATGTGGCCGCGAG  
 CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG  
 AACCAGCAACTAATATACCTGAGGCTACCCCCAAAACTGCTACAAATACCATCTAA

YOL048C\_homolog 247aa (SEQ ID NO 442)

MFSLFFPPQAIVYTLLMGLGVIGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRECANDV  
 VLMGKLRRYRKLPIRVRRAREYLKAIPDFSIFPFSLLKLLVFFGIYFIPFVGPIIVLFFQSSKRGLK  
 AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPPFINMFFMFTNTLGAALWAVDIEQQE  
 KAVTENVAATTTATDTNSVNQQLVIPVHNEPATNIPEATPKTATNTI

YOR027W\_homolog 2270bp PathoSeq: 1..947/1781..1828, public:  
 948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)

GCATTTTACTTATTTAGATATTACTTCATATTGCTTTTATTTAGATTGATTTTGTTTAACAGTGAA  
 AGTTTTTATTTTGTTTTAAAGTTTATTTTGTTTTAAAGTTTGTATTATACAA  
 TATTTAAATTATAGTAATCATCCTATAAAATTTCAAAGTCAAAGACAGATCTTAAGTCTAATTA  
 TAACTCTCTATGGCCTTCTGTGTCAAATTTGTGTCGTTTGATAACAAGTTTGGAACGGTAATGGTT  
 GAAATTAGAAAAGAAAAAATTACACATGGTAGCAGCTGATGTATAGAAGTTTCTAGCAAAAAA  
 AAAGAAAGAATTTTCTTCCATTTTCAAATTTGAGAGATCGAAATAATTTTCTTGAATTTA  
 TTAAGGGAACCCCTTCCGAAAAATCCAAAACCAAACTTCCACCCAAATATCAAATAACTAAC  
 TTATCATTTCCAACAGATAATATTTCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG  
 AAGGTAACAAATATTTTGCTGCTAAAGATTTTGAAGGCGATTGAAGCATTACATAAGCAATTG  
 AAGCATCACCTGAACCAAAACCATGTTCTTTTCAAATCGTTCTGGATCTTATGCCTCTTTAAAG  
 ATTTTAACAACGCATTAAAAGATGCTCAAGAATGTGTCAAGATCAATCCTAGTTGGGCCAAAGGGT  
 ATAATAGAATTGCTGGGGCTGAATTTGGTTTAAAGTAATTTTGATCAAGCCAAATCCAATTATGAAA  
 AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAATCAGTTGAATCTGCTT  
 TATCATCTGGTGGTGGTGATGACAAGGATTTAGGATTTGGTAAAAATTTTAAATGATCCTAATCTTT  
 ATACTAAATTTGAAAAATAATCCTAAAACAAGTGAATTTATGAATGATCCTCAATTTGTTGCTAAAC  
 TTGAACGCTTTAAACTAATCCACAATTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA  
 CGGCTTTTGCTGCTTTAATGGGTATTGACATGGATTTACCAAAATATGGGATTCACTGCTCCAAACG  
 AATCACAATCCAATGCATCAGAACCAAAACCTGGAACCAAAATCAGTACCAGAATCTAAACCAGAAC  
 CAAAAGCAGAACAAAAGGAAGAAGATCAACCTCAGCCAAAGATGAAGACACTCCAATGACTGATG  
 CCCAAGACGACACTAATGATAATGATGCCAAAACCCAAGCTGACAATGCTAAAGCTGAAGGTAATG  
 CCTTATACAAGAAACGTCATTTGATGAAGCAATGCGCGCTATAATAAGGCTTGGGAATTACATA  
 AGGATATCACTTATTTAAACAATCGTGTCTGCTGCCAATATGAAAAAGGTGATTATGCTGCTA  
 TTGCTACATGTAAGGATGATGAAGGTAGAGACATGAGAGCTGATTATAAATTGATTGCTA  
 AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTACCCGAAGCAGTGAAAAAT  
 TTGAAAAATCTTTAACTGAACATCGTACCCCTGATGTTTTAAATAAATTAAGATCAACTCAACGTG  
 AAATTAAGAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG  
 GTAAAGAATATTTACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA  
 GAGCACCAGAAGATGCTAGAGGATATTTCTAATCGTGTGCTGCATTTGGCAAAATTTGTTATCATTTT  
 CTGATGCTATACAAGATTGTAATAAAGCCATTTGAAAAAGATCCAAATTTTATTAGAGCTTATATTA  
 GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTGATGATACTTTAACCGAGGCAA  
 GAATAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAAGCTA  
 CTTATCAAAGATTTCAAGCCATTGAAGGTGAACTCCTGAACAAAC'TATGGAAAAGAGTTTCTAAAG  
 ATCCAGAAATTTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA  
 ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG  
 CTGCTGGTGTTATTCGTACCAGATAA

YOR027W\_homolog 589aa (SEQ ID NO 444)

MTTAEYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLYSNRSYSYASLKDFNNALKDAQECV  
 KINPSWAKGYNRIAGAEFLGNFDQAKSNYEKCLELDPNNMAKEGLKSVESALSSGGGDDKDLGF  
 GKILNDPNLYTKLKNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTAFALMGIDMDL  
 PNMGFTAPNESQSNASEPKSEPKSVPEKPEPKAEQKEEESTSAKDEDTPTMDAQDDTNDNDAKTQ

ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYKGDYDAAIATCEKAIDEGRD  
MRADYKLIAKSFARLGNIIYLKKDELPEAVKNFEKSLTEHRTDPVLNKLKLRSTQREIKTRELNAYIDP  
EKAEEARLQGKEYFTKGDWPNVAVKAYTEMIKRAPEDARGYSNRAAALAKLLSFPDAIQDCNKAIEK  
DPNFIRAYIRKANAQLAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMNKATYQRFQAIEGETP  
EQTMERVSKDPEIVQILQDPVMQGILAQARENPAALQDHMKNPEVYKKINMLIAAGVIRTR

YOR312C\_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)

CCACTAACAACTTTTTTTTGACTATACACCCTGAAAAAAAAAAAAATTTTTGTAAAAAATCT  
TAAGAATTTTCAGTTTAGAAGGTATTCAACAACAACCGAAGAGTATGTTCAACATCGTTATAATAGA  
ATAGAATAAGAGCATGACAACAAAGGGATACAAGCTTGAAAAAAGAAAAAGGGTGGGATATCTTAA  
AATTATTAAAGAGTTTTTTTTTATAACATGTCATTGAGATTGAGATTGGGAATACTGAATTCGATT  
TAAAGTCATTGGATGGGAGAGTTAATTATTCGTTTTATTATTAGGATTACCAATGAATAGTAATGA  
AGTGATGGAGAGATAGAATGAAAGTATTCAGAAGAGCATCAAGTCCCTTATAAGTTTGTGAGACAT  
AATATGTCTACCCCTTGTCAACTTGTCTATAAATTTTATTGCTCGTCTTTAAAAGAAATGAATAA  
AAAGATTTACTAACTTAATTTCAATTATTTATAGAAAGATGTCTAGATTAAACGAATATCAAGTTA  
TTGGTCGTAATTTACCAACTGAATCCGTTCCAGAACCAAAGTTGTTTCAAGATGAGAATTTTTGTCTC  
CAAACACCGTTGTTGCCAAATCAAGATATTGGTATTTCTTGCAAAAATGCATAAAGTTAAAAAAG  
CTTCTGGTGAAATTGTATCTGTCAACATTATTTCTGAAGCTAAACCAACTAAAGTTAAAACTTTTG  
GTATTTGGTTAAGATATGAATCCAGATCTGGTATTCATAACATGTACAAAGAATACAGAGATGTTA  
CTAGAGTTGGTGCTGTTGAAACCATGTACCAAGATTTAGCTGCTAGACACAGAGCTAGATTTAGAA  
GTATCCATATTTTGAAGTTGTTGAATTAGAAAAAACTGATGATGTTAAAAGACAATACGTTAAAC  
AATTTTGTACTAAAGATTTGAAATTTCCATTACCACACAGAGTCCAAAAATCTAAGAAATTTGTTCC  
AAGCTACTGCTCCAACCACTTTCTACTAA

YOR312C\_homolog 172aa (SEQ ID NO 446)

MSRLNEYQVIGRNLPTESVPEPKLFRMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIISE  
AKPTKVKTFGIWLRYESRSGIHNMYKEYRDVTRVGAVETMYQDLAARHRARFRSIHILKVVELEKT  
DDVKRQYVVKQFLTKDLKFPLPHRVQKSKKLFQATAPTTFY

YOR369C\_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS: 501..929 (SEQ ID NO 447)

TGTTTACTTTTTCTGTAGTTTTTAAAGTTTCCTAATTTAACTTCCAAAAGTTTCATTAACAACAATA  
TTAACATACCTTTGTCACAAGCAATTATATTGAAGTTTTTTTGATACAAGTGTGTTGTTTTTTGTG  
TACATGTGAGATATATAATTGTGTATATACAGTCACGTGAATAGAGCAGAAAAATTACGAAGTAGA  
AATATTGGTAGCGCTTAGGGCTATAGCCCTATTTAGTTTGTGCACCACACGACTTACAATTTTTT  
TTTTTTTTCTTTCTTAGAATCCTTGAGGCACTGACACTGTACTCTCTCTCTCTCTCTCTCTCTCG  
TAGGTAGTGAAAAATTTCCACTAGTCTTCCCATACCCACCTAGGTTCTTTC'TTTTGGAACCACT  
GAGCAGTAAATCAATTTACTTGACGAAGAAGTCTATACATAAATATAAACTTGTCCCTCCCCCCC  
CTTTTTTTTTTAACTAACTAAGAAGAAAAAATTAAAAAAATGTCTGACGTTGAACAAGAACAATTG  
TTGAAGAAGTTGTTGTTGAAGAACAATCCGGTGCCATCACCATTGAAGATGCTTTAAAAGTTGTTT  
TAAGAAGCTCTTTAGTCCATGATGGTTTAGCTAGAGGTTTAAGAGAAGCTTCTAAAGCTTTATCTA  
AAAGAGAAGCTCAATTATGTGTTTTGTGTGACTCTGTTACTGAAGAATCAATCATCAAATTGGTTG  
AAGCTTTATGTAATGAACCAGAAGAAAAAATCCCATTGATTAAAGTTTCCGATGCTAAATTATTGG  
GTGAATGGGCTGGTTTATGTCAATTAGATAGAGATGGTAATGCTAGAAAAGTTGTTGGTGCCTCTT  
GTGTTGTTGTCAAAAACCTGGGGTGCTGATTCTGATGAAAGAAACATCTTGTGGAACACTTTTCTC  
ACAATAA

YOR369C\_homolog 143aa (SEQ ID NO 448)

MSDVEQEQIVEEVVVVEEQSGAITIEDALKVVLRTSLVHDGLARGLREASKALSKREAQLCVLCDSV  
TEESIIKLVEALCNEPEEKIPLIKVSDAKLLGEWAGLCQLDRDGNARKVVGASCVVVKNWGADSDE  
RNILLEHFSQQ

YPL047W\_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS: 501..878 (SEQ ID NO 449)

YPL047W\_homolog 126aa (SEQ ID NO 450)  
MLFCFII TKICFFFFSKADSIFNDLINNI IKQHTLTSLTNIKDHSLLNSSNSNTNSNTNGTIASN  
GGNGTTSDENNEIENSTIODKSKLKOLETSRYFRCLNCGRNIAGRFASHISKLERKRK

YPL137C\_homolog 5344bp public: 1..3342, PathoSeq: 3343..5344; CDS: 1250..5341 (SEQ ID NO 451)

CTCTAGAAGTAGGACATCGTATAGTGTTATAAACACTCAATAAGTAATGAAGAAACACGTTTTGTGTG  
TGCAATGTTAGCTGGCGAGCTCAATAATGGGGTCTCTCCGCCGCTCTGTCTGCCTTGCATTCTACTTT  
TTTTTCTCCTTATGGAAACATTAGTACTAGTAGTGGTGGGTAGTAGTTGCTGTTGTTTGCATCTTGC  
ACGTAGTGTGTTTTCCCTTCATCTTTTCATCTGATTATCTGTCTTTGTTAACTGCATACAAAGGGA  
GGGGAAGAAGAAACAACAAAAGGGGAATTTGAATATACGTCAATCTTTTAAATCCTACTACCACGGG  
GGGGGGGGGGGTCATACTTCTTGGTGTAATAATGTATGGAGATTGAGGTTATTAGACTTTTAGAA  
AGAGGTCTTGGTTGAGTAAGGCGGGATAGCACAAATAATGCGTGTCTAATTGGTCAGAGAATAATA  
TGCTTTGGGGAACAATAGAAAGATGTAAGCGAGAGAAATAGAATTNCAAGGGTAAGGATGATTAAC  
TTTTTTT'TTT'TTTAATGCTTGGAGTACTTTGTTGTTGGAAAGAGTATTCAGAGAATATAGTTTAA  
AAAAGAAAAGTATATAACTTTTAGTAATCGGGAACAATGGAATCAATATTTGAAAATATAGTTTT  
TATAGAGTAACCTGGGTCGAGGTGAACCCGAATTCATATTTGGT'TTTCGGTTGTTATATGCTACAT  
AACCATCCTCATCTTGAATGAAACAAGGATAATAGAAATGAGTATATTAACAAACAACATTATGT  
TGTTACTGTTGTATTCTGT'TTTTTTGGTCATTGCCATGGTAATTTTCATATTTAGTAACAATTTAGTG  
TTCATCGTAAGTCTCTCCTTCTCTGGGAGATGTTCTCTCTCTCTTCTCTCTCTGTTGTTGTTGT  
TGTTAATTTGTTAATTTGTTGATTATTTGATTGTTTCCCCAATAAAAATCCCGATAAACTGAACAATA  
ATTGTCATCATAAATTTTTTTTTTAGAAAACTCACTCCATAAATTAATTTATTTATATATTAATTT  
TAAATCGGAAC'TCCGTCFAATTTGGATTCGGTTTTTTTTTTTTTTTATTTGTTTCATTTATTTCTTGAT  
TTTATTTTCTTTTTTGCTTCCTACTTCTCTTTTATTTTCTTAGTTTCATAATTTTTGACAGATAATA  
CTTGAAACTGGTTAATTTTAAATCAACTTCGTGATTTTTTTTCCGGAATCTAATAATATCAATGAC  
CAGTAATCTGCCACCACTTGGTTCTACAACCTAACGATCAGAGACTACCCCAAAGCGGAGTTTTCATC  
CATACCCACAAATAAAATGGCTTTTACC'TAATGCCAATGAAGATTTGCCACGGGTGTGTCGAATGG  
AGATGTTGACTGGCTATTTTCGAGGTAAATCAAGAAATTTGGGGAAAAAGATGGCTAACAAACAATGC  
CAATAAGGATGAACGAAAGAATAGTCATGGTAACATCAAAAACCTCGGAAAAAACTACCGCAAAACC  
CAATGAAACTAAACATGAGTCTAATGGTGAGAAGTTAGAATTCAATGTTCCAAAATCTGTAATGCC  
AACAAAGCATACATCGTCTGGGAACCCAAAAGCACCTACCAATGGACAAATCTCAAATGTAACACC  
AAGTCAACCAAGTCCGAAACAGACCACTTCTGGGTCAACAAATGCAAATGATATACCTCCAATTTCT  
TCCTAAACAACACAGAAAAGGCATCAAAAGTTGAATAAACTAAAAATGGGCGTTCAAGATCGTCTTC  
TGCATCAACAGTCGTACCTTCATCTACAACAGCTTCAACTACTACTAATCTCGAGATCTCTAAAG  
TCAACCAAAAAGACGGAGCAGTAGTTTTTAAC'TTGT'TTACTCCTTCTTGCAGGATGATTTGGCATA  
TGACGATCCTGCATTGGTATCTCAATTATCAAAACAATTCAAATTCCTCTGAACCTATCCTCGCCTAA  
TGTTTCTCGTTCAAATAGCAAAAAAGGTGGGTTATTCAGTTCACCTTTCATCAAAATTTAGATCAAG  
CTCGGCTTCATCTAAACAACCACAACCTGCATTCATCGTCTACACCATCAACCACAACGACAAATGG  
TGGCGGTAACCTCGTCCGCTGCTCCAAAATCATCCCATCACTCCCCCAAATTTAATCCTTCATCTGT  
TGGTCCAGATCAAAAGCACATAAGCTGAGAAGCTGAAGATTTGGTGCTCTTACCAATACTTTGCCTGC  
TGGGAGTGAATACCAATTAACAGCTAAACCATCAATATCGGGAAATTCAAATTTTCAAAGATTCATT

TCTCGATGATGCAAGTTCTTCACCGTCATCTTCATTAAACTCTGATGGGGGGCTTAAGTTTTTCAG  
GAGACGTTCTCTGTGGCATCTACACCATCAACACACGCGTCAACACCTCGAGTGATTTTGAACAA  
AAACCCCAATAGGAGAAAAGTACCCATTGAAGAAATATCTGAAGTTCGATTGCGTTCGGGTACCTT  
TTCTGTTGATAAACTCGAGCACGATCCGCAACAGCAGATTCCCTTCAAGAAGACCTAAACGAGGTAA  
TGTTTTAATTCACAGGACATCAATGCACCACCTCCAAGACTATGTCTTGGGATTTTCAGTTAATGA  
ACCAATAATAAAGATGACGGTAAATCACACAACCATTCCAAATATAGTGATCATGAAATTGCATT  
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AGCAGTTGATAAGAAATTGGCAAATGATGTTTCTGTGGATGGACCGTTGCATGTCCACGAACAACA  
TTTTGAAGAAGAAATTGAAAGCAAAACAGGTGAAAAGACCATTTCATTGGAAACAATCTATACAAG  
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ACCGTTGGAAGTGTTAAAGATGCTCAACCCAAAACCAACTTTAATTGATGTGTTATCTTTTTTCAGA  
TTTTATTGCCATTACACCTATTAACACGGTCATTTTTTGATAACGTGACTATGACAACAGAGATGTT  
GAAAACTTTCTTGGATCGTTGACATATAATAACAATTTGAAAAGTTATCGTTGAGAAATGTTTC  
CATTGATGAGTTGGGATGGAAGTATTTGTGTGAATTTTTTGGCAACAAAATAAACAGTTAAGAAATT  
GGATATATCACAACAACGTATCAAGCCAGATACCCAGACACAAGCATTCGTGGTAATATGAAGT  
GGACTTATTTATTCGATCATTAATTTTGGTGGTGGAAATAGAAGATTGGTTATCAATGGATGTAA  
ACTATCCGATGCAATATTTGAAAAGTTTCATCAATCAAGCGGTTAAGAAGTCAACCTATCGATTAGG  
TATTGCTGGTATTGATTTGAATGTTAAAAAATCAGAAATGGTCACATCGTGGTTAACTGATGGTAA  
TTCTCAATGTGTTGGTGTGATATTGCTTTTAATGATTTGAGCAAGGGACAATTACGTCCATTTCAT  
TAATGCGTTTAAACACTGGCAAGTCAACAATTTAGTGTTTTTTTTTCATTGAATTC AACCAATTTACT  
GAACATTGAAGAACTTCTGACTTGATCAAGTCAATTAATTAATGTTAAACATTACGATTTTTTGA  
TTTAAGTTCCATACCTAATATCTTCCCGAAAATAATTACCCATTTGACAAAATCTTGGCCAGATA  
TCTTAATCTTTCGAAGAATACATTTTGATCTTAATGAATTAACCGCACAAAGCTATTGGGTCATTGGC  
GGGGTGTTTACTGAAAATGCCCAATTAGTTTCATGTCTCGTTATTGGGTAATAGAAATTTGTCAAC  
TACGTCAGCAGCTACATTATACGGAGCAGTTAAACAATCCAAGACCTTGTTTGTCTTGTATTGGA  
CTACGATTTAATACCTGATCAATTATCACAACGTATTGCCTTTTTATTGATGAGAACTTGGAAATA  
CACTTTGAAGCCATCTCATGGCGGCAATATTGAAAGCAATCCAGAAAAACCAGAGGATTTGATGTA  
TGATGGATCGTTATTAATGGAAACAGCTGAAAAATTATTAGTTGAAATAGAAAAGGGTAAGAAAGA  
GGATATCAAAATGCAAGAATTATATCCGATTACAGTATTGGAAAGAACAGATCGATTTCGTAAGGA  
TATTCACAAAACCATTGATACATTATTTCGAACAAAGAAAATTTAGGTAAATTATCATTTGAAGGTAA  
AGAGAATTTAGTTTCGATTTTGTATTATTAGATTCGTCTTTAGAAAAATTTGGTTGTTATGGTTGAGGA  
ACATGCCAACGGATTATTATTAAACACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC  
GCCATCGGTCACTGTTGATACAAATCCATGAAAGTGCAAAATGAGTTGATTACTGCTGGACCAATTTT  
ATCACCATGTCAATAGGAAAGCAGAACAAAGCTCGTATTTCCAGTGTTTGGCCAATATGATAA  
TTTGACCCTCATCTAAGTTGTCTGTTGAGTCAAATGATGAAGGTAGAGATGTTCCAATAGATAAAAT  
GACAGGACGACCAGTTTGTGATTCGATCAATTAGTCAAACCTTCTGTGCATGCAAAAGAGCAAGAAAT  
TGAAGAAGGGGAGCTTCATAAATTTGGATTCTTTATTCAACAAAAAGAGAGACAAAAACAACA  
ACAACAACAACAACAAGAACTCACACCACCAGCACCAACCGGCCAGCTGATCCAACAAGAAAA  
CCAGCTGCCGCTGCCACAACAAGGAAAATATGAAGATTTACCGATATTAAATACATTACCGTCAGG  
ACCAGAGTTGAGAGATGCTATAATGGCAGCTAAGGGAGTAGCAAATGTTACTGAATTAATTGATCG  
AATTAATAATCATCGTGTTAAAATCGATGCACCATCGACAAAACACCATCATGAATTGAACAAACC  
AAATTCGTGACAAAGTAGTTGAGGATGAAGTTGAAGTTTCTGATAATGCCTCTATTGATTCTACTAA  
TGGTGACGATTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTACGGTTGATCCCATGGT  
TAGTGAAGTTTATGACAAGTTGTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C\_homolog 1364aa (SEQ ID NO 452)

MTSNPPLGSTTNDQRLPQSGVSSIPTNKLPLPNANEDFATGVSNGDVDWLFGRGSKKLKGMANN  
NANKDERKNSHGNINKSEKTTAKPNETKHESNGEKLEFNVPKSVMPKHTSSGNPKAPTNGQISNV  
TPSQPSPKQTTSGSTNANDIPPISPKQPEKASKLNKLKIGRSRSSASTVVPSSSTASTTTNPGDP  
KSQPKRRSSSFNFVTPSLTSDLAYDDPALVSQLSNNSNSNSSSPNVSRNSKKGGLFSSLSKFR  
SSSASSKQPQSHSSSTPSTTTTNGGGNSSAAPKSSHHSPKFNPSLVGPVSKHNREEDLVSLTNTL  
PAGSGIPIKRKPSISGNSIFKDSFLDDASSPSSSLNSDGLKFFRRRSSVASTPSTHASTPRVIL  
NKNPNRRKVPIEEEISEVRLRRVTFVVDKLEHDPQQQIPSRPRKRGNVLI PQDINAPPPRLCLGISV

NEPNMKDDGKSHNHSKYSDEHIALAEDAQRRAIIEAEKHAQEAHRQAKKIAQEVSGYRSHRFISIK  
EGGSVGNSTNGNDNDEDDDEVEEAVDKKLANDVSDGPLHVHEQHFEIEIESKTGEKTISLETIY  
TRCCHLREILPIPATLKLKNTAPLEVLKMLNPKPTLIDVLSFSDFIATPINTVIFDNVTMTTE  
MLKNFLGSLTYNKQLEKLSLRNVSIDELGWKYLCEFLATNKTVKKLDISQQRIKPDTPDTSIRGNM  
NWDLFIRSLIRGGIEELVINGCKLSDAIFEKFINQAVKKSTYRLGIAGIDLNVKKSEMVTSWLTD  
GNSQCVGVDFNDLSKGQLRPFINAFNTGKVNNLVFFSLNSTNLSNIEETSDLIKSLINVKTLRF  
LDLSSIPNIFPKIITHLDKYLPRYPNLRRIHFDLNELTAQAIGSLAGCLSKMPQLVHVSLGNRNL  
STTSAATLYGAVKQSKTLFALDLDYDLIPDQLSQRIAFYLMRNLEYTLKPSHGGNIESNPEKPEDL  
MYDGSLLMETAEKLLVEIEKGKKEDIKMQRIIISDSVLERTRSIRKDIHKTIDTLFEQQRNLGKLSFE  
GKENLVRFCLLDSSLEKLVVMVEEHANGLLLTPTTSTDDLRSRAMSPSVTVDTIHESANELITAGP  
ILSPHVNRKAEQSSYFPVFANNDNLTPHQVVVESNDEGRDVPIDKMTGRPVLIRSISQTSVHAKEQ  
EIEEGELHKFGFFIQQKERQKQQQQQQQNSHHQHPAQSIQQENQSPSPQQGKYEDLPILNTLP  
SGPELRDAIMAAKGVANVTELIDRINNHRVKIDAPSTKHHHELNKPNSDKVVEDEVEVSDNASIDS  
TNGDDLHQLGDGKHNGNGTVDPMVSEVYDKLLNDAERVRSNRDI

YPL175W\_homolog 1859bp public: 1..393/395..1859, PathoSeq:  
394;CDS: 501..1856 (SEQ ID NO 453)

ACGGAATAATGTTATGCGAACAGAGTAAGTGGATTATCAACAAGCATCAGTCAATTTCAAAAACCT  
CGGCTGCTTCTTTGCCCTAGTGATGCATTTGTACAATAGAATTATAATTAAAAGAAAGGTAGAATAG  
AATTCAATGTAGGTGATATCACTTTCTGAGAGTTCTTATTACGATATATAAAATACATAGCCAAAA  
TTATAATGAAGTAAAAACATGTAAGTGTGTAATTTTATTCAAGTCCAAAGGTATTGATTAATATTG  
TAGAGTGTGAGCATTTAAATATGAAGGAAGACCGATAACCTAAAGTTTTCTCAGGGTGTGCGAA  
GGCTAGGAGGAATAAAATCTGAGTAGAGAACTTTCGTTTATATCAGTTTTTTCGAAGAAAAAGG  
AAAAACAAAACAAAATAACACACCAAGCAATTAACACACACATCCTAAACACCACTCTGTGGAG  
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ATTTTTTTTACCCTCAACCTGGAGGAGTAGAGTTTCATGTGTATCATTTATCACAAAACTCATTG  
AACTAGGACACTCAGTGGTTATCATAACTCATAATTATTCATCAAGAAATGGTGTACGAGTATTAA  
CGAATGGTTTGAAAGTGTATTATGTACCCTTTGGGTGATCTATAGAAGCTCAGTTTTCCCAACTG  
TATTTCTGTGCTTCCCAATATTGAGGAATATCTTACATACGAGAAAACATTGAGATTATTCACGGAC  
ATGGTTCCCTTCAGCACATTATGCCACGAAGCTATTACATGGCCGAACAATGGGATTAAAAACAG  
TCTTCACTGATCATTCACTTTTTTGGATTTCGCCGAGATTGGATCAATTATGGGGAATAAAGCATTAA  
AGTTCACTTTTCAGTGATGTTGGCCATGTTATCTGTGTCTAGTCACACCTGTAAAGAAAACACGGTTT  
TAAGAGGATCAATAGACCCCATAAAAGTGAGTGTGATACCGAATGCAGTTATTCTGAAAGATTTC  
AGCCCAAAATCGCATTGTGTTAACAAGAACTATACTAAAGAGATCACCATTGTGGTGATCACGAGAT  
TGTTTTCCAAATAAAGGAGCCGATCTATTAAACGGCTGTTATCCCCAAAATTTGCCAGTTGAAACCAA  
AAGTGAAATTTCTAATTGCTGGTGACGGCCCCAGTTTTTTAGATTTAGAACAAATGAGAGAAAAGT  
ACTTTCTTTCAGGAAAGGGTTACATTAGTAGGCGCTATAAAACACGAAGAAGTAAGAGATGTAATGG  
TCCAAGGTGACATATACTTACATCCTTCATTAACAGAGGCGTTTGGTACAGTTATTGTGGAAGCTG  
CATCATGTGGGTTATATGTTGTCCTACAAAAGTTGGAGGCATACCCGAAGTCTTACCAAACGAAA  
TGACAAGCTTTGCTGAACCGGAAGAAAACCTCACTTATTGATGCTGCTATAGATGCTATAAATAAAA  
TTGAAAGTAATGAAATCGATACCTCAAAATTTACGATGCGGTTGCAAAGATGTACAGTTGGAATG  
ATATTGCAAGAAGAACAGAAAATGTTTATAAATTCATTGATTAGACAAACTAAACGAGTCTTTAC  
TTCACCGATTACAAAGATACCTATTGTTGTGGTATAATAGCAGGCAAACTTTATGCTTTATGTGTAA  
TAGTGATATTTTTATTTTCGTGATACTAGAATGGTTGTATCCCGCTGATCATATCGATAAAGCAA  
CAAAATGGCCACTGGCTATCAAGGAAGAAGACGAGCTGGAAGAAGAAACATTTATTTTTCCGAACA  
AAGTAAATTAG

YPL175W\_homolog 452aa (SEQ ID NO 454)

MGYNIAMVTDFYPQPGVEFHVYHLSQKLIELGHSVVIITHNYSSRNGVRVLTNGLKVVYVPLWV  
IYRSSVFPTVFSFPILRNIFIRENIEIIHGHGSFSTLCHEAILHGRMTGLKTVFTDHSLFGFAEI  
GSIMGNKALKFTFSDVGHVICVSHTCKENTVLRGSIDPIKVSVIPNAVISKDFKPKSHCVNKNYTK  
EITIVVITRLFPNKGADLLTAVIPKICQLKPKVKFLIAGDGPFLDLEQMREKYFLQERVTLVGAI  
KHEEVRDVMVQGDIIYLHPSLTEAFGTVIVEAASCGLYVVTTKVGGIPEVLPNEMTSFAEPEENSLI  
DAIDAINKIESNEIDTSKFHDAVAKMYSWNDIARRTENYNSLDLKLNESLLHRLQRYCYCCGII  
AGKLYALCVIVDIFIFVILEWLYPADHIDKATKWPSAIKEEDESEETFIKPNKVN

10/030019

156/161

YPL218W\_homolog 1231bp PathoSeq: 1..407, public: 408..1231; exon 1: 501..518, intron 1: 519..676, exon 2: 677-1228 (SEQ ID NO 455)  
GATACAAATTCACGACCTCTAATTTCCCTTAGTGATAGGTTAATCATGAAATATATAAAATGTCTAGA  
AATAATTGAATAATGATATAAATATAATGTTGTGAAACTTGTGGAAAAATTTGACAGCCTAGTAAC  
TCAAGTGTGTTACACTCTTGTATTATTATTATATCGTTTACAAGTAGATTTCTCATTTTGA  
ACAGCAAATACTGTCGTTAATAGGAATCAGAGGCAGAAAAGAGAGAGAGAAAAAAGGACA  
CATTTACACGTACACCTTAACTTGAAGGAAAAAACAACAAGAGAGACAAAGAAAGAGACAAA  
GAAATACTTTCAACAACGAAAGATTGAGATATTGGTGATTTTCACAAACCAAAAAAAGAATAC  
ACAACCTGTAGATTAAACAGAATTTGAACATTTCTAGAGTTTCTTATATTCCCCCAAGGTGGACAA  
TTAATAATAACATTTGATTATACAAGAACATTTCAATCATGTGGATTTTGTACTGGTGTATGTAAT  
GATTTATCTTTACCGAATCAATACTTTATTTATGAGTGATTGGTTGGTTGGTTATAATACCACCAC  
TTTATTCTATTAAACCAAGTTTGATCTAATTACTGATCTGTATATACTAACCAAATATTTACCTTAT  
CACTTAATTATTTACAGTTCAAGATATATTATCATCATTAGGATTTATGGAATAAACATGCCAAATT  
ATTATTTTATAGGGTTAGATAATGCTGGTAAACTACTCTTTTACATATGTTAAAGAATGATAGATT  
GGCCACTTTTACAACCAACATTACATCCAACCTTCAGAAGAATTGGCCATTGGATCAGTTAGATTTAC  
TACTTTTGTATTTAGGTGGACATCAACAAGCTAGAAGATTATGGAAAGATTATTTCCCTGAAGTCAA  
TGGTATTGTCTTTTTAGTTCGATGCTGCTGATACCGAAAGATTTGCTGAATCCAAAGCTGAATTGGA  
AAGTTTATTTAGAATTGAAGAATTGAGTCAAGTTCATTTGTTATTTTGGGTAATAAGATTGATGT  
TCCTACTGCAGTAGGGGAAATGGAATTGAAAAATGCCCTTGGATTATATAATACTACTGGTAAAGA  
TACTGGTAAATTGCCTGAAGGTACTAGACCAATTGAAGTGTATGGTTTCCGTTGTTATGAGATC  
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YPL218W\_homolog 190aa (SEQ ID NO 456)  
MWIFDWQDILSSLGLWNKHAKLLFLGLDNAGKTTLLHMLKNDRLATLQPTLHPTSEELAIGSVRF  
TTFDLGGHQARRLWKDYFPEVNGIVFLVDAADTERFAESKAELESLEFRIEELSQVPFVILGNKID  
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YOL127W\_homolog 429 bp, public: 1..429, CDS: <1..429 (SEQ ID NO 475)  
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YOL127W\_homolog 142 aa (SEQ ID NO 476)  
LIATTKASAAKKAALKGVNGKKALKVVRTSTTFRLPKTLKLTRSPKYQRKSVPHYNRLDAHKIIIVAP  
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YJL188C\_homolog 117 bp public: 1..117, CDS: <1..>117 (SEQ ID NO 477)  
TTAGATACCCAACTTAGTTCTTCTCCAGTGTCTTCTTTTAGCATTGTATCTGATTTTGTGTGTCAGT  
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YJL188C\_homolog 39 aa (SEQ ID NO 478)  
LDTQLSSSPVSSFSIVSDFVSSQSDPLWQWSVLLLSLS

YGR183C\_homolog 198 bp public: 1..198, CDS: 1..198 (SEQ ID NO 479)  
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GCTTTTGTCTTTCCAAGGTTTTTTCGATGTTGCAGTGAACAAATGGTGGGAGGAACACAACAAAGCT  
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YGR183C\_homolog 65 aa (SEQ ID NO 480)  
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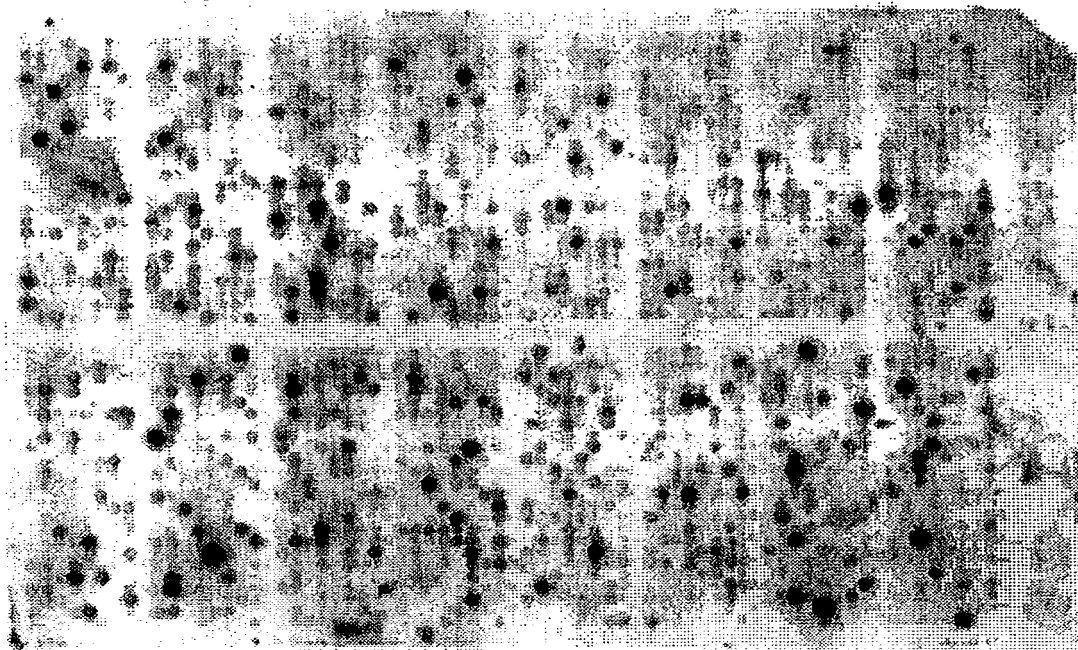
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YDR529C\_homolog 151 aa (SEQ ID NO 482)  
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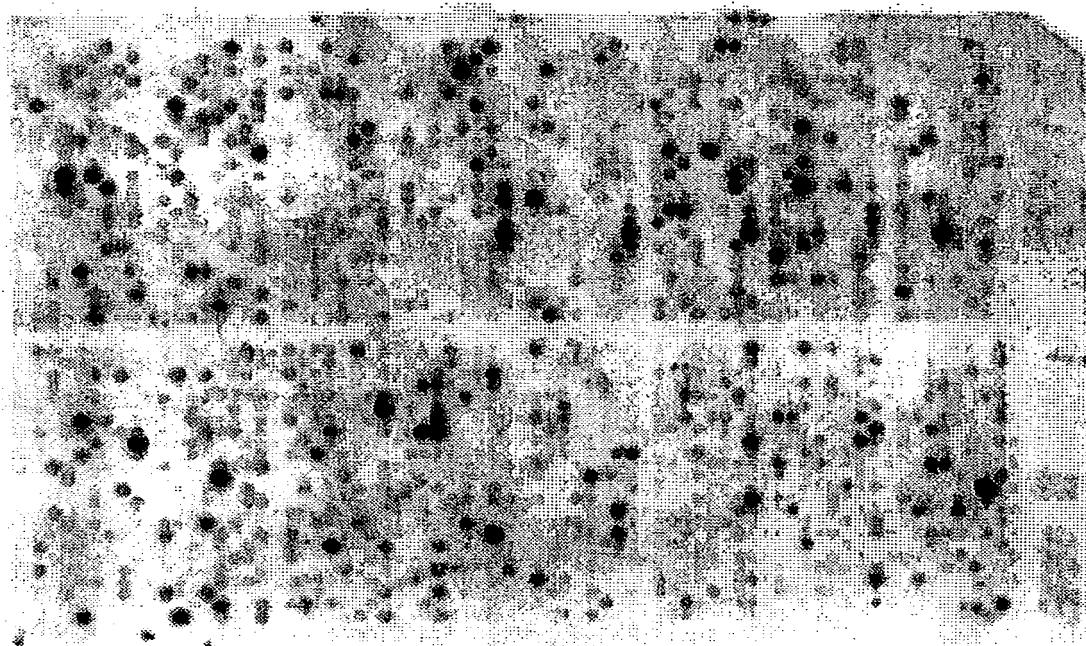
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YBL003C\_YDR225W\_homolog 132 aa (SEQ ID NO 484)  
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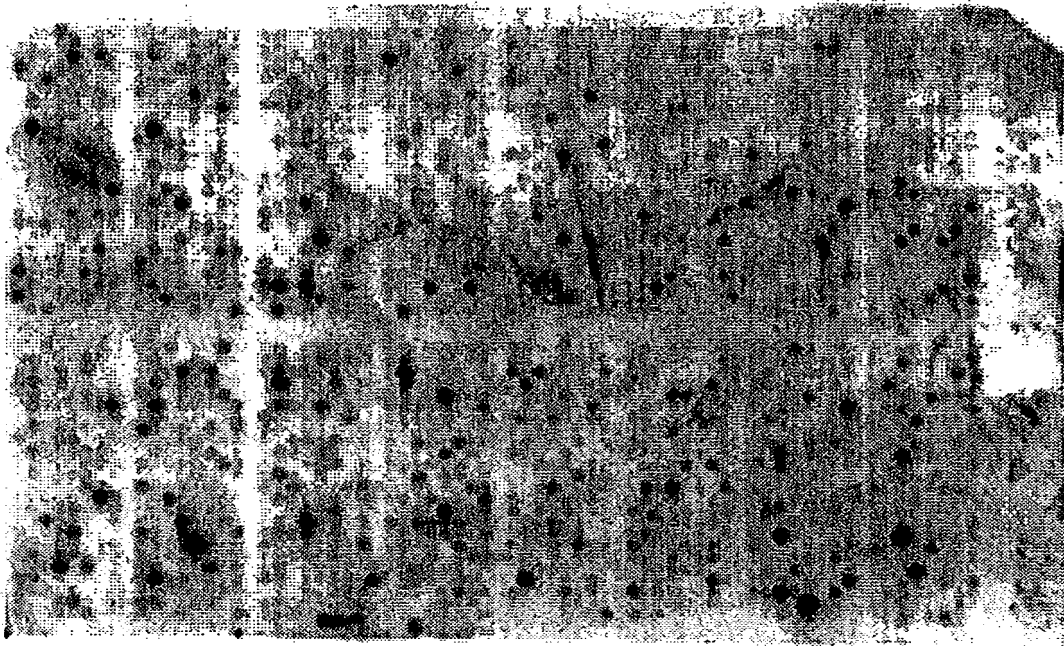
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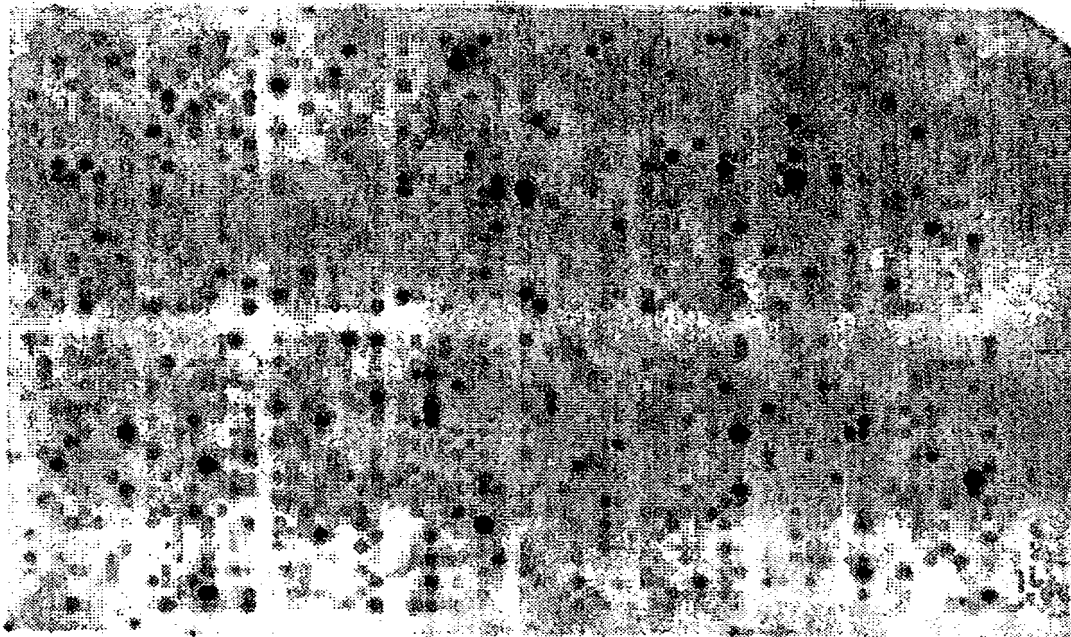
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FIG. 3A

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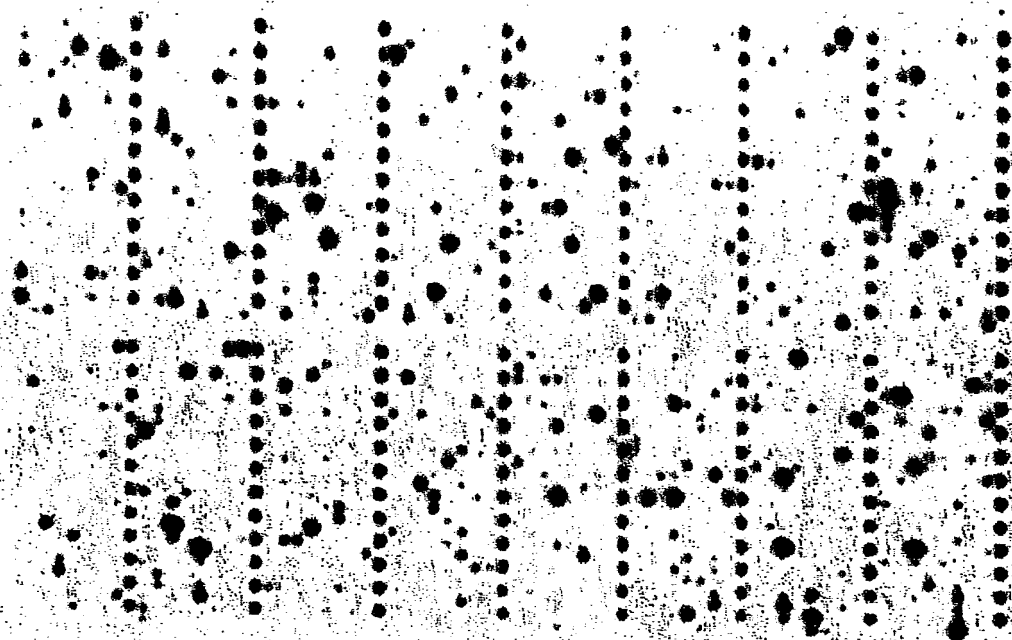
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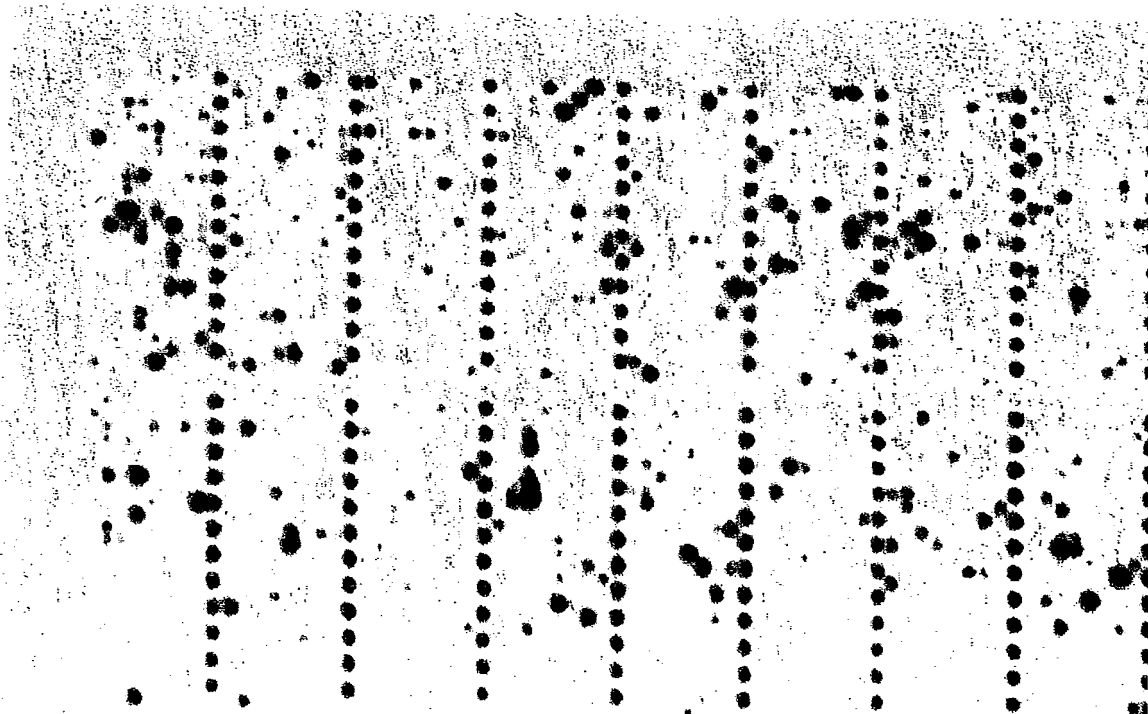
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FIG. 3B

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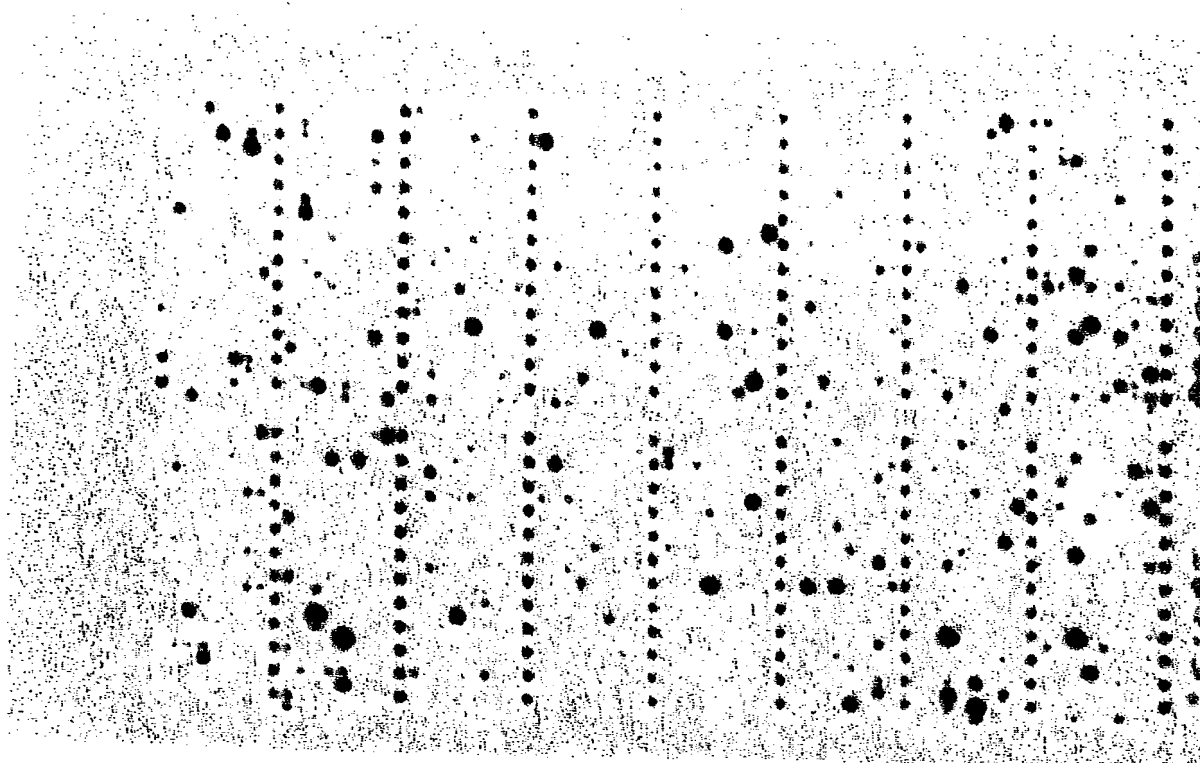
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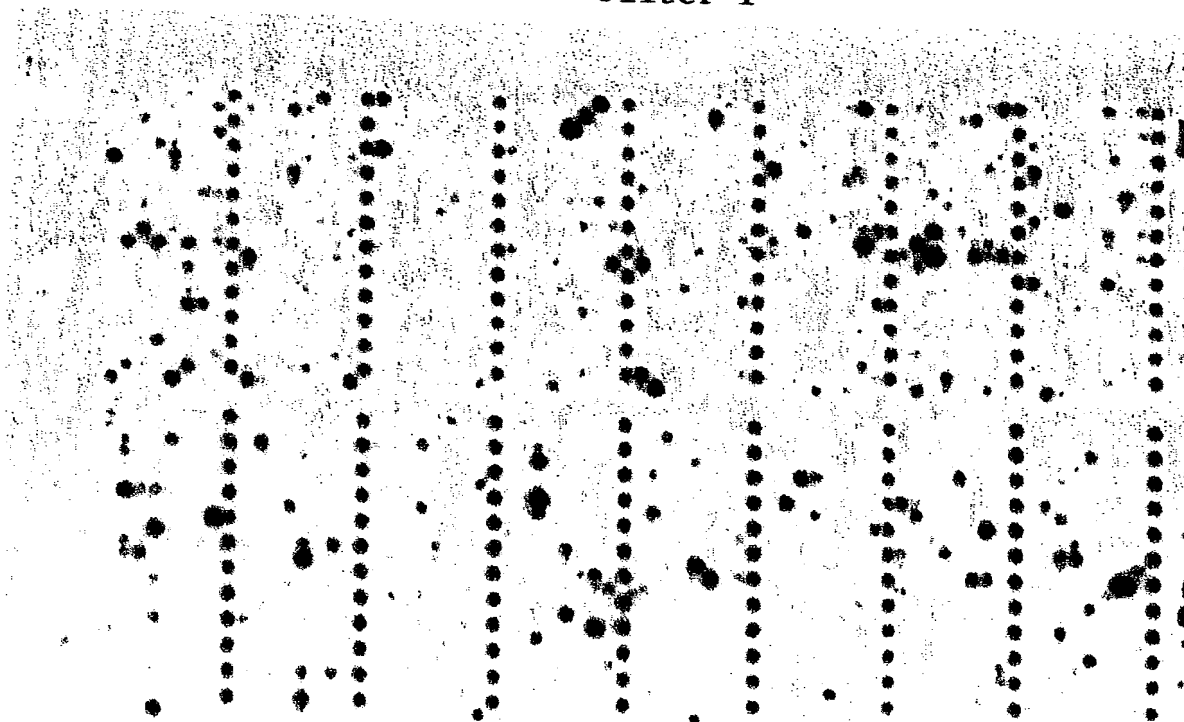
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FIG. 4A

161/161



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## DECLARATION — Utility or Design Patent Application

I hereby claim the benefit under 35 U.S.C. 120 of any United States application(s), or 365(c) of any PCT international application designating the United States of America, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

U.S. Parent Application or PCT Parent Number	Parent Filing Date (MM/DD/YYYY)	Parent Patent Number (if applicable)

☐ Additional U.S. or PCT international application numbers are listed on a supplemental priority data sheet PTO/SB/02B attached hereto.

As a named inventor, I hereby appoint the following registered practitioner(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

☐ Customer Number

OR

☒ Registered practitioner(s) name/registration number listed below

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Name	Registration Number	Name	Registration Number
Michael Stark	32,495	Myra McCormack	36,602
Steven P. Berman	24,772	Ellen C. Coletti	34,140
Andrea L. Colby	30,194	Mary A. Appollina	34,087

☐ Additional registered practitioner(s) named on supplemental Registered Practitioner Information sheet PTO/SB/02C attached hereto.

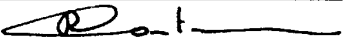
Direct all correspondence to: ☐ Customer Number  OR ☒ Correspondence address below

Name	Philip S. Johnson				
Address	Johnson & Johnson				
Address	One Johnson & Johnson Plaza				
City	New Brunswick	State	NJ	ZIP	08933-7003
Country	USA	Telephone	(732) 524-2359	Fax	(732) 524-2808

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. 1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Name of Sole or First Inventor:

☐ A petition has been filed for this unsigned inventor

Given Name (first and middle [if any])		Family Name or Surname	
Roland Henri		Contreras	
Inventor's Signature			Date
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			Belgium BEX
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Post Office Address			
City	Schelderode/Merelbeke	State	Country
			Belgium
ZIP	9820		

☒ Additional inventors are being named on the 2 supplemental Additional Inventor(s) sheet(s) PTO/SB/02A attached hereto

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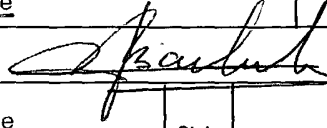
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## DECLARATION

## ADDITIONAL INVENTOR(S) Supplemental Sheet Page 3 of 4

Name of Additional Joint Inventor, if any:		<input type="checkbox"/> A petition has been filed for this unsigned inventor	
Given Name (first and middle [if any])		Family Name or Surname	
Marianne Denise		De Backer	
Inventor's Signature			Date 10/16/2001
Residence: City	Beerse	State	Country Belgium BEX Citizenship BE
Post Office Address	c/o Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse, Belgium		
Post Office Address			
City	San Diego	State CA	ZIP 92122 Country USA
Name of Additional Joint Inventor, if any:		<input type="checkbox"/> A petition has been filed for this unsigned inventor	
Given Name (first and middle [if any])		Family Name or Surname	
Walter Herman Maria Louis		Luyten	
Inventor's Signature			Date
Residence: City	Beerse	State	Country Belgium BEX Citizenship BE
Post Office Address	c/o Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse, Belgium		
Post Office Address			
City	Turnhout	State	ZIP 2300 Country Belgium
Name of Additional Joint Inventor, if any:		<input type="checkbox"/> A petition has been filed for this unsigned inventor	
Given Name (first and middle [if any])		Family Name or Surname	
Isabelle Karin Pieter		Lenaerts	
Inventor's Signature			Date
Residence: City	Gent	State	Country Belgium BEX Citizenship BE
Post Office Address	c/o University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium		
Post Office Address			
City	Zoersel	State	ZIP 2980 Country Belgium

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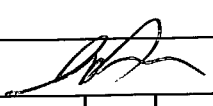
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5-00

<b>Name of Additional Joint Inventor, if any:</b>				<input type="checkbox"/> A petition has been filed for this unsigned inventor			
Given Name (first and middle [if any])				Family Name or Surname			
<u>Bart Jozef Maria</u>				<u>Nelissen</u>			
Inventor's Signature				Date	<u>10/26/01</u>		
Residence: City	<u>Beerse</u>	State		Country	<u>Belgium</u> <u>BEX</u>	Citizenship	<u>BE</u>
Post Office Address <u>c/o Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse, Belgium</u>							
Post Office Address							
City	<u>Meerhout</u>	State		ZIP	<u>2450</u>	Country	<u>Belgium</u>

6-00

<b>Name of Additional Joint Inventor, if any:</b>				<input type="checkbox"/> A petition has been filed for this unsigned inventor			
Given Name (first and middle [if any])				Family Name or Surname			
<u>Rieka Josephina</u>				<u>Reekmans</u>			
Inventor's Signature				Date			
Residence: City	<u>Gent</u>	State		Country	<u>Belgium</u> <u>BEX</u>	Citizenship	<u>BE</u>
Post Office Address <u>c/o University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium</u>							
Post Office Address							
City	<u>Wevelgem</u>	State		ZIP	<u>8560</u>	Country	<u>Belgium</u>

<b>Name of Additional Joint Inventor, if any:</b>				<input type="checkbox"/> A petition has been filed for this unsigned inventor			
Given Name (first and middle [if any])				Family Name or Surname			
Inventor's Signature				Date			
Residence: City		State		Country		Citizenship	
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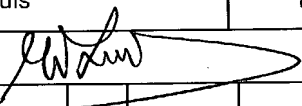
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<b>DECLARATION</b>	<b>ADDITIONAL INVENTOR(S)</b> <b>Supplemental Sheet</b> Page <u>3</u> of <u>4</u>
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<b>Name of Additional Joint Inventor, if any:</b>		<input type="checkbox"/> A petition has been filed for this unsigned inventor					
Given Name (first and middle [if any])		Family Name or Surname					
Marianne Denise		De Backer					
Inventor's Signature					Date		
Residence: City	Beerse	State		Country	Belgium	Citizenship	BE
Post Office Address	c/o Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse, Belgium						
Post Office Address							
City	San Diego	State	CA	ZIP	92122	Country	USA
<b>Name of Additional Joint Inventor, if any:</b>		<input type="checkbox"/> A petition has been filed for this unsigned inventor					
Given Name (first and middle [if any])		Family Name or Surname					
Walter Herman Maria Louis		Luyten					
Inventor's Signature					Date	10/26/01	
Residence: City	Beerse	State		Country	Belgium	Citizenship	BE
Post Office Address	c/o Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse, Belgium						
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Given Name (first and middle [if any])		Family Name or Surname					
Isabelle Karin Pieter		Lenaerts					
Inventor's Signature					Date		
Residence: City	Gent	State		Country	Belgium	Citizenship	BE
Post Office Address	c/o University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium						
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City	Zoersel	State		ZIP	2980	Country	Belgium

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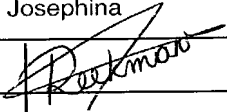
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Inventor's Signature					Date		
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Isabelle Karin Pieter		Lenaerts					
Inventor's Signature	<i>Lenaerts</i>				Date	10/03/01	
Residence: City	Gent	State		Country	Belgium	Citizenship	BE
Post Office Address	c/o University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium						
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Inventor's Signature					Date		
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Post Office Address		c/o Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse, Belgium					
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Given Name (first and middle [if any])				Family Name or Surname			
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Inventor's Signature					Date		10/03/0
Residence: City		Gent	State		Country	Belgium	Citizenship BE
Post Office Address		c/o University of Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium					
Post Office Address							
City		Wevelgem	State		ZIP	8560	Country Belgium
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Inventor's Signature					Date		
Residence: City			State		Country		Citizenship
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Luyten, Walter  
Lanaerts, Isabelle  
Nelissen, Bart  
Reekmans, Rieka

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Met Pro Tyr His Tyr Leu Phe Leu Ala Leu Phe Thr Tyr Leu Ala Thr
 1             5             10             15

Ser Asn Val Val Ser Gly Ser Thr Gln Ala Cys Leu Pro Val Gly Pro
 20             25             30

Arg Lys Asn Gly Met Asn Val Asn Phe Tyr Lys Tyr Ser Leu Leu Asp
 35             40             45

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<400> 4
Met Ala Ala Ile Arg Asp Tyr Lys Thr Ala Leu Asp Leu Thr Lys Ser
  1                               10                          15

Leu Pro Arg Pro Asp Gly Leu Ser Val Gln Glu Leu Met Asp Ser Lys
          20                25                30

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Thr Gln Lys Val Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr  
 340 345 350

Asn Val Cys Glu Phe Ala Asn Gln Phe Gly Val Pro Cys Met Ala Asp  
 355 360 365

Gly Gly Val Gln Lys His Trp Ser Tyr Tyr Tyr Gln Ser Phe Gly Ser  
 370 375 380

Trp Phe Phe Tyr Cys Tyr Asp Gly Trp Tyr Val Gly Arg Tyr Tyr Arg  
 385 390 395 400

Ile Thr Arg

<210> 5  
 <211> 812  
 <212> DNA  
 <213> Candida albicans

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 agcatcgatc gcaaaaaaac gtgagcttca tcacctacgg ttgtagacat tgcaagacac 180  
 atctttccag ttccctccag attatttcta gagattatag gggtaggacc ggaactgctt 240  
 atttaatgaa caaagttgtt aatgtcggtt aaggaaaggc cgagcaacga agaattgtga 300  
 ctggcgacta cttagtctgt gatattcttt gtcattggtg caagaggaac gtaggttgga 360  
 aatacttgca gagcagcaat gatgatcagc agtataagga aggaaagtgt atcttagagc 420  
 tgaaaaacat ttgtaaatgt acttgatgtc ttcccttggtc tgctatctag cacctctcgt 480  
 ctttttagtgc ttttttagcgt atgattcttt ttaagaatct ggtctttctt ccttctattt 540  
 tgattgggta tattttctatt cgtgtttcat tactgggtctg ggtaattgg gttttgggtt 600  
 ggtccagttg ttttcaagta gcctttattt ttccattgtg gtattttatc ttatcgattt 660  
 atactttttt ttattcaaag aaaattaaac agataatctc ttatgagcct agctactttg 720  
 tttttttcta cagggccatt gacttatgcc ctgaacgagt cttactttac tttttttgta 780  
 ttttcaataa tgtcgtgttt cccatgttgt aa 812

<210> 6  
 <211> 103  
 <212> PRT  
 <213> Candida albicans

<400> 6  
 Met Ile Leu Phe Lys Asn Leu Val Phe Leu Pro Ser Ile Leu Ile Gly  
 1 5 10 15

Tyr Ile Ser Ile Arg Val Ser Leu Leu Val Trp Val Asn Trp Val Leu  
 20 25 30

Val Trp Ser Ser Cys Phe Gln Val Ala Phe Ile Phe Ser Leu Trp Tyr  
 35 40 45

Phe Ile Leu Ser Ile Tyr Thr Phe Phe Tyr Ser Lys Lys Ile Lys Gln  
 50 55 60



Ile Ile Ser Tyr Glu Pro Ser Tyr Phe Val Phe Ser Tyr Arg Ala Ile  
 65 70 75 80

Asp Leu Cys Pro Glu Arg Val Leu Leu Tyr Phe Phe Cys Ile Phe Asn  
 85 90 95

Asn Val Val Phe Pro Met Leu  
 100

&lt;210&gt; 7

&lt;211&gt; 2507

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 7

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Gln Gln Ser Ile Glu Thr Arg Asp Ala Ile Asp Lys Glu Asn Gly Val  
35 40 45

Gln Thr Glu Thr Gly Glu Asn Ser Ala Lys Asn Ala Glu Gln Asn Val  
50 55 60

Ser Ser Thr Asn Leu Asn Asn Ala Pro Thr Asn Gly Ala Leu Asp Asp  
65 70 75 80

Asp Val Ile Pro Asn Ala Ile Val Ile Lys Asn Ile Pro Phe Ala Ile  
85 90 95

Lys Lys Glu Gln Leu Leu Asp Ile Ile Glu Glu Met Asp Leu Pro Leu  
100 105 110

Pro Tyr Ala Phe Asn Tyr His Phe Asp Asn Gly Ile Phe Arg Gly Leu  
115 120 125

Ala Phe Ala Asn Phe Thr Thr Pro Glu Glu Thr Thr Gln Val Ile Thr  
130 135 140

Ser Leu Asn Gly Lys Glu Ile Ser Gly Arg Lys Leu Lys Val Glu Tyr  
145 150 155 160

Lys Lys Met Leu Pro Gln Ala Glu Arg Glu Arg Ile Glu Arg Glu Lys  
165 170 175

Arg Glu Lys Arg Gly Gln Leu Glu Glu Gln His Arg Ser Ser Ser Asn  
180 185 190

Leu Ser Leu Asp Ser Leu Ser Lys Met Ser Gly Ser Gly Asn Asn Asn  
195 200 205

Thr Ser Asn Asn Gln Leu Phe Ser Thr Leu Met Asn Gly Ile Asn Ala  
210 215 220

Asn Ser Met Met Asn Ser Pro Met Asn Asn Thr Ile Asn Asn Asn Ser  
225 230 235 240

Ser Asn Asn Asn Asn Ser Gly Asn Ile Ile Leu Asn Gln Pro Ser Leu

	245		250		255										
Ser	Ala	Gln	His	Thr	Ser	Ser	Ser	Leu	Tyr	Gln	Thr	Asn	Val	Asn	Asn
	260							265					270		
Gln	Ala	Gln	Met	Ser	Thr	Glu	Arg	Phe	Tyr	Ala	Pro	Leu	Pro	Ser	Thr
	275						280					285			
Ser	Thr	Leu	Pro	Leu	Pro	Pro	Gln	Gln	Leu	Asp	Phe	Asn	Asp	Pro	Asp
	290					295					300				
Thr	Leu	Glu	Ile	Tyr	Ser	Gln	Leu	Leu	Leu	Phe	Lys	Asp	Arg	Glu	Lys
305					310					315					320
Tyr	Tyr	Tyr	Glu	Leu	Ala	Tyr	Pro	Met	Gly	Ile	Ser	Ala	Ser	His	Lys
			325						330					335	
Arg	Ile	Ile	Asn	Val	Leu	Cys	Ser	Tyr	Leu	Gly	Leu	Val	Glu	Val	Tyr
			340					345					350		
Asp	Pro	Arg	Phe	Ile	Ile	Ile	Arg	Arg	Lys	Ile	Leu	Asp	His	Ala	Asn
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Leu	Gln	Ser	His	Leu	Gln	Gln	Gln	Gly	Gln	Met	Thr	Ser	Ala	His	Pro
	370					375					380				
Leu	Gln	Pro	Asn	Ser	Thr	Gly	Gly	Ser	Met	Asn	Arg	Ser	Gln	Ser	Tyr
385					390					395					400
Thr	Ser	Leu	Leu	Gln	Ala	His	Ala	Ala	Ala	Ala	Ala	Asn	Ser	Ile	Ser
				405				410						415	
Asn	Gln	Ala	Val	Asn	Asn	Ser	Ser	Asn	Ser	Asn	Thr	Ile	Asn	Ser	Asn
			420					425					430		
Asn	Gly	Asn	Gly	Asn	Asn	Val	Ile	Ile	Asn	Asn	Asn	Ser	Ala	Ser	Ser
	435						440					445			
Thr	Pro	Lys	Ile	Ser	Ser	Gln	Gly	Gln	Phe	Ser	Met	Gln	Pro	Thr	Leu
	450					455					460				
Thr	Ser	Pro	Lys	Met	Asn	Ile	His	His	Ser	Ser	Gln	Tyr	Asn	Ser	Ala
465					470					475					480
Asp	Gln	Pro	Gln	Gln	Pro	Gln	Pro	Gln	Thr	Gln	Gln	Asn	Val	Gln	Ser
					485				490					495	
Ala	Ala	Gln	Gln	Gln	Gln	Ser	Phe	Leu	Arg	Gln	Gln	Ala	Thr	Leu	Thr
			500					505					510		
Pro	Ser	Ser	Arg	Ile	Pro	Ser	Gly	Tyr	Ser	Ala	Asn	His	Tyr	Gln	Ile
		515					520					525			
Asn	Ser	Val	Asn	Pro	Leu	Leu	Arg	Asn	Ser	Gln	Ile	Ser	Pro	Pro	Asn
	530					535					540				
Ser	Gln	Ile	Pro	Ile	Asn	Ser	Gln	Thr	Leu	Ser	Gln	Ala	Gln	Pro	Pro

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<211> 3674
<212> DNA
<213> Candida albicans
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caattaattg	gcagccagct	gacgatgtca	ttattcctcc	ctctgtctcc	aatgatgagg	180
cgaaggctaa	atttgggtcaa	tttaatgaaa	ttaaacccta	tttaagattc	accaagtcga	240
aataagcttt	gaaataaacg	actttactat	atacagggtat	atgaagtatc	tctaactaaa	300
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<400> 10
Met Val Lys Asp Asn Arg Asp Ser Asp Gln Asp Gln Asp Phe Ser Ser
  1                    5                10                15

Ala His Met Lys Arg Gln Pro Glu Gln Gln Gln Leu Gln Gln His Gln
  20                25                30

Phe Pro Ser Lys Lys Gln Arg Ile Ser His His Asp Asp Ser His Gln
  35                40                45

Ile Asn His Arg Pro Val Thr Ser Cys Thr His Cys Arg Gln His Lys
  50                55                60

Ile Lys Cys Asp Ala Ser Gln Asn Phe Pro His Pro Cys Ser Arg Cys

```



370	375	380
Val Met Leu Thr Ala Cys Leu Ser Asp Pro Glu Pro Thr Met Tyr Cys 385 390 395 400		
Lys Leu Ser Ser Leu Ile Lys Gln Leu Ala Ile Glu Thr Cys Trp Ile 405 410 415		
Arg Thr Pro Arg Ser Thr His Ile Ser Gln Ala Leu Leu Ile Leu Cys 420 425 430		
Ile Trp Pro Leu Pro Asn Gln Lys Val Leu Asp Asp Cys Ser Tyr Arg 435 440 445		
Phe Val Gly Leu Ala Lys Ser Leu Ser Tyr Gln Leu Gly Leu His Arg 450 455 460		
Gly Glu Phe Ile Ser Glu Phe Thr Arg Thr Gln Thr Ser Met Pro Asn 465 470 475 480		
Ala Glu Lys Trp Arg Thr Arg Thr Trp Leu Gly Ile Phe Phe Ala Glu 485 490 495		
Leu Cys Trp Ala Ser Ile Leu Gly Leu Pro Pro Thr Ser Gln Thr Asp 500 505 510		
Tyr Leu Leu Glu Lys Ala Leu Ser Cys Gly Asp Glu Glu Ser Glu Glu 515 520 525		
Asp Asn Asn Asp Ser Ile Asp Asn Asn Asn Asn Asp Lys Arg Asn Lys 530 535 540		
Lys Asp Glu Pro His Val Glu Ser Lys Tyr Lys Leu Pro Gly Ser Phe 545 550 555 560		
Arg Arg Leu Leu Ser Leu Ala Asn Phe Gln Ala Lys Leu Ser His Ile 565 570 575		
Ile Gly Ser Ser Thr Ser Ser Pro Asp Gly Leu Leu Glu Pro Lys Tyr 580 585 590		
Arg Ala Glu Thr Leu Ser Ile Leu Gly Lys Glu Leu Asp Leu Leu Ala 595 600 605		
Lys Thr Leu Asn Phe Gln Ser Asp Asp Thr Val Asn Ile Tyr Phe Leu 610 615 620		
Tyr Val Lys Leu Thr Val Cys Cys Phe Ala Phe Leu Pro Glu Thr Pro 625 630 635 640		
Pro Thr Asp Gln Ile Pro Tyr Val Thr Glu Ala Tyr Leu Thr Ala Thr 645 650 655		
Lys Ile Val Thr Leu Leu Asn Asn Leu Leu Glu Thr His Gln Leu Ile 660 665 670		
Glu Leu Pro Ile Tyr Ile Arg Gln Ala Ala Thr Phe Ser Ala Leu Ile		

675	680	685
Leu Phe Lys Leu Gln Leu Thr Pro Leu Leu Pro Asp Lys Tyr Phe Asp 690 695 700		
Ser Ala Arg Gln Ser Val Val Thr Ile His Arg Leu Tyr Arg Asn Gln 705 710 715 720		
Leu Thr Ala Trp Ala Thr Ser Val Glu Asn Asp Ile Ser Arg Thr Ala 725 730 735		
Ser Met Leu Glu Lys Leu Asn Phe Val Leu Ile Met His Pro Glu Val 740 745 750		
Phe Val Glu Glu Asp Gly Ile Ile Ser Arg Met Arg Ser His Leu Thr 755 760 765		
Gly Ser Leu Phe Tyr Asp Leu Val Trp Cys Val His Glu Ala Arg Arg 770 775 780		
Arg Glu Met Asp Pro Glu Tyr Asn Lys Gln Ala Leu Glu Lys Ala Ala 785 790 795 800		
Lys Lys Arg Lys Phe Ser Ser Asn Gly Ile Tyr Asn Gly Thr Ser Ser 805 810 815		
Thr Gly Gly Ile Thr Asp Arg Lys Leu Tyr Pro Leu Pro Leu Tyr Asn 820 825 830		
His Ile Ser Arg Asp Asp Phe Glu Thr Val Thr Lys Thr Thr Pro Ser 835 840 845		
Gly Thr Thr Val Thr Thr Leu Val Pro Thr Lys Asn Ala Leu Lys Gln 850 855 860		
Ala Glu Lys Leu Ala Lys Thr Asn Asn Gly Asp Ser Asp Gly Ser Ile 865 870 875 880		
Met Glu Ile Asn Gly Ile Pro Leu Ser Met Leu Gly Glu Thr Gly Ser 885 890 895		
Val Lys Phe Gln Ser Leu Phe Ala Asn Thr Ser Asn Ser Asn Asp Tyr 900 905 910		
Asn Asn Asn Arg Thr Leu Leu Asp Ala Ser Asn Asp Ile Ser Ile Pro 915 920 925		
Ser Asn Ser Ile Tyr Pro Val Ala Ser Val Pro Ala Ser Asn Asn Asn 930 935 940		
Pro Gln Ser Thr Lys Val Asp Tyr Tyr Ser Asn Gly Pro Ser Val Ile 945 950 955 960		
Pro Asp Leu Ser Met Lys Arg Ser Val Ser Thr Pro Val Asn His Phe 965 970 975		
Pro Ala Ser Val Pro Gly Leu Arg Asn His Pro Val Gly Asn Leu Ser		



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<400> 12
Met Lys Ser Thr Phe Lys Ser Glu Tyr Pro Phe Glu Lys Arg Lys Ala
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Glu Ser Glu Arg Ile Ala Asp Arg Phe Lys Asn Arg Ile Pro Val Ile
          20             25             30
Cys Glu Lys Ala Glu Lys Ser Asp Ile Pro Glu Ile Asp Lys Arg Lys
      35             40             45

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14

Tyr Leu Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val Ile  
50 55 60

Arg Lys Arg Ile Met Leu Pro Pro Glu Lys Ala Ile Phe Ile Phe Val  
65 70 75 80

Asn Asp Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile Tyr Gln  
85 90 95

Glu His Lys Asp Lys Asp Gly Phe Leu Tyr Val Thr Tyr Ser Gly Glu  
100 105 110

Asn Thr Phe Gly Arg  
115

&lt;210&gt; 13

&lt;211&gt; 1145

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 13

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&lt;210&gt; 14

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 14

Met Ser Phe Asn Ser Pro Phe Phe Asp Phe Phe Asp Asn Ile Asn Asn  
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Glu Val Asp Ala Phe Asn Arg Leu Leu Gly Glu Gly Gly Leu Arg Gly  
20 25 30

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tatatgagtt	gatgaataaa	tagttataaa	aacttgcttt	ggcttcgata	tatgaccgtt	240
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 370 375 380  
 Lys Phe Gln Cys Ser Asn Asp Thr Tyr Val Arg Tyr Val Ile Asn Asp  
 385 390 395 400  
 Ala Val Val Pro Ile Glu Thr Cys Ser Thr Gly Pro Gly Phe Ser Cys  
 405 410 415  
 Glu Ile Asn Asp Phe Tyr Asp Tyr Ala Glu Lys Arg Val Ala Gly Thr  
 420 425 430  
 Asp Phe Leu Lys Val Cys Asn Val Ser Ser Val Ser Asn Ser Thr Glu  
 435 440 445  
 Leu Thr Phe Tyr Trp Asp Trp Asn Thr Thr His Tyr Asn Ala Ser Leu  
 450 455 460  
 Leu Arg Gln  
 465

&lt;210&gt; 21

&lt;211&gt; 1563

&lt;212&gt; DNA

<213> *Candida albicans*

&lt;400&gt; 21

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&lt;210&gt; 22

&lt;211&gt; 236

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 22

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Met Lys Leu Asn Ile Ser Tyr Pro Val Asn Gly Ser Gln Lys Thr Phe
 1             5             10             15

Glu Ile Asp Asp Glu His Arg Ile Arg Val Phe Phe Asp Lys Arg Ile
      20             25             30

Gly Gln Glu Val Asp Gly Glu Ala Val Gly Asp Glu Phe Lys Gly Tyr
      35             40             45

Val Phe Lys Ile Ser Gly Gly Asn Asp Lys Gln Gly Phe Pro Met Lys
      50             55             60

Gln Gly Val Leu Leu Pro Thr Arg Ile Lys Leu Leu Leu Thr Lys Asn
      65             70             75             80

Val Ser Cys Tyr Arg Pro Arg Arg Asp Gly Glu Arg Lys Arg Lys Ser
      85             90             95

Val Arg Gly Ala Ile Val Gly Pro Asp Leu Ala Val Leu Ala Leu Val

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Ile Val Lys Lys Gly Glu Gln Glu Leu Glu Gly Leu Thr Asp Thr Thr		
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Val Pro Lys Arg Leu Gly Pro Lys Arg Ala Asn Asn Ile Arg Lys Phe		
130	135	140
Phe Gly Leu Ser Lys Glu Asp Asp Val Arg Asp Phe Val Ile Arg Arg		
145	150	155
Glu Val Thr Lys Gly Glu Lys Thr Tyr Thr Lys Ala Pro Lys Ile Gln		
165	170	175
Arg Leu Val Thr Pro Gln Arg Leu Gln Arg Lys Arg His Gln Arg Ala		
180	185	190
Leu Lys Val Arg Asn Ala Gln Ala Gln Arg Glu Ala Ala Ala Glu Tyr		
195	200	205
Ala Gln Leu Leu Ala Lys Arg Leu Ser Glu Arg Lys Ala Glu Lys Ala		
210	215	220
Glu Ile Arg Lys Arg Arg Ala Ser Ser Leu Lys Ala		
225	230	235

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 <211> 893  
 <212> DNA  
 <213> Candida albicans

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 gcactaacca ctatgaatac accaacaaca gtatagctaa attggacgcg cagagagtta 780  
 gtagaagaag aaggaagaaa agggaagcgg agagaagaga ttatgacaca taaaaactac 840  
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<210> 24  
 <211> 130  
 <212> PRT  
 <213> Candida albicans

<400> 24



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aggcggttta	ttatctttgt	ccctttatac	tgttgtgttt	cttgcttatt	gcttcagtag	180	
gcagcgtata	gtataaccag	aaaaaagtga	aaaaataact	aaaaaagcac	tatgagatga	240	
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cattccgcac	ccgagtatga	tccatcttat	aagctgatcc	agttgacacc	agagttactg	360	
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<210> 26

<211> 309

<212> PRT

<213> Candida albicans

<400> 26

Met Arg Glu Phe Val Pro Glu Gln Pro Ile Thr Phe Asp Glu Thr Leu  
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Leu Phe Gly Leu Ser Lys Pro Tyr Met Asp Val Val Gly Phe Ala Lys  
 20 25 30

Thr Glu Ser Glu Phe Glu Thr Arg Glu Thr His Gly Glu Leu Asn Leu  
 35 40 45

Asn Ser Val Pro Ile Tyr Asn Gly Glu Leu Asp Phe Ser Asp Lys Ile  
 50 55 60

Met Lys Arg Ser Ser Thr Lys Val Ile Gly Thr Leu Glu Glu Leu Leu  
 65 70 75 80

Glu Asn Ser Pro Cys Ser Ala Leu Glu Gly Ile Ser Lys Trp His Lys  
 85 90 95

Ile Gly Gly Ser Val Lys Asp Gly Val Leu Cys Ile Leu Ser Gln Asp  
 100 105 110

Phe Leu Phe Lys Ala Leu His Val Leu Leu Met Ser Ala Met Ala Glu  
 115 120 125

Ser Leu Asp Leu Gln His Leu Asn Val Glu Asp Thr His His Ala Val  
 130 135 140

Gly Lys Asp Ile Glu Asp Glu Phe Asn Pro Tyr Thr Arg Glu Ile Ile  
 145 150 155 160

Glu Thr Val Leu Asn Lys Phe Ala Val Gln Glu Gln Glu Ala Glu Asn  
 165 170 175

Asn Thr Trp Arg Leu Arg Ile Pro Phe Ile Ala Gln Trp Tyr Gly Ile  
 180 185 190

Gln Ala Leu Arg Lys Tyr Val Ser Gly Ile Ser Met Pro Ile Asp Glu  
 195 200 205

Phe Leu Ile Lys Trp Lys Ser Leu Phe Pro Pro Phe Phe Pro Cys Asp  
 210 215 220

Ile Asp Ile Asp Met Leu Arg Gly Tyr His Phe Lys Pro Thr Asp Lys  
 225 230 235 240

Thr Val Gln Tyr Ile Ala Lys Ser Thr Leu Pro Met Asp Pro Lys Glu  
 245 250 255



<211> 483

<212> PRT

<213> *Candida albicans*

<400> 28

Met Val Thr Gln Thr Asn Pro Val Pro Val Thr Tyr Pro Thr Asp Ala  
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Tyr Ile Pro Thr Tyr Leu Pro Asp Asp Lys Val Ser Asn Leu Ala Asp  
20 25 30

Leu Lys Lys Leu Ile Glu Met Asp Ser Arg Leu Asp Leu Tyr Leu Thr  
35 40 45

Arg Arg Arg Leu Asp Thr Ser Ile Asn Leu Pro Thr Asn Thr Lys Thr  
50 55 60

Lys Asp His Pro Pro Asn Lys Glu Met Leu Arg Ile Tyr Val Tyr Asn  
65 70 75 80

Thr Thr Glu Ser Ser Pro Arg Ser Asp Ser Gly Thr Pro Ala Asp Ser  
85 90 95

Gly Lys Thr Thr Trp Thr Leu Arg Ile Glu Gly Lys Leu Leu His Glu  
100 105 110

Ser Ala Asn Gly Lys His Pro Phe Ser Glu Phe Leu Glu Gly Val Ala  
115 120 125

Val Asp Phe Lys Arg Leu Lys Pro Leu Gly Met Gly Lys Lys Arg Lys  
130 135 140

Arg Asp Ser Ser Leu Ser Leu Pro Leu Asn Leu Gln Gln Pro Glu Tyr  
145 150 155 160

Asn Asp Gln Asp Ser Thr Met Gly Asp Asn Asp Asn Gly Glu Asp Glu  
165 170 175

Asp Ser Ala Glu Ala Glu Ser Arg Glu Glu Ile Val Asp Ala Leu Glu  
180 185 190

Trp Asn Tyr Asp Glu Asn Asn Val Val Glu Phe Asp Gly Ile Asp Ile  
195 200 205

Lys Arg Gln Gly Lys Asp Asn Leu Arg Cys Ser Ile Thr Ile Gln Leu  
210 215 220

Arg Gly Val Asp Gly Gly Lys Val Gln Tyr Ser Pro Asn Leu Ala Thr  
225 230 235 240

Leu Ile Gly Met Gln Thr Gly Ser Val Asn Asp Ala Val Tyr Ser Ile  
245 250 255

Tyr Lys Tyr Ile Leu Ile Asn Asn Leu Phe Val Thr Glu Gln Thr Glu  
260 265 270

Ala Gln Asp Gly Ser Asn Asp Ala Glu Asp Ser Ser Asn Glu Asn Asn

275                      280                      285  
 Asn Lys Asn Gly Ala Gly Asp Asp Asp Gly Val Glu Gly Ser Thr Pro  
     290                      295                      300  
 Lys Asp Lys Pro Glu Leu Gly Glu Val Lys Leu Asp Ser Leu Leu Gln  
     305                      310                      315                      320  
 Lys Val Leu Asp Thr Asn Ala Ala His Leu Pro Leu Met Asn Val Val  
                     325                      330                      335  
 Gln Thr Val Asn Lys Leu Val Ser Pro Leu Pro Pro Ile Ile Leu Asp  
                     340                      345                      350  
 Tyr Thr Ile Asp Leu Ser Lys Asp Thr Thr Tyr Gly Ala Thr Thr Leu  
                     355                      360                      365  
 Asp Val Asp Val Ser His Ile Leu His Gln Pro Gln Pro Gln Pro Asn  
     370                      375                      380  
 Leu Gln Lys Glu Glu Glu Thr Asp Ala Glu Asp Thr Ala Lys Leu Arg  
     385                      390                      395                      400  
 Glu Ile Thr Lys Leu Ala Leu Gln Leu Asn Ser Ser Ala Gln Lys Tyr  
                     405                      410                      415  
 Gln Phe Phe His Glu Leu Ser Leu His Pro Arg Glu Thr Leu Thr His  
                     420                      425                      430  
 Tyr Leu Trp Ser Ser Lys Gln Asn Glu Leu Val Leu Gln Gly Asp Gln  
     435                      440                      445  
 Tyr Phe Asn Glu Asp Ala Ala Arg Thr Ser Asp Ile Tyr Ser Asn Asn  
     450                      455                      460  
 Asn Asn Asp Arg Ser Leu Met Gly Asn Ile Ser Leu Leu Tyr Ser Gln  
     465                      470                      475                      480  
 Gly Arg Leu

&lt;210&gt; 29

&lt;211&gt; 911

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 29

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gaatgcagcg cagacagcac agtttttcat acccggtttt gcgccatttg gcaattagca 420
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<400> 31						
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&lt;210&gt; 32

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 32

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Met Thr Thr Thr Val Pro Lys Ile Phe Ala Phe His Glu Phe Ser Asp
  1             5             10             15

```

```

Val Ala Glu Ala Val Ala Asp His Val Val His Ala Gln Asp Gly Ala
      20             25             30

```

```

Leu Ala Pro Lys Asn Glu Arg Lys His Ser Val Pro Asn Ile Ser Met
    35             40             45

```

```

Asn Ala Leu Asp Met Thr Arg Glu Ala Ser Cys Lys Ser Thr Ala Ser
    50             55             60

```

```

Ala Ala Glu Gly Lys Ser Gly Ser Ser Gly Ser Gly Ser Gly Ser Ser
    65             70             75             80

```

```

Lys Pro Lys Lys Glu Lys Arg Phe Lys Ile Ala Leu Ser Gly Gly Ser
      85             90             95

```

```

Leu Ile Glu Val Leu His Glu Gly Leu Leu Lys Arg Asp Asp Val Arg
    100            105            110

```

```

Trp Gly Asp Trp Asp Ile Tyr Phe Ala Asp Glu Arg Leu Val Pro Phe
    115            120            125

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```

Ser Ser Asn Glu Ser Asn Tyr Gly Cys Ala Lys Arg Lys Ile Leu Asp
    130            135            140

```

```

Leu Ile Asp Thr Ala Lys Tyr Gly Thr Pro Lys Val Tyr His Ile Asp
    145            150            155            160

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Glu Ser Leu Ile Asp Asp Pro Gln Glu Cys Val Asp Asn Tyr Glu Lys  
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 Val Leu Ile Arg Gly Phe Ala Gly Arg Asp Ser Val Lys Leu Pro Met  
 180 185 190  
 Phe Asp Leu Phe Leu Leu Gly Cys Ala Pro Asp Gly His Ile Ala Ser  
 195 200 205  
 Leu Phe Pro Asn Phe Gln Asp Asn Leu Arg Glu Lys Leu Ala Trp Val  
 210 215 220  
 Val Pro Val Glu Asn Ala Pro Ser Gly Pro Ser Thr Arg Ile Ser Leu  
 225 230 235 240  
 Thr Ile Pro Val Ile Cys His Ser His Arg Val Thr Phe Val Val Glu  
 245 250 255  
 Gly Ala Thr Lys Ala Pro Ile Ile Lys Thr Ile Met Glu Arg Pro Glu  
 260 265 270  
 Lys Gly Leu Pro Ser Ser Ile Val Asn Glu Gly Ala Ala Gly Arg Val  
 275 280 285  
 Ser Trp Phe Val Asp Asp Asp Ala Leu Thr Asp Val Leu Val Thr Lys  
 290 295 300  
 Lys Lys Tyr Lys Phe His Gln Gly Leu Ser Ile  
 305 310 315

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 <211> 1196  
 <212> DNA  
 <213> Candida albicans

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 gaggtaatga agaaatcaag aaactgcaca ctcaaggga acttttagaa tcattacaag 1140



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<210> 34

<211> 231

<212> PRT

<213> Candida albicans

<400> 34

Met Ile Pro Ser Asn Lys Arg Asn Ala Arg Ile Leu Ser Ile Thr Thr  
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Leu Leu Leu Leu Leu Val Phe Phe Val Ala Gln Asn Ala Asn Phe Leu  
20 25 30

Thr Val Glu Ile Lys Glu Glu Thr Ser Lys Ala Phe Ser Thr Asn Met  
35 40 45

Asp Asn Met Ala Gly Gly Ser Ser Arg Glu Tyr Ala Ala Met Pro Thr  
50 55 60

Ser Thr Thr Asn Lys Gly Ser Ser Glu Val Asp Glu Glu Ile Asn Glu  
65 70 75 80

Ile Lys Gln Lys Val Gly Leu Gln Gln Pro Ile Ala Ser Val Asp Asp  
85 90 95

Ser Leu Ser Ala Ile Lys Asn Asp Lys Gly Ser Arg Ile Thr Lys Ala  
100 105 110

Phe Asn Val Gln Lys Glu Tyr Ser Leu Ile Leu Asp Leu Ser Pro Ile  
115 120 125

Ile Ile Phe Ser Lys Ser Thr Cys Ser Tyr Ser Lys Gly Met Lys Glu  
130 135 140

Leu Leu Glu Asn Glu Tyr Gln Phe Ile Pro Asn Tyr Tyr Ile Ile Glu  
145 150 155 160

Leu Asp Lys His Gly His Gly Glu Glu Leu Gln Glu Tyr Ile Lys Leu  
165 170 175

Val Thr Gly Arg Gly Thr Val Pro Asn Leu Leu Val Asn Gly Val Ser  
180 185 190

Arg Gly Gly Asn Glu Glu Ile Lys Lys Leu His Thr Gln Gly Lys Leu  
195 200 205

Leu Glu Ser Leu Gln Val Trp Ser Asp Gly Lys Phe Ser Val Glu Gln  
210 215 220

Arg Glu Lys Pro Ser Asn Asn  
225 230

<210> 35

<211> 1889

<212> DNA

<213> Candida albicans

<400> 35

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caataccagg	tacgactcct	gatccaataa	ttgaggcgca	gaacgataat	gatagtagtg	180
atagtagcgg	catagatttg	atagccttct	taagaaatgg	accattataa	agtttttgta	240
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$\langle 210 \rangle$  36

<211> 462

&lt;212&gt; PRT

<213> Candida albicans

<400> 36

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Ala Gly Asn Ala Thr Ser Asn Glu Phe Asp Glu His Leu Gln Asn Glu  
35 40 45

Val Glu Arg Glu Arg Glu Ile Gln Lys Lys Lys Lys Ile Lys Arg Thr  
50 55 60

Gln	Ser	Lys	Lys	Ser	Pro	Asp	Leu	Ile	Asn	Lys	Ser	Thr	Phe	Gln	Ser		
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Tyr	Glu	Ile	Val	Ile	Asp	Gly	Pro	Leu	Arg	Lys	Ile	Lys	Pro	Tyr	His		
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Phe	Thr	Tyr	Arg	Thr	Phe	Cys	Lys	Glu	Arg	Trp	Arg	Asp	Lys	Lys	Leu		
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Ser	His	Gln	Ile	Arg	Val	His	Leu	Gln	Tyr	Leu	Gly	His	Pro	Ile	Ala		
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 Tyr Gly Glu Val Leu Arg Gln Glu Lys Cys Ser Ile Cys Glu Ser Asp  
 405 410 415  
 Leu Tyr Thr Asp Pro Gly Pro Asn Asp Leu Asp Leu Trp Leu His Ala  
 420 425 430  
 Tyr Leu Tyr Glu Ser Thr Glu Thr Glu Glu Gly Thr Glu Lys Lys Lys  
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&lt;210&gt; 37

&lt;211&gt; 1364

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 37

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&lt;210&gt; 38

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 38

41

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 Thr Ala Val Ala His Val Lys Ala Gly Lys Gly Leu Ile Lys Val Asn  
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 Gly Ser Pro Ile Thr Leu Val Glu Pro Glu Ile Leu Arg Phe Lys Val  
 35 40 45  
 Tyr Glu Pro Leu Leu Leu Val Gly Leu Asp Lys Phe Ser Asn Ile Asp  
 50 55 60  
 Ile Arg Val Arg Val Thr Gly Gly Gly His Val Ser Gln Val Tyr Ala  
 65 70 75 80  
 Ile Arg Gln Ala Ile Ala Lys Gly Leu Val Ala Tyr His Gln Lys Tyr  
 85 90 95  
 Val Asp Glu Gln Ser Lys Asn Glu Leu Lys Lys Ala Phe Thr Ser Tyr  
 100 105 110  
 Asp Arg Thr Leu Leu Ile Ala Asp Ser Arg Arg Pro Glu Pro Lys Lys  
 115 120 125  
 Phe Gly Gly Lys Gly Ala Arg Ser Arg Phe Gln Lys Ser Tyr Arg  
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&lt;210&gt; 39

&lt;211&gt; 1088

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 39

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&lt;210&gt; 40

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<211> 158  
<212> PRT  
<213> Candida albicans

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35 40 45  
Phe Leu Asp Ile Gln Pro Thr Ala Glu Gly His Ala Leu Ile Ile Pro  
50 55 60  
Lys Tyr His Gly Ala Lys Leu His Asp Ile Pro Asp Glu Phe Leu Thr  
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Asp Ala Met Pro Ile Ala Lys Arg Leu Ala Lys Ala Met Lys Leu Asp  
85 90 95  
Thr Tyr Asn Val Leu Gln Asn Asn Gly Lys Ile Ala His Gln Glu Val  
100 105 110  
Asp His Val His Phe His Leu Ile Pro Lys Arg Asp Glu Lys Ser Gly  
115 120 125  
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<211> 578  
<212> DNA  
<213> Candida albicans

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50 55 60

Ala Val Arg Gln Leu Tyr Lys Gly Lys Lys Tyr Gln Pro Lys Asp Leu  
65 70 75 80

Arg Ala Lys Lys Thr Arg Ala Leu Arg Arg Ala Leu Thr Lys Phe Glu  
85 90 95

Ala Ser Gln Val Thr Glu Lys Gln Arg Lys Lys Gln Ile Ala Phe Pro  
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Gln Arg Lys Tyr Ala Ile Lys Ala  
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<210> 45

<211> 2660

<212> DNA

<213> Candida albicans

<400> 45

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Ala	Glu	Thr	Leu	Val	Cys	His	Tyr	Gly	Thr	Asn	Ser	Leu	Pro	Ser	Ile				
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Glu	Val	Asn	Gly	Thr	Thr	Lys	Ser	Leu	Glu	Ser	Ala	Met	Val	Gln	Leu				
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Asp	Lys	Asp	Ile	His	Asp	Val	Ile	Gly	Asn	Asp	Asp	Phe	Val	Leu	Val				
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Ser	Leu	Tyr	Ser	Thr	Trp	His	Ile	Arg	Val	Thr	Leu	Pro	Arg	Gln	Ala				
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 260 265 270  
 Trp Ser Leu Asn Asn Ser Pro Tyr Val Glu Asp Gln Asp Ser Ile Ser  
 275 280 285  
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 290 295 300  
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 305 310 315 320  
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 325 330 335  
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 340 345 350  
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 370 375 380  
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 385 390 395 400  
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ccccattgca	gatggacgat	attttaacaa	gacgaacctg	acctcgtctt	ctataaaaact	420	
ggacttctaa	gcaactctca	tttatcttat	atccggtcca	ttttgtacta	aaagaaccag	480	
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48

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578

&lt;210&gt; 48

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 48

Met Arg Ala Lys Trp Arg Lys Lys Arg Thr Arg Arg Leu Lys Arg Lys  
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Arg Arg Lys Val Arg Ala Arg Ser Lys  
 20 25

&lt;210&gt; 49

&lt;211&gt; 1354

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 49

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 tttccacaa agaaagtacg ctattaaggc ttaa 1354

&lt;210&gt; 50

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 50

Met Ala Gly Val Lys Ala Tyr Glu Leu Arg Thr Lys Ser Lys Glu Gln  
 1 5 10 15

Leu Ala Ser Gln Leu Val Asp Leu Lys Lys Glu Leu Ala Glu Leu Lys  
 20 25 30  
 Val Gln Lys Leu Ser Arg Pro Ser Leu Pro Lys Ile Lys Thr Val Arg  
 35 40 45  
 Lys Ser Ile Ala Cys Val Leu Thr Val Ile Asn Glu Gln Gln Arg Glu  
 50 55 60  
 Ala Val Arg Gln Leu Tyr Lys Gly Lys Lys Tyr Gln Pro Lys Asp Leu  
 65 70 75 80  
 Arg Ala Lys Lys Thr Arg Ala Leu Arg Arg Ala Leu Thr Lys Phe Glu  
 85 90 95  
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 100 105 110  
 Gln Arg Lys Tyr Ala Ile Lys Ala  
 115 120

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 <211> 3254  
 <212> DNA  
 <213> Candida albicans

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 aggagagtca tttagaaggc gtattgctca atagtagaaa gcaggcctgt gcacatgaat 180  
 taattaaaaa atataaagggt agtgattaga cgacacatgt ccataggtaa cctgtcataa 240  
 ttttgaacaa tttcccttct tttctttttt ttttttgggt gcggcgatat gtagcttggt 300  
 aatttacaca tcatgtactt ttctgcatca aaatatgaaa ggcgatagta gctaaagaaa 360  
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 acaatttttg tagctcgaca caatatagt gtaccttgct gagaactccc aaccaaataa 600  
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Gly	Ser	Ser	Thr	Gln	Tyr	Ser	Gly	Thr	Leu	Ser	Arg	Thr	Pro	Asn	Gln	
			20					25					30			
Ile	Ile	Glu	Leu	Glu	Lys	Pro	Ser	Thr	Leu	Ser	Pro	Leu	Ser	Arg	Gly	
		35					40					45				
Lys	Lys	Trp	Thr	Glu	Lys	Leu	Ala	Arg	Phe	Gln	Arg	Ser	Ser	Ala	Lys	
	50					55					60					
Lys	Lys	Arg	Phe	Ser	Pro	Ser	Pro	Ile	Ser	Ser	Ser	Thr	Phe	Ser	Phe	
65					70					75					80	
Ser	Pro	Lys	Ser	Arg	Val	Thr	Ser	Ser	Asn	Ser	Ser	Gly	Asn	Glu	Asp	
				85					90					95		
Gly	Asn	Leu	Met	Asn	Thr	Pro	Ser	Thr	Val	Ser	Thr	Asp	Tyr	Leu	Pro	
			100					105					110			
Gln	His	Pro	His	Arg	Thr	Ser	Ser	Leu	Pro	Arg	Pro	Asn	Ser	Asn	Leu	

115	120	125
Phe His Ala Ser Asn Ser Asn Leu Ser Arg Ala Asn Glu Pro Pro Arg 130 135 140		
Ala Glu Asn Leu Ser Asp Asn Ile Pro Pro Lys Val Ala Pro Phe Gly 145 150 155 160		
Tyr Pro Ile Gln Arg Thr Ser Ile Lys Lys Ser Phe Leu Asn Ala Ser 165 170 175		
Cys Thr Leu Cys Asp Glu Pro Ile Ser Asn Arg Arg Lys Gly Glu Lys 180 185 190		
Ile Ile Glu Leu Ala Cys Gly His Leu Ser His Gln Glu Cys Leu Ile 195 200 205		
Ile Ser Phe Gly Thr Thr Ser Lys Ala Asp Val Arg Ala Leu Phe Pro 210 215 220		
Phe Cys Thr Lys Cys Lys Lys Asp Thr Asn Lys Ala Val Gln Cys Ile 225 230 235 240		
Pro Glu Asn Asp Glu Leu Lys Asp Ile Leu Ile Ser Asp Phe Leu Ile 245 250 255		
His Lys Ile Pro Asp Ser Glu Leu Ser Ile Thr Pro Gln Ser Arg Phe 260 265 270		
Pro Pro Tyr Ser Pro Leu Leu Pro Pro Phe Gly Leu Ser Tyr Thr Pro 275 280 285		
Val Glu Arg Gln Thr Ile Tyr Ser Gln Ala Pro Ser Leu Asn Pro Asn 290 295 300		
Leu Ile Leu Ala Ala Pro Pro Lys Glu Arg Asn Gln Ile Pro Gln Lys 305 310 315 320		
Lys Ser Asn Tyr Thr Phe Leu His Ser Pro Leu Gly His Arg Arg Ile 325 330 335		
Pro Ser Gly Ala Asn Ser Ile Leu Ala Asp Thr Ser Val Ala Leu Ser 340 345 350		
Ala Asn Asp Ser Ile Ser Ala Val Ser Asn Ser Val Arg Ala Lys Asp 355 360 365		
Asp Glu Thr Lys Thr Thr Leu Pro Leu Leu Arg Ser Tyr Phe Ile Gln 370 375 380		
Ile Leu Leu Asn Asn Phe Gln Glu Glu Leu Gln Asp Trp Arg Ile Asp 385 390 395 400		
Gly Asp Tyr Gly Leu Leu Arg Leu Val Asp Lys Leu Met Ile Ser Lys 405 410 415		
Asp Gly Gln Arg Tyr Ile Gln Cys Trp Cys Phe Leu Phe Glu Asp Ala		





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aagattatcg	tgatgctaata	gctagaagta	atatatcgcg	tcaggactct	gtctccacaa	180
cgaactctga	tgtggtagac	ctcagctatt	ctctggggca	tggcttgctg	gtggcaaac	240
ctgattcaga	ccgagaatga	tatccttctc	tgtagttttg	tagatgtcat	atatgtacgt	300
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ccgtgtactc	gctacacgta	gaaagaaatc	agaaaacaac	agctcgacaa	gtgaaatttg	420
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tcgatccttc	tcgagtagtg	gagacttac	cgagattccg	ttttcagaaa	gctcttgaaa	600
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<400> 54  
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1 5 10 15





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 Glu Glu Val Lys Leu Leu Glu Val Ala Phe Leu Asp Thr Thr Lys Ser  
 645 650 655  
 Ser Phe Lys Arg Gln Ile Glu Ile Ala Lys Lys Asn Lys His Lys Arg  
 660 665 670  
 Ala Leu Lys Asp Ser Cys Lys Asn Ile Glu Pro Ile Asp Thr Pro Ile  
 675 680 685  
 Ser Phe Arg Gln Phe Ala Gly Val Asp Ser Thr Asn Val Gln Lys Asp  
 690 695 700  
 Ser Ile Glu Glu Asp Leu Gln Leu Ala Met Lys Gly Asp Ala Ile His  
 705 710 715 720  
 Ala Thr Ser Ser Ser Ser Ile Ser Lys Leu Lys Lys Ile Val Pro Leu  
 725 730 735  
 Cys Gly Phe Ser Asp Pro Val Tyr Ala Glu Ala Cys Ile Thr Asn Asn  
 740 745 750  
 Gln Phe Asp Val Val Leu Asp Val Leu Leu Val Asn Gln Thr Lys Glu  
 755 760 765  
 Thr Leu Lys Asn Leu His Val Gln Phe Ala Thr Leu Gly Asp Leu Lys  
 770 775 780  
 Ile Ile Asp Thr Pro Gln Lys Thr Asn Val Ile Pro His Gly Phe His  
 785 790 795 800  
 Lys Phe Thr Val Thr Val Lys Val Ser Ser Ala Asp Thr Gly Val Ile  
 805 810 815  
 Phe Gly Asn Ile Ile Tyr Asp Gly Ala His Gly Glu Asp Ala Arg Tyr  
 820 825 830  
 Val Ile Leu Asn Asp Val His Val Asp Ile Met Asp Tyr Ile Lys Pro  
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 Ala Thr Ala Asp Asp Glu His Phe Arg Thr Met Trp Asn Ala Phe Glu  
 850 855 860  
 Trp Glu Asn Lys Ile Ser Val Lys Ser Gln Leu Pro Thr Leu His Ala  
 865 870 875 880  
 Tyr Leu Arg Glu Leu Val Lys Gly Thr Asn Met Gly Ile Leu Thr Pro  
 885 890 895  
 Ser Glu Ser Leu Gly Glu Asp Asp Cys Arg Phe Leu Ser Cys Asn Leu  
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 Pro Ser Pro Gln Ile Ala Gln Pro Ser Thr Ser Gln Lys Leu Pro Tyr  
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 Arg Ile Asn Pro Thr Thr Thr Asn Gly Asp Thr Asp Ile Ser Val Asn  
           50                  55                  60  
 Ser Asn Pro Ile Gln Pro Pro Leu Pro Asn Leu Met His Leu Ser Gly  
           65                  70                  75                  80  
 Pro Ser Asp Tyr Arg Ser Met His Gln Ser Pro Ile His Pro Ser Tyr  
                   85                  90                  95  
 Ile Ile Pro Pro His Ser Asn Glu Arg Lys Gln Ser Ala Ser Tyr Asn  
                   100                  105                  110  
 Arg Pro Gln Asn Ala His Val Ser Ile Gln Pro Ser Val Val Phe Pro  
           115                  120                  125  
 Pro Lys Ser Tyr Ser Ile Ser Tyr Ala Pro Tyr Gln Ile Asn Pro Pro  
           130                  135                  140  
 Leu Pro Asn Gly Leu Pro Asn Gln Ser Ile Ser Leu Asn Lys Glu Tyr  
           145                  150                  155                  160  
 Ile Ala Glu Glu Gln Leu Ser Thr Leu Pro Ser Arg Asn Thr Ser Val  
                   165                  170                  175  
 Thr Thr Ala Pro Pro Ser Phe Gln Asn Ser Ala Asp Thr Ala Lys Asn  
                   180                  185                  190  
 Ser Ala Asp Asn Asn Asp Asn Asn Asp Asn Val Thr Lys Pro Val Pro  
           195                  200                  205  
 Asp Lys Asp Thr Gln Leu Ile Ser Ser Ser Gly Lys Thr Leu Arg Asn  
           210                  215                  220  
 Thr Arg Arg Ala Ala Gln Asn Arg Thr Ala Gln Lys Ala Phe Arg Gln  
           225                  230                  235                  240  
 Arg Lys Glu Lys Tyr Ile Lys Asn Leu Glu Gln Lys Ser Lys Ile Phe  
                   245                  250                  255  
 Asp Asp Leu Leu Ala Glu Asn Asn Asn Phe Lys Ser Leu Asn Asp Ser  
           260                  265                  270  
 Leu Arg Asn Asp Asn Asn Ile Leu Ile Ala Gln His Glu Ala<sup>^</sup> Ile Arg  
           275                  280                  285  
 Asn Ala Ile Thr Met Leu Arg Ser Glu Tyr Asp Val Leu Cys Asn Glu  
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 Asn Asn Met Leu Lys Asn Glu Asn Ser Ile Ile Lys Asn Glu His Asn  
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2270

&lt;210&gt; 58

&lt;211&gt; 589

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 58

Met	Ser	Gly	Val	Ser	Asn	Lys	Thr	Val	Ser	Ile	Asn	Gly	Trp	Tyr	Gly
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Met	Pro	Ile	His	Leu	Leu	Arg	Glu	Glu	Gly	Asp	Phe	Ala	Gln	Phe	Met
			20					25					30		

Ile	Leu	Thr	Ile	Asn	Glu	Leu	Lys	Ile	Ala	Ile	His	Gly	Tyr	Leu	Arg
		35					40					45			

Asn	Thr	Pro	Trp	Tyr	Asn	Met	Leu	Lys	Asp	Tyr	Leu	Phe	Val	Ile	Phe
	50					55					60				

Cys	Tyr	Lys	Leu	Ile	Ser	Asn	Phe	Phe	Tyr	Leu	Leu	Lys	Val	Tyr	Gly
65					70					75					80

Pro	Val	Arg	Leu	Ala	Val	Arg	Thr	Tyr	Glu	His	Ser	Ser	Arg	Arg	Leu
			85						90					95	

Phe	Arg	Trp	Leu	Leu	Asp	Ser	Pro	Phe	Leu	Arg	Gly	Thr	Val	Glu	Lys
			100					105					110		

Glu	Val	Thr	Lys	Val	Lys	Gln	Ser	Ile	Glu	Asp	Glu	Leu	Ile	Arg	Ser
		115				120						125			

Asp	Ser	Gln	Leu	Met	Asn	Phe	Pro	Gln	Leu	Pro	Ser	Asn	Gly	Ile	Pro
	130					135					140				

Gln	Asp	Asp	Val	Ile	Glu	Glu	Leu	Asn	Lys	Leu	Asn	Asp	Leu	Ile	Pro
145					150					155					160

His	Thr	Gln	Trp	Lys	Glu	Gly	Lys	Val	Ser	Gly	Ala	Val	Tyr	His	Gly
				165					170					175	

Gly	Asp	Asp	Leu	Ile	His	Leu	Gln	Thr	Ile	Ala	Tyr	Glu	Lys	Tyr	Cys
			180				185						190		

Val	Ala	Asn	Gln	Leu	His	Pro	Asp	Val	Phe	Pro	Ala	Val	Arg	Lys	Met
		195					200					205			

Glu	Ser	Glu	Val	Val	Ser	Met	Val	Leu	Arg	Met	Phe	Asn	Ala	Pro	Ser
	210					215					220				

Asp	Thr	Gly	Cys	Gly	Thr	Thr	Thr	Ser	Gly	Gly	Thr	Glu	Ser	Leu	Leu
225					230					235					240

Leu	Ala	Cys	Leu	Ser	Ala	Lys	Met	Tyr	Ala	Leu	His	His	Arg	Gly	Ile
				245					250					255	

Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp  
 260 265 270  
 Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp  
 275 280 285  
 Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn  
 290 295 300  
 Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly  
 305 310 315 320  
 Ile Ala Asp Asp Ile Glu Gly Leu Gly Lys Ile Ala Gln Lys Tyr Lys  
 325 330 335  
 Leu Pro Leu His Val Asp Ser Cys Leu Gly Ser Phe Ile Val Ser Phe  
 340 345 350  
 Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Leu Asp Phe Arg Val  
 355 360 365  
 Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala  
 370 375 380  
 Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met  
 385 390 395 400  
 His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser  
 405 410 415  
 Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp  
 420 425 430  
 Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln  
 435 440 445  
 Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn  
 450 455 460  
 Ile Pro Asp Leu Asn Ile Met Gly Asn Pro Arg Tyr Ser Val Ile Ser  
 465 470 475 480  
 Phe Ser Ser Lys Thr Leu Asn Ile His Glu Leu Ser Asp Arg Leu Ser  
 485 490 495  
 Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His  
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 Met Ala Phe Thr Arg Leu Ser Ala His Val Val Asp Glu Ile Cys Asp  
 515 520 525  
 Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys  
 530 535 540  
 Pro Ser Pro Asp Gly Thr Ser Ala Leu Tyr Gly Val Ala Gly Ser Val  
 545 550 555 560

Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala  
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Leu Tyr Lys Leu Gly Pro Gly Glu Asp Thr Ala Thr Lys  
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<210> 59

<211> 3470

<212> DNA

<213> Candida albicans

<400> 59

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tatatattaga	agagaggaaa	ttatttttct	catgtccttt	ttaaatccct	ttgggtggcg	300
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			20					25					30			
Arg	Ile	Leu	Pro	Val	Pro	Glu	Leu	Arg	Leu	Thr	Ala	Val	Asp	Leu	Val	
		35					40					45				
His	Ser	Gln	Thr	Gly	Ala	Glu	His	Leu	His	Ile	Asp	Arg	Asp	Asp	Lys	
	50					55					60					
Asn	Asn	Val	Phe	Ser	Ile	Ala	Phe	Lys	Thr	Asn	Pro	Pro	Asp	Ser	Thr	
65					70					75					80	
Gly	Val	Pro	His	Ile	Leu	Glu	His	Thr	Thr	Leu	Cys	Gly	Ser	Val	Lys	
				85					90					95		
Tyr	Pro	Val	Arg	Asp	Pro	Phe	Phe	Lys	Met	Leu	Asn	Lys	Ser	Leu	Ala	
			100					105					110			
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		115					120					125				
Ser	Thr	Thr	Asn	Pro	Gln	Asp	Phe	Ala	Asn	Leu	Arg	Gly	Val	Tyr	Leu	
	130					135					140					
Asp	Ser	Thr	Leu	Asn	Pro	Leu	Leu	Lys	Gln	Glu	Asp	Phe	Asp	Gln	Glu	
145					150					155					160	
Gly	Trp	Arg	Leu	Glu	His	Lys	Asn	Ile	Thr	Asp	Pro	Glu	Ser	Asn	Ile	
				165					170					175		
Val	Phe	Lys	Gly	Val	Val	Tyr	Asn	Glu	Met	Lys	Gly	Gln	Ile	Ser	Asn	



				485						490							495	
Leu Arg Glu Lys Ile Thr Ala Leu Asp Glu Gln Asp Lys Lys Asn Ile 500                    505                    510	Phe Lys Arg Gly Ile Leu Leu Gln Glu Lys Gln Asn Glu Lys Glu Asp 515                    520                    525	Leu Ser Cys Leu Pro Thr Leu Gln Ile Lys Asp Ile Pro Arg Ala Gly 530                    535                    540	Asp Lys Tyr Ser Ile Glu Gln Lys Asn Asn Thr Met Ser Arg Ile Thr 545                    550                    555                    560	Asp Thr Asn Gly Ile Thr Tyr Val Arg Gly Lys Arg Leu Leu Asn Asp 565                    570                    575	Ile Ile Pro Phe Glu Leu Phe Pro Tyr Leu Pro Leu Phe Ala Glu Ser 580                    585                    590	Leu Thr Asn Leu Gly Thr Thr Thr Glu Ser Phe Ser Glu Ile Glu Asp 595                    600                    605	Gln Ile Lys Leu His Thr Gly Gly Ile Ser Thr His Val Glu Val Thr 610                    615                    620	Ser Asp Pro Asn Thr Thr Glu Pro Arg Leu Ile Phe Gly Phe Asp Gly 625                    630                    635                    640	Trp Ser Leu Asn Ser Lys Thr Asp His Ile Phe Glu Phe Trp Ser Lys 645                    650                    655	Ile Leu Leu Glu Thr Asp Phe His Lys Asn Ser Asp Lys Leu Lys Val 660                    665                    670	Leu Ile Arg Leu Leu Ala Ser Ser Asn Thr Ser Ser Val Ala Asp Ala 675                    680                    685	Gly His Ala Phe Ala Arg Gly Tyr Ser Ala Ala His Tyr Arg Ser Ser 690                    695                    700	Gly Ala Ile Asn Glu Thr Leu Asn Gly Ile Glu Gln Leu Gln Phe Ile 705                    710                    715	Asn Arg Leu His Ser Leu Leu Asp Asn Glu Glu Thr Phe Gln Arg Glu 725                    730                    735	Val Val Asp Lys Leu Thr Glu Leu Gln Lys Tyr Ile Val Asp Thr Asn 740                    745                    750	Asn Met Asn Phe Phe Ile Thr Ser Asp Ser Asp Val Gln Ala Lys Thr 755                    760                    765	Val Glu Ser Gln Ile Ser Lys Phe Met Glu Arg Leu Pro His Gly Ser 770                    775                    780	Cys Leu Pro Asn Gly Pro Lys Thr Ser Asp Tyr Pro Leu Ile Gly Ser

785		790		795		800
Lys Cys Lys His Thr Leu Ile Lys Phe Pro Phe Gln Val His Tyr Thr						
		805		810		815
Ser Gln Ala Leu Leu Gly Val Pro Tyr Thr His Lys Asp Gly Ser Ala						
		820		825		830
Leu Gln Val Met Ser Asn Met Leu Thr Phe Lys His Leu His Arg Glu						
		835		840		845
Val Arg Glu Lys Gly Gly Ala Tyr Gly Gly Gly Ala Ser Tyr Ser Ala						
		850		855		860
Leu Ala Gly Ile Phe Ser Phe Tyr Ser Tyr Arg Asp Pro Gln Pro Leu						
		865		870		880
Lys Ser Leu Glu Thr Phe Lys Asn Ser Gly Arg Tyr Ile Leu Asn Asp						
		885		890		895
Ala Lys Trp Gly Val Thr Asp Leu Asp Glu Ala Lys Leu Thr Ile Phe						
		900		905		910
Gln Gln Val Asp Ala Pro Lys Ser Pro Lys Gly Glu Gly Val Thr Tyr						
		915		920		925
Phe Met Ser Gly Val Thr Asp Asp Met Lys Gln Ala Arg Arg Glu Gln						
		930		935		940
Leu Leu Asp Val Ser Leu Leu Asp Val His Arg Val Ala Glu Lys Tyr						
		945		950		955
Leu Leu Asn Lys Glu Gly Val Ser Thr Val Ile Gly Pro Gly Ile Glu						
		965		970		975
Gly Lys Thr Val Ser Pro Asn Trp Glu Val Lys Glu Leu						
		980		985		

&lt;210&gt; 61

&lt;211&gt; 1612

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 61

```

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ctctaatagt tactctatta ttgctgttaa ttgacaatgt ttagtcacgt gcaacacaat 180
tcaagtcacg tggaaaggcc ttccatggt gatccatctt ctacatcttc atcgggtcctg 240
cataaagtca taatatgggg ctactggaat gtatgcactt aacagtacta ttatatgggtg 300
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```

```

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```

&lt;210&gt; 62

&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 62

```

Met Asn Arg Val Gly Ile Asp Val Asp His Met Ile Gly Val Leu Leu
  1             5             10             15

```

```

Leu Ala Val Val Val Val Phe Trp Val Gly Ala Ser Cys Leu Thr Asn
      20             25             30

```

```

Glu Leu Leu Glu Thr Asn Ala Tyr Asn Lys Pro Phe Phe Leu Thr Tyr
    35             40             45

```

```

Leu Asn Ile Ser Ser Phe Ala Leu Tyr Leu Thr Pro Asp Leu Trp Arg
    50             55             60

```

```

Ile Ile Gln Ser Arg Arg Lys Ser Leu Gln Glu Arg Thr Glu Arg Thr
    65             70             75             80

```

```

Leu Pro Ile His Thr Gln Glu Ser Phe Ser Glu Phe Leu Pro Leu Leu
      85             90             95

```

```

Ser Ser Thr Pro Ser Thr Ser Ser Asn Leu Ser Ser Ile Ala Asp Thr
    100             105             110

```

```

Lys Val Lys Asp Thr Met Arg Leu Ser Leu Leu Phe Cys Val Leu Trp
    115             120             125

```

```

Phe Val Ala Asn Leu Ala Ala Asn Ala Ala Leu Ser Tyr Thr Thr Val
    130             135             140

```

```

Ala Ser Ser Thr Ile Leu Ser Ser Thr Ser Ser Phe Phe Thr Leu Phe
    145             150             155             160

```

```

Leu Ala Thr Ser Leu Gly Ile Glu Thr Phe Ser Thr Lys Lys Leu Leu
    165             170             175

```



Gly Leu Phe Val Ser Leu Phe Gly Ile Ile Leu Ile Val Met Gln Ser  
 180 185 190  
 Ser Lys Gln Gln Asp Ser Val Ser Ala Ser Ser Phe Leu Val Gly Asn  
 195 200 205  
 Thr Leu Ala Leu Leu Gly Ser Leu Gly Tyr Ser Val Tyr Thr Thr Leu  
 210 215 220  
 Leu Lys Tyr Glu Ile Ser Ser Lys Gly Leu Arg Leu Asp Ile Gln Met  
 225 230 235 240  
 Phe Leu Gly Tyr Val Gly Ile Phe Thr Phe Leu Leu Phe Trp Pro Ile  
 245 250 255  
 Leu Ile Ile Leu Asp Ile Thr His Met Glu Thr Phe Glu Leu Pro Ser  
 260 265 270  
 Asn Phe His Ile Ser Phe Leu Val Met Leu Asn Cys Ile Ile Ile Phe  
 275 280 285  
 Val Ser Asp Tyr Phe Trp Cys Lys Ala Leu Ile Leu Thr Ser Pro Leu  
 290 295 300  
 Val Val Thr Val Ala Leu Thr Phe Thr Ile Pro Leu Ala Met Phe Ala  
 305 310 315 320  
 Asp Phe Val Trp Arg Glu Ala Phe Phe Thr Pro Trp Tyr Ile Ile Gly  
 325 330 335  
 Val Ile Phe Ile Phe Val Ser Phe Phe Leu Val Asn His Arg Gly Glu  
 340 345 350  
 Ser Ala Val Glu Lys Asp Cys Ala Ala Val Glu Lys Gly Pro Ile Leu  
 355 360 365  
 Asp Ala  
 370

&lt;210&gt; 63

&lt;211&gt; 1376

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 63

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 cgtgtctggc aacaaaaaag tacattttaat ttcaatgatt aaaaagacat taaacatccg 180  
 tacattacgc acccatgcat gctatctgaa aatattctac atgctgcttt tagaaaatttg 240  
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<210> 65
<211> 1289
<212> DNA
<213> Candida albicans
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&lt;400&gt; 65

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atgtatatat ttgtaacttt gtatatatct tttgtttttt gacctttttc ttcctctatg 480
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&lt;210&gt; 66

&lt;211&gt; 262

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 66

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Gly Gly Ser Gln Asp Trp Leu Lys His Ser Tyr Lys Leu Phe Lys Ala
      20           25           30

Ile Met Asn Arg Ile Phe Gly Tyr Gly Asn Lys Lys Ser His Asp Gln
      35           40           45

Leu Leu Gln Glu Ser Asn Gln Ser Met Asn Gln Ala Gln Gln Ser Leu
      50           55           60

Ser Asn Arg Ile Ser Gln Leu Asp Thr Gln Ile Ala Gln Leu Asn Phe
      65           70           75           80

Gln Leu Gln Asn Ile Gln Lys Asn Leu Gln Arg Ser Asn Asn Lys Gln
      85           90           95

Pro Ser Leu Arg Lys Gln Ala Leu Lys Ile Leu Asn Lys Arg Lys Gln
      100          105          110

Leu Glu Asn Met Lys Asp Ser Leu Asp Ser Gln Ser Trp Ser Met Thr
      115          120          125

Gln Ala Gln Leu Thr Asn Asp Asn Leu Gln Asn Thr Met Ile Thr Ile

```

[illegible]

<210> 68  
 <211> 136  
 <212> PRT  
 <213> Candida albicans

<400> 68  
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 Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly  
                   20                  25                  30  
 Ser Lys Ser His Pro Phe Gly His Ala Leu Val Ala Gly Ile Glu Arg  
           35                  40                  45  
 Tyr Pro Ser Lys Val Thr Lys Lys His Gly Ala Lys Lys Val Ala Lys  
           50                  55                  60  
 Arg Thr Lys Ile Lys Pro Phe Ile Lys Val Val Asn Tyr Asn His Leu  
           65                  70                  75                  80  
 Leu Pro Thr Arg Tyr Thr Leu Asp Val Glu Ala Phe Lys Ser Val Val  
                   85                  90                  95  
 Ser Thr Glu Thr Phe Glu Gln Pro Ser Gln Arg Glu Glu Ala Lys Lys  
                   100                  105                  110  
 Val Val Lys Lys Ala Phe Glu Glu Arg His Gln Ala Gly Lys Asn Gln  
           115                  120                  125  
 Trp Phe Phe Ser Lys Leu Arg Phe  
           130                  135

<210> 69  
 <211> 2744  
 <212> DNA  
 <213> Candida albicans

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 cttacaaaga gctattagta tcttggttct tctattdtct tcgattattg gtgatttdtc 360  
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 aaataaaaag caaacaaata cgcgatagtg cagcaaactg caacacaaatc atcaaactct 480  
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 catcagcagc attacaaaca caaattccca ctacttdtga gggtacaacg accacattaa 660  
 acaataaaca gagtaaaaat gataaccaac tgggttaacca actgaataaa gctcaagggtg 720  
 aagcaagcat gcttcgtgat aaaataaact ttdttgaacat tgaaagggaa aaggaaaaga 780  
 atattcaagc cgtcaaagtt aatgaattgc aagtcaagca tcttcaagag ttggctaaat 840  
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<400> 70
Met Arg Arg Glu Thr Val Gly Glu Phe Ser Ser Asp Asp Asp Asp Asp
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Ile Leu Leu Glu Leu Gly Thr Arg Pro Pro Arg Phe Thr Gln Ile Pro
      20                      25                      30

Pro Ser Ser Ala Ala Leu Gln Thr Gln Ile Pro Thr Thr Leu Glu Val
      35                      40                      45

Thr Thr Thr Thr Leu Asn Asn Lys Gln Ser Lys Asn Asp Asn Gln Leu
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caatttatga taaattgcac caggccaagg attctgaagt gtctactgaa gataccgtac 2040
atgatgaatt ataa                                     2054

```

<210> 76  
 <211> 517  
 <212> PRT  
 <213> Candida albicans

<400> 76  
 Met Gln Val Thr Thr Arg Phe Ile Ser Ala Ile Val Ser Phe Cys Leu  
 1 5 10 15  
 Phe Ala Ser Phe Thr Leu Ala Glu Asn Ser Ala Arg Ala Thr Pro Gly  
 20 25 30  
 Ser Asp Leu Leu Val Leu Thr Glu Lys Lys Phe Lys Ser Phe Ile Glu  
 35 40 45  
 Ser His Pro Leu Val Leu Val Glu Phe Phe Ala Pro Trp Cys Leu His  
 50 55 60  
 Ser Gln Ile Leu Arg Pro His Leu Glu Glu Ala Ala Ser Ile Leu Lys  
 65 70 75 80  
 Glu His Asn Val Pro Val Val Gln Ile Asp Cys Glu Ala Asn Ser Met  
 85 90 95  
 Val Cys Leu Gln Gln Thr Ile Asn Thr Tyr Pro Thr Leu Lys Ile Phe  
 100 105 110  
 Lys Asn Gly Arg Ile Phe Asp Gly Gln Val Tyr Arg Gly Val Lys Ile  
 115 120 125

Thr Asp Glu Ile Thr Gln Tyr Met Ile Gln Leu Tyr Glu Ala Ser Val  
 130 135 140  
 Ile Tyr Leu Asn Ser Glu Asp Glu Ile Gln Pro Tyr Leu Glu Asn Ala  
 145 150 155 160  
 Thr Leu Pro Val Val Ile Asn Arg Gly Leu Thr Gly Leu Asn Glu Thr  
 165 170 175  
 Tyr Gln Glu Val Ala Leu Asp Leu Ala Glu Asp Tyr Val Phe Leu Ser  
 180 185 190  
 Leu Leu Asp Ser Glu Asp Lys Ser Leu Ser Ile His Leu Pro Asn Thr  
 195 200 205  
 Thr Glu Pro Ile Leu Phe Asp Gly Asn Val Asp Ser Leu Val Gly Asn  
 210 215 220  
 Ser Val Ala Leu Thr Gln Trp Leu Lys Val Val Ile Leu Pro Tyr Phe  
 225 230 235 240  
 Thr Asp Ile Glu Pro Asp Leu Phe Pro Lys Tyr Ile Ser Ser Asn Leu  
 245 250 255  
 Pro Leu Ala Tyr Phe Phe Tyr Thr Ser Glu Glu Glu Leu Glu Asp Tyr  
 260 265 270  
 Thr Asp Leu Phe Thr Gln Leu Gly Lys Glu Asn Arg Gly Gln Ile Asn  
 275 280 285  
 Phe Ile Ala Leu Asn Ser Thr Met Phe Pro His His Val Arg Phe Leu  
 290 295 300  
 Asn Met Arg Glu Gln Phe Pro Leu Phe Ala Ile His Asn Met Ile Asn  
 305 310 315 320  
 Asn Leu Lys Tyr Gly Leu Pro Gln Leu Pro Glu Glu Glu Tyr Ala Lys  
 325 330 335  
 Leu Glu Lys Pro Gln Pro Leu Asp Arg Asp Met Ile Val Gln Leu Val  
 340 345 350  
 Lys Asp Tyr Arg Glu Gly Thr Ala Lys Pro Ile Val Lys Ser Glu Glu  
 355 360 365  
 Ile Pro Lys Glu Gln Lys Ser Asn Val Tyr Lys Ile Val Gly Lys Thr  
 370 375 380  
 His Asp Asp Ile Val His Asp Asp Asp Lys Asp Val Leu Val Lys Tyr  
 385 390 395 400  
 Tyr Ala Thr Trp Cys Ile His Ser Lys Arg Phe Ala Pro Ile Tyr Glu  
 405 410 415  
 Glu Ile Ala Asn Val Leu Ala Ser Asp Glu Ser Val Arg Asp Lys Ile  
 420 425 430



<400> 80  
Met Gly Ile Ser Arg Asp Ser Arg His Lys Arg Ser Ala Thr Gly Ala  
1 5 10 15

<400>	81						
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tagaagcgga	aagagaagga	gctgaagagg	ttaattcatc	gatggaaggc	aactggggtt	120	
ggattttccga	gacatcgttg	gcattttgggc	ccgtcgaatt	aaatcttttg	gcctgaaaaa	180	
agatccatga	cggatggggc	cggggccaata	ctatggttcg	agcggatggcc	agctcggaag	240	
aggcagcaaaa	ccttgacgtg	acgagtcgag	aggtgagttt	gaacgatcgtc	ggggagggtta	300	
ttctgtggct	ccgcttgtag	gtgaacagat	acgtatagag	ggcgcagccac	tgggttaaatt	360	
tttcatggct	cggattactt	ccgtactgct	ggctaaaatc	gaaatctcgg	cctgctgaga	420	
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ggtcgcgaat	actgttaagc	agtttaaacg	ggaaaaatgtc	cgatgcactg	gcgcgtgtgc	600	
gtcagcagca	gcagaccagc	gtggatgtgg	agctgctgca	cacgatgcta	gcgcgagccg	660	
ctgcgccttgc	ccatgccgac	actatagcat	acatgtggta	tcagcatgtg	atgccacgcc	720	

<400>	82																
Met	Leu	Thr	Ile	Thr	Lys	Arg	Leu	Val	Thr	Thr	Asp	Val	Arg	Ser	Arg		
1				5					10					15			
Ile	Leu	Leu	Ser	Ser	Leu	Asn	Gly	Lys	Met	Ser	Asp	Ala	Leu	Ala	Leu		
			20					25					30				
Leu	Arg	Gln	Gln	Gln	Gln	Thr	Ser	Val	Asp	Val	Glu	Leu	Leu	His	Thr		
		35					40					45					
Met	Leu	Ala	Arg	Ala	Ala	Ala	Leu	Ala	His	Ala	Asp	Thr	Ile	Ala	Tyr		
	50					55					60						
Met	Trp	Tyr	Gln	His	Val	Met	Pro	Arg	Arg	Leu	Pro	Val	Glu	Gly	Arg		
65					70					75					80		
Leu	Leu	Cys	Glu	Met	Ala	Gly	Val	Ala	Leu	Tyr	Gln	Asp	Arg	Leu	Phe		
				85					90					95			
Leu	Pro	Ala	Gln	Phe	Leu	Gln	His	Tyr	Gln	Ala	Met	Asn	Arg	Asp	Arg		
			100					105					110				
Arg	Thr	Ser	Pro	Glu	Asp	Glu	Leu	Ile	Glu	Tyr	Glu	Leu	Arg	Arg	Ile		
		115					120					125					
Lys	Val	Glu	Ala	Phe	Ala	Arg	Gly	Thr	Met	His	Ser	Thr	Ala	Leu	Arg		
	130					135					140						
Glu	Lys	Trp	Lys	Val	Phe	Leu	Gln	Glu	Met	Asp	Thr	Leu	Pro	Gly	Gln		
145					150					155					160		
Pro	Pro	Leu	Arg	Leu	Arg	Asp	Phe	Pro	Gln	Met	Thr	Lys	Ala	Met	Gly		
				165					170					175			
Ile	Ala	Leu	Met	Gln	Gln	Asp	Glu	Gln	Ala	Ala	Ala	Leu	Ala	Leu	Phe		
			180					185					190				
Gly	Arg	Gln	Pro	Leu	Val	Ile	Lys	Asn	Glu	Trp	Ser	Leu	Pro	Leu	Leu		
		195					200					205					

```

<400> 84
Met Ser Asp Ala Gly Arg Lys Gly Phe Gly Glu Lys Ala Ser Glu Ala
  1              5              10              15
Leu Lys Pro Asp Ser Gln Lys Ser Tyr Ala Glu Gln Gly Lys Glu Tyr
          20              25              30
Ile Thr Asp Lys Ala Asp Lys Val Ala Gly Lys Val Gln Pro Glu Asp
          35              40              45
Asn Lys Gly Val Phe Gln Gly Val His Asp Ser Ala Glu Lys Gly Lys
  50              55              60
Asp Asn Ala Glu Gly Gln Gly Glu Ser Leu Ala Asp Gln Ala Arg Asp
  65              70              75              80
Tyr Met Gly Ala Ala Lys Ser Lys Leu Asn Asp Ala Val Glu Tyr Val
          85              90              95

```

```
<210> 85
<211> 995
<212> DNA
<213> Candida albicans
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<400>	85						
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taccttggtc	agcgtatgac	ttttgagagt	ctggcctcaa	agcttcagaa	gctttttcac		180
cgaatccttt	tctacctgcg	tcagacattg	ttgtatttag	ttttttttgt	tttgagttgt		240
ttgtttgaga	ttatcgaata	atcagatggg	ttttttttct	atatattaga	gagagattaa		300
ataagatcaa	acgcaattga	ggaagtga	cgaattcac	cgctctattt	atacgtttta		360
atatagcttt	agagaataag	ctttcagatc	aagaggggga	cgaccggaac	ctcaaagttg		420
accaaacgat	tttcagggg	ctgtagatct	agttactctc	cgctagagtg	gcttctggtc		480
tgtgtttgtg	ggttgtatta	atgcttgctg	atacctttcc	ttctttcaat	ttctacgtca		540
atgggttttt	ttccttcctt	ttccttttcc	ttttcctttt	cccctcttta	ctacgtttct		600
atgttatttt	gtgccgcccc	ctgcaagttg	caacatatcc	ccttaacaga	tgccagcaat		660
attctagtct	tgctattttt	accgcctctg	gctttttggc	tctagtctct	gtcccaagag		720
ccaagggccc	gtcaaacagt	cgtcattgct	accgccagct	ggcaccaca	catcaccgac		780
cctttttttt	catttttcgc	tgggcggtta	gtgggattcc	cccgctcccg	gagattttca		840
cttggaattg	cgcgtcccc	ttttttcttc	attctctgac	tccccctacc	ttctccact		900
tttctgtgta	tcaagaggaa	aagaaggaga	aaaggagaac	tccgaaaaat	accgaacaag		960
agggtaacag	aatgtgcatt	tggtatgagcg	ggtaa				995

```
<210> 86
<211> 164
<212> PRT
<213> Candida albicans
```

```

<400> 86
Met Leu Ala Tyr Thr Phe Pro Ser Phe Asn Phe Tyr Val Asn Gly Phe
  1                      5                      10                      15

Phe Ser Phe Leu Phe Leu Phe Leu Phe Leu Phe Pro Ser Leu Leu Arg
                20                      25                      30

Phe Tyr Val Ile Leu Cys Arg Pro Leu Gln Val Ala Thr Tyr Pro Leu
          35                      40                      45

Asn Arg Cys Gln Gln Tyr Ser Ser Leu Ala Ile Phe Thr Ala Ser Gly
  50                      55                      60

Phe Trp Leu Leu Val Leu Val Pro Arg Ala Lys Gly Pro Ser Thr Arg
  65                      70                      75                      80

Arg His Cys Tyr Arg Gln Leu Ala Pro Thr His His Arg Pro Phe Phe
          85                      90                      95

Ser Ile Phe Gly Trp Ala Val Ser Gly Ile Arg Pro Leu Pro Glu Ile
          100                      105                      110

```



Phe Thr Trp Ile Cys Ala Ser Pro Phe Phe Leu His Ser Leu Thr Pro  
 115 120 125

Pro Thr Phe Ser His Phe Ser Val Tyr Gln Glu Glu Lys Lys Glu Lys  
 130 135 140

Arg Arg Thr Pro Lys Asn Thr Glu Gln Glu Gly Asn Arg Met Cys Ile  
 145 150 155 160

Trp Met Ser Gly

<210> 87  
 <211> 2702  
 <212> DNA  
 <213> Candida albicans

<400> 87  
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 ctatcctttt gcataatatt ttcgtcacca ttatcttggt gcggtgtttt tattttaaaac 120  
 aatagaactc gcctaaaggg gaaattttcg atataaaaaat tcaaaaaaat ggctttcatg 180  
 gatcgagtat ttgtttgtcg aaaaaggatc actggagtga cgttactacg ctacgaagcc 240  
 tccttcgggc ttagccctgt tgattacgaa tttggatcag ttggtatttg attcctcgga 300  
 agagttaact tcacgcgggt aaatcacttg tgatgcggtt tattctctat acggctaata 360  
 gatgaatcag ggtgttttaa agtgcgtata aacccttttg ctattttcgt ttatataatt 420  
 ggcgttgata aagagccaat atctattgtt gctacataga ggcagctctc ttagcaaaat 480  
 aaaaatacaa aaagttcgac atgggcttca gtagcggtaa atcaactaag aaaaagcctc 540  
 tgcttttcga tatcagactt aaaaatgttg acaacgatgt aatactcctc aaaggtcctc 600  
 caaacgaggc cccctcggtg cttttatctg gttgcacgtt tttatcgatt aacgaaccca 660  
 tgcagatcaa aagcatatca ttgagacttt atgggaagat acaaataagac gtaccattag 720  
 agaggcccca ggacgctagt tcttcgtcgt tgtcttcac gccgccaaag atcagaaagt 780  
 acaacaaggt tttttataat tacgcatggg ataattgtta cctcaaggag tatctgagt 840  
 gtttaagagg gcaatctggc cttgcgggca gtagctcatc aagtaatatc ttggggcactc 900  
 gccaaagagc tcagtcacaa agttccttga agtcttttaa ggggtcctcc tcaccctctt 960  
 catgtacttt agataagggc aactacgatt ttcccttttag tgctattttg cctgggtcgt 1020  
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 ttgaacgcag caaaaattat agtgatttga tctgtaggaa aaatattaga gttctgagaa 1140  
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 acaaagtgga ttattctatt tcagtaacca acaaagccgt agctattggt tcagccacc 1260  
 ctataaatat ttccattgta cctctttcga aaggtttgaa attgggctca atcaaagtcg 1320  
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 catcagtcac aggggttgaa ttattagcgg atatgcgtag cggtggctct gttcctacca 1860  
 tttcagactt gatgacgcc ccaaattatg aaatgcacgt atatgatcgt ctttatagcg 1920  
 gttctttcac tcgcacggct gtggaaacgt ctggaacatg tactcctttg ggaagcgaat 1980  
 gttcgactgt cgaggatcag caacaggatt tagaagattt acgtatacgg ttgacaaaaa 2040  
 ttagaaatca acgtgacaat ctagggtctac caccgtctgc ctgctctgct gccgcttcca 2100  
 gatcgctatc tccattacta aacgttccag caccagagga tggcacggag agaattctac 2160  
 ctcagagtgc tcttggtccc aatagtggct ctgtgccagg agtacatagt aacgtatcac 2220

```

ctgttttact ttcaagatcc ccagcccca gcggtgcagc ccatgaagtg ttaccagtgc 2280
cctcgggctt aaattatcca gagactcaaa acctgaacaa gggtccatcg tatggcaagg 2340
caatgaaata tgatatcatt ggtgaggacc ttctccttc ctacccttgt gcgatacaaa 2400
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cttctatacc aactagcttt cattcctcta gttttatgag tagcactgct tcccctattt 2520
ccataattaa tggctctaga agtagttcta gtgggggtatc tcttaatata cttaatgagt 2580
taacttcgaa aacttcgaat aacccatcca gtaatagtat gaaaagggtca ccaacaagac 2640
ggaggggtac ttcttttagct gggtttatgg gaggttttct atcaaagggt aacaaaacgat 2700
ag 2702

```

&lt;210&gt; 88

&lt;211&gt; 733

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 88

```

Met Gly Phe Ser Ser Gly Lys Ser Thr Lys Lys Lys Pro Leu Leu Phe
  1             5             10             15

Asp Ile Arg Leu Lys Asn Val Asp Asn Asp Val Ile Leu Leu Lys Gly
      20             25             30

Pro Pro Asn Glu Ala Pro Ser Val Leu Leu Ser Gly Cys Ile Val Leu
      35             40             45

Ser Ile Asn Glu Pro Met Gln Ile Lys Ser Ile Ser Leu Arg Leu Tyr
      50             55             60

Gly Lys Ile Gln Ile Asp Val Pro Leu Glu Arg Pro Gln Asp Ala Ser
      65             70             75             80

Ser Ser Ser Leu Ser Ser Ser Pro Pro Lys Ile Arg Lys Tyr Asn Lys
      85             90             95

Val Phe Tyr Asn Tyr Ala Trp Asp Asn Val Asn Leu Lys Glu Tyr Leu
      100            105            110

Ser Gly Leu Arg Gly Gln Ser Gly Leu Ala Gly Ser Ser Ser Ser Ser
      115            120            125

Asn Ile Leu Gly Thr Arg Gln Arg Ala Gln Ser Thr Ser Ser Leu Lys
      130            135            140

Ser Leu Lys Gly Ser Ser Ser Pro Ser Ser Cys Thr Leu Asp Lys Gly
      145            150            155            160

Asn Tyr Asp Phe Pro Phe Ser Ala Ile Leu Pro Gly Ser Leu Pro Glu
      165            170            175

Ser Val Glu Ser Leu Pro Asn Cys Phe Val Thr Tyr Ser Met Glu Ser
      180            185            190

Val Ile Glu Arg Ser Lys Asn Tyr Ser Asp Leu Ile Cys Arg Lys Asn
      195            200            205

Ile Arg Val Leu Arg Thr Ile Ser Pro Ala Ala Val Glu Leu Ser Glu

```

210	215	220
Thr Val Cys Val Asp	Asn Ser Trp Pro Asp	Lys Val Asp Tyr Ser Ile
225	230	235 240
Ser Val Pro Asn Lys	Ala Val Ala Ile Gly	Ser Ala Thr Pro Ile Asn
245	250	255
Ile Ser Ile Val Pro	Leu Ser Lys Gly	Leu Lys Leu Gly Ser Ile Lys
260	265	270
Val Val Leu Phe Glu	Asn Tyr Gln Tyr Cys Asp	Pro Phe Pro Pro Val
275	280	285
Ile Ser Glu Asn Arg	Gln Val Thr Glu Leu Asn	Leu Glu Asp Pro Leu
290	295	300
Asn Glu Ser Ser Gly	Glu Phe Asn Gly Asn Gly	Cys Phe Val Asn Asn
305	310	315 320
Pro Phe Phe Gln Pro	Asp His Ser Phe Gln Asp	Lys Trp Glu Ile Asp
325	330	335
Thr Ile Leu Gln Ile	Pro Asn Ser Leu Ser Asn	Cys Val Gln Asp Cys
340	345	350
Asp Val Arg Ser Asn	Ile Lys Val Arg His Lys	Leu Lys Phe Phe Ile
355	360	365
Ile Leu Ile Asn Pro	Asp Gly His Lys Ser Glu	Leu Arg Ala Ser Leu
370	375	380
Pro Ile Gln Leu Phe	Ile Ser Pro Phe Val Ala	Leu Ser Ile Lys Pro
385	390	395 400
Leu Ser Ser Ser Asn	Leu Tyr Ser Leu Phe Ser	Thr Thr Asn Gln Lys
405	410	415
Asp Glu Asn Ser Ser	Gln Glu Glu Glu Glu Tyr	Leu Phe Ser Arg
420	425	430
Ser Ala Ser Val Thr	Gly Leu Glu Leu Leu Ala	Asp Met Arg Ser Gly
435	440	445
Gly Ser Val Pro Thr	Ile Ser Asp Leu Met Thr	Pro Pro Asn Tyr Glu
450	455	460
Met His Val Tyr Asp	Arg Leu Tyr Ser Gly Ser	Phe Thr Arg Thr Ala
465	470	475 480
Val Glu Thr Ser Gly	Thr Cys Thr Pro Leu Gly	Ser Glu Cys Ser Thr
485	490	495
Val Glu Asp Gln Gln	Gln Asp Leu Glu Asp Leu	Arg Ile Arg Leu Thr
500	505	510
Lys Ile Arg Asn Gln	Arg Asp Asn Leu Gly Leu	Pro Pro Ser Ala Ser

<400> 89						
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aaatccagca	aaccttcgcc	catattttatt	ctttttataac	agaagaagag	actatatctt	240
caaaacctcg	tatatattata	tacatatctt	ccaaacaaac	tcccaagttt	cactttctctg	300
gattttacctt	ggcatttcctt	ttccccatcc	tctttataatg	gtaatgcgca	tccttaatta	360
tgatattcaca	atagacgaag	ggcacacacc	aattttgccac	cgtaagcgata	gagtaagtta	420
aatggctaac	tcattataat	cttcattgcta	aatcatataa	gggcagagac	gaagcaaagc	480

```

gaaaaaaaca tattacaatc atgtcgggtg ctgctgctgc atctgctgct ggttatgaca 540
ggcacatcac tatcttttcc cccgaggggtc gtttatatca agtagaatat gccttttaaag 600
cgactaatca aactaacata aactcactag cggtcagagg taaagattgt acagtgggtga 660
taagtcagaa aaagggtccct gataaactgt tggatccaac tactgtttcg tatatttttt 720
gtatttcaag aacaattgggt atggtagtga acggaccaat accggatgca agaaatgcgg 780
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ttaatgaaga atcatgggag aagggtgtag aaattgctat tactcatatg attgacgcac 1140
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```

&lt;210&gt; 90

&lt;211&gt; 252 \*

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 90

```

Met Ser Gly Ala Ala Ala Ala Ser Ala Ala Gly Tyr Asp Arg His Ile
  1              5              10              15

```

```

Thr Ile Phe Ser Pro Glu Gly Arg Leu Tyr Gln Val Glu Tyr Ala Phe
      20              25              30

```

```

Lys Ala Thr Asn Gln Thr Asn Ile Asn Ser Leu Ala Val Arg Gly Lys
      35              40              45

```

```

Asp Cys Thr Val Val Ile Ser Gln Lys Lys Val Pro Asp Lys Leu Leu
      50              55              60

```

```

Asp Pro Thr Thr Val Ser Tyr Ile Phe Cys Ile Ser Arg Thr Ile Gly
      65              70              75              80

```

```

Met Val Val Asn Gly Pro Ile Pro Asp Ala Arg Asn Ala Ala Leu Arg
      85              90              95

```

```

Ala Lys Ala Glu Ala Ala Glu Phe Arg Tyr Lys Tyr Gly Tyr Asp Met
      100              105              110

```

```

Pro Cys Asp Val Leu Ala Lys Arg Met Ala Asn Leu Ser Gln Ile Tyr
      115              120              125

```

```

Thr Gln Arg Ala Tyr Met Arg Pro Leu Gly Val Ile Leu Thr Phe Val
      130              135              140

```

```

Ser Val Asp Glu Glu Leu Gly Pro Ser Ile Tyr Lys Thr Asp Pro Ala
      145              150              155              160

```

```

Gly Tyr Tyr Val Gly Tyr Lys Ala Thr Ala Thr Gly Pro Lys Gln Gln
      165              170              175

```

```

Glu Ile Thr Thr Asn Leu Glu Asn His Phe Lys Lys Ser Lys Ile Asp
      180              185              190

```

His Ile Asn Glu Glu Ser Trp Glu Lys Val Val Glu Phe Ala Ile Thr  
 195 200 205

His Met Ile Asp Ala Leu Gly Thr Glu Phe Ser Lys Asn Asp Leu Glu  
 210 215 220

Val Gly Val Ala Thr Lys Asp Lys Phe Phe Thr Leu Ser Ala Glu Asn  
 225 230 235 240

Ile Glu Glu Arg Leu Val Ala Ile Ala Glu Gln Asp  
 245 250

<210> 91

<211> 968

<212> DNA

<213> Candida albicans

<400> 91

ccaagttaag caagacacca agacaataac ttgagaggta tgtccctata tgatgatgat 60  
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 agagcttcag atagccaata caccggaatt tagactttga caggattgtg gcttggtcca 180  
 gtataactta taatatatgt caacctttga gcaggaaaacc caatgaaaat gcttcattac 240  
 atatatatga tatggagaag catgaaaaat aacagcgtga gatgttatcc atgttgcaag 300  
 aacctagtaa aatgaattct gaatttgcaa aaagtccata ttccacggt ctctcttcc 360  
 tacaattttg cgaacgcctg aacaaccatg cggattacca ttatttatat tgacaagatg 420  
 gctacctatg aaaagcatag acttactaac attttttttt tcaaatatgt ttgaaaaacg 480  
 tggattaata tagtgataaa atgaagggtg aaatcgattc tttttcaggt gccaaaatct 540  
 acccaggcag aggtaccttg tttgtccgtg gtgactccaa aatcttcaga ttccaaaact 600  
 ccaaactctgc ctctttgttc aagcaaagaa agaaccceaag aagaatcgct tggactgtct 660  
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 gatctttgaa gccagaagt agaaaggcta acagagaaga aaaattgaag gccaaacaaag 840  
 aaaagaagaa ggctgaaaag gctgctagaa aggctgaaaa ggctaagtct gctgggtactc 900  
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 ctcgtaa 968

<210> 92

<211> 155

<212> PRT

<213> Candida albicans

<400> 92

Met Lys Val Glu Ile Asp Ser Phe Ser Gly Ala Lys Ile Tyr Pro Gly  
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Arg Gly Thr Leu Phe Val Arg Gly Asp Ser Lys Ile Phe Arg Phe Gln  
 20 25 30

Asn Ser Lys Ser Ala Ser Leu Phe Lys Gln Arg Lys Asn Pro Arg Arg  
 35 40 45

Ile Ala Trp Thr Val Leu Phe Arg Lys His His Lys Lys Gly Ile Thr  
 50 55 60



100

50                      55                      60  
 Val Ser Asn Cys Gly Ser His Pro Ser Thr Thr Ser Lys Gly Ser Pro  
 65                      70                      75                      80  
 Ile Asn Thr Gln Tyr Val Phe  
 85

<210> 95  
 <211> 1430  
 <212> DNA  
 <213> Candida albicans

<400> 95  
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 ctagaagtga ctcggttctc ttaggaaatt ctaaaccgaa gatttctctt atgggtgattg 240  
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<210> 96  
 <211> 309  
 <212> PRT  
 <213> Candida albicans

<400> 96  
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 1                      5                      10                      15  
 Lys Ser Asn Asp Ala Ala Val Leu Glu Ile Leu His Val Leu Asp Lys  
 20                      25                      30  
 Glu Phe Val Pro Thr Glu Lys Leu Leu Arg Glu Thr Lys Val Gly Val  
 35                      40                      45





<210> 99  
<211> 1461

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 99

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aattgaaatc tacgatactt gatgttgaca ttatagcact agttcccagg aaaccttttc 180
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caacaagctc atttctggaa gccagtcctg aacttggaca aattgtggac attgatccca 1260
gaagacaaga gagaccaata cttgaaatct gcttctaagg aaactgctcc agttattgac 1320
actttggcag ccggttacgg taagatcttg ggtaagggtg gaattccaaa tgttccagtt 1380
atcgtcaaag ctgattcgt ctccaagttg gctgaagaaa aaatcagagc tgctgggtgg 1440
gttggtgaat tgatcgctta a                                     1461

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&lt;210&gt; 100

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 100

```

Met Pro Ser Arg Phe Thr Lys Thr Arg Lys His Arg Gly His Val Ser
 1              5              10              15

Ala Gly Lys Gly Arg Ile Gly Lys His Arg Lys His Pro Gly Gly Arg
      20              25              30

Gly Met Ala Gly Gly Gln His His His Arg Ile Asn Met Asp Lys Tyr
      35              40              45

His Pro Gly Tyr Phe Gly Lys Val Gly Met Arg Tyr Phe His Lys Gln
      50              55              60

Gln Ala His Phe Trp Lys Pro Val Leu Asn Leu Asp Lys Leu Trp Thr
      65              70              75              80

Leu Ile Pro Glu Asp Lys Arg Asp Gln Tyr Leu Lys Ser Ala Ser Lys
      85              90              95

Glu Thr Ala Pro Val Ile Asp Thr Leu Ala Ala Gly Tyr Gly Lys Ile
      100              105              110

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Leu Gly Lys Gly Arg Ile Pro Asn Val Pro Val Ile Val Lys Ala Arg  
 115 120 125

Phe Val Ser Lys Leu Ala Glu Glu Lys Ile Arg Ala Ala Gly Gly Val  
 130 135 140

Val Glu Leu Ile Ala  
 145

<210> 101  
 <211> 1880  
 <212> DNA  
 <213> Candida albicans

<400> 101  
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 tgaactaatt tagtatctat ttccatttca ttataattca cgtttttagc agcctctctt 180  
 cttctaggta attggaaatc ttcttcttta ggcatacggt gaccagctga aaggcagatg 240  
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 tagtcctttt gaaagcaata tcataaaaata tatatagttc tccatgatgt tcgggtcagt 360  
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 gtggaatacg atctgttata tctaaactaa agctaactaa cggaataagc aaatacgaat 480  
 cgaccgctaa tttaacaaat atgggttttag caatggaaag tagagtggca ccggaaattc 540  
 ctgggctcat tcaacctggg aatgtcacgc aagacttgaa gatgatggc tgtaaattat 600  
 tgaattcccc aaaacctacg aaaacattcc ctgggtccca gcctgtgtcc ttccagcatt 660  
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 ttgataggga aaataactat tatctgggta atggatttag gtttcccaga ttacccccaaa 840  
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 caccttacac tgccggcgga aaagattcat tgttattaaa atggaagcca gaacaagaaa 1260  
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 aagatgatcg gaacaggtgg tattacaatt atgacgttaa gccagtttcc agcttatatg 1380  
 tctggcaagg cggagctgat gtcaattcac gtttaaaaca ttccgaccag cctttcgata 1440  
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<210> 102  
 <211> 459  
 <212> PRT  
 <213> Candida albicans

&lt;400&gt; 102

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Ile	Gln	Pro	Gly	Asn	Val	Thr	Gln	Asp	Leu	Lys	Met	Met	Val	Cys	Lys
			20					25					30		
Leu	Leu	Asn	Ser	Pro	Lys	Pro	Thr	Lys	Thr	Phe	Pro	Gly	Ser	Gln	Pro
		35					40					45			
Val	Ser	Phe	Gln	His	Ser	Asp	Val	Glu	Glu	Lys	Leu	Leu	Ala	His	Asp
	50					55					60				
Tyr	Tyr	Val	Cys	Glu	Lys	Thr	Asp	Gly	Leu	Arg	Val	Leu	Met	Phe	Ile
65					70					75					80
Val	Ile	Asn	Pro	Val	Thr	Gly	Glu	Gln	Gly	Cys	Phe	Met	Ile	Asp	Arg
				85					90					95	
Glu	Asn	Asn	Tyr	Tyr	Leu	Val	Asn	Gly	Phe	Arg	Phe	Pro	Arg	Leu	Pro
			100					105					110		
Gln	Lys	Lys	Lys	Glu	Glu	Leu	Leu	Glu	Thr	Leu	Gln	Asp	Gly	Thr	Leu
		115						120				125			
Leu	Asp	Gly	Glu	Leu	Val	Ile	Gln	Thr	Asn	Pro	Met	Thr	Lys	Leu	Gln
	130					135					140				
Glu	Leu	Arg	Tyr	Leu	Met	Phe	Asp	Cys	Leu	Ala	Ile	Asn	Gly	Arg	Cys
145					150					155					160
Leu	Thr	Gln	Ser	Pro	Thr	Ser	Ser	Arg	Leu	Ala	His	Leu	Gly	Lys	Glu
				165					170					175	
Phe	Phe	Lys	Pro	Tyr	Phe	Asp	Leu	Arg	Ala	Ala	Tyr	Pro	Asn	Arg	Cys
			180					185					190		
Thr	Thr	Phe	Pro	Phe	Lys	Ile	Ser	Met	Lys	His	Met	Asp	Phe	Ser	Tyr
		195					200					205			
Gln	Leu	Val	Lys	Val	Ala	Lys	Ser	Leu	Asp	Lys	Leu	Pro	His	Leu	Ser
	210					215					220				
Asp	Gly	Leu	Ile	Phe	Thr	Pro	Val	Lys	Ala	Pro	Tyr	Thr	Ala	Gly	Gly
225					230					235					240
Lys	Asp	Ser	Leu	Leu	Leu	Lys	Trp	Lys	Pro	Glu	Gln	Glu	Asn	Thr	Val
			245						250					255	
Asp	Phe	Lys	Leu	Ile	Leu	Asp	Ile	Pro	Met	Val	Glu	Asp	Pro	Ser	Leu
			260					265					270		
Pro	Lys	Asp	Asp	Arg	Asn	Arg	Trp	Tyr	Tyr	Asn	Tyr	Asp	Val	Lys	Pro
		275					280					285			
Val	Phe	Ser	Leu	Tyr	Val	Trp	Gln	Gly	Gly	Ala	Asp	Val	Asn	Ser	Arg
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[illegible]



<400> 106															
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			20					25					30		
Ser	Gly	Asp	Gly	Tyr	Leu	Lys	Val	Trp	Asp	Asn	Lys	Leu	Leu	Asp	Asn
		35					40					45			
Glu	Asn	Pro	Lys	Asp	Lys	Ser	Tyr	Ser	His	Phe	Val	His	Lys	Ser	Gly
	50					55					60				
Leu	His	His	Val	Asp	Val	Leu	Gln	Ala	Ile	Glu	Arg	Asp	Ala	Phe	Glu
65					70					75					80
Leu	Cys	Leu	Val	Ala	Thr	Thr	Ser	Phe	Ser	Gly	Asp	Leu	Leu	Phe	Tyr
				85					90					95	
Arg	Ile	Thr	Arg	Glu	Asp	Glu	Thr	Lys	Lys	Val	Ile	Phe	Glu	Lys	Leu
			100					105					110		
Asp	Leu	Leu	Asp	Ser	Asp	Met	Lys	Lys	His	Ser	Phe	Trp	Ala	Leu	Lys
		115					120					125			
Trp	Gly	Ala	Ser	Asn	Asp	Arg	Leu	Leu	Ser	His	Arg	Leu	Val	Ala	Thr



130		135		140
Asp Val Lys Gly Thr Thr Tyr Ile Trp Lys Phe His Pro Phe Ala Asp				
145		150		155
Glu Ser Asn Ser Leu Thr Leu Asn Trp Ser Pro Thr Leu Glu Leu Gln				
	165		170	175
Gly Thr Val Glu Ser Pro Met Thr Pro Ser Gln Phe Ala Thr Ser Val				
	180		185	190
Asp Ile Ser Glu Arg Gly Leu Ile Ala Thr Gly Phe Asn Asn Gly Thr				
	195		200	205
Val Gln Ile Ser Glu Leu Ser Thr Leu Arg Pro Leu Tyr Asn Phe Glu				
	210		215	220
Ser Gln His Ser Met Ile Asn Asn Ser Asn Ser Ile Arg Ser Val Lys				
225		230		235
Phe Ser Pro Gln Gly Ser Leu Leu Ala Ile Ala His Asp Ser Asn Ser				
	245		250	255
Phe Gly Cys Ile Thr Leu Tyr Glu Thr Glu Phe Gly Glu Arg Ile Gly				
	260		265	270
Ser Leu Ser Val Pro Thr His Ser Ser Gln Ala Ser Leu Gly Glu Phe				
	275		280	285
Ala His Ser Ser Trp Val Met Ser Leu Ser Phe Asn Asp Ser Gly Glu				
	290		295	300
Thr Leu Cys Ser Ala Gly Trp Asp Gly Lys Leu Arg Phe Trp Asp Val				
305		310		315
Lys Thr Lys Glu Arg Ile Thr Thr Leu Asn Met His Cys Asp Asp Ile				
	325		330	335
Glu Ile Glu Glu Asp Ile Leu Ala Val Asp Glu His Gly Asp Ser Leu				
	340		345	350
Ala Glu Pro Gly Val Phe Asp Val Lys Phe Leu Lys Lys Gly Trp Arg				
	355		360	365
Ser Gly Met Gly Ala Asp Leu Asn Glu Ser Leu Cys Cys Val Cys Leu				
	370		375	380
Asp Arg Ser Ile Arg Trp Phe Arg Glu Ala Gly Gly Lys				
385		390		395

&lt;210&gt; 107

&lt;211&gt; 1037

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

Val	Lys	Glu	Asp	Met	Val	Asn	Arg	Leu	Leu	Arg	Thr	Cys	Lys	Gly	Asn
145					150					155					160



<400> 111  
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<210> 112

<211> 174

<212> PRT

<213> *Candida albicans*

<400> 112

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Leu Val Leu Asn Ile Ser Val Gly Glu Ser Gly Asp Arg Leu Thr Arg  
 20 25 30

Ala Ser Lys Val Leu Glu Gln Leu Ser Gly Gln Thr Pro Val Gln Ser  
 35 40 45

Lys Ala Arg Tyr Thr Val Arg Thr Phe Gly Ile Arg Arg Asn Glu Lys  
 50 55 60

Ile Ala Val His Val Thr Val Arg Gly Pro Lys Ala Glu Glu Ile Leu  
 65 70 75 80

Glu Arg Gly Leu Lys Val Lys Glu Tyr Gln Leu Arg Asp Arg Asn Phe  
 85 90 95

Ser Ala Thr Gly Asn Phe Gly Phe Gly Ile Asp Glu His Ile Asp Leu  
 100 105 110

Gly Ile Lys Tyr Asp Pro Ser Ile Gly Ile Phe Gly Met Asp Phe Tyr  
 115 120 125

Val Val Met Asn Arg Pro Gly Ala Arg Val Thr Arg Arg Lys Arg Cys  
 130 135 140

Lys Gly Thr Val Gly Asn Ser His Lys Thr Thr Lys Glu Asp Thr Val  
 145 150 155 160

Ser Trp Phe Lys Gln Lys Tyr Asp Ala Asp Val Leu Asp Lys  
 165 170

<210> 113  
 <211> 1258  
 <212> DNA  
 <213> Candida albicans

<400> 113  
 agccatgctg gtcgcactag actttttcttc tcaactgtcac ttacctgttt gaaatcatgt 60  
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 taccctatat acaccatac cctatttttta aatataaaaa gtaaacttca ttttgaaaga 180  
 ccactctgca tcagcacgcg ggctctggaa ggaagaaatg acgtttcggc ggaataccct 240  
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 tacgcccaga gtacactgcc gtaatatcac aatgtttcga ctaacgggtta cagtacgtta 420  
 aattagatac tgcctatgaa ttgacatatt agataatgtc aaattttaca aaaacctaag 480  
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 aaccccctat tgtgatatcg ttttaggtga aggaaatgtt gtgagctctg gagtgataaa 660  
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 caacggaatc atttttttac taacagtttt tttttattat tatagccgtt gggccgaaaa 900  
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<210> 114  
 <211> 145  
 <212> PRT  
 <213> Candida albicans

<400> 114  
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 Val His Arg Arg Asn Asn Arg Trp Ala Glu Asn Asn Tyr Lys Lys Arg  
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 Leu Leu Gly Thr Ala Phe Lys Ser Ser Pro Phe Gly Gly Ser Ser His  
 35 40 45  
 Ala Lys Gly Ile Val Leu Glu Lys Leu Gly Ile Glu Ser Lys Gln Pro  
 50 55 60  
 Asn Ser Ala Ile Arg Lys Cys Val Arg Val Gln Leu Ile Lys Asn Gly  
 65 70 75 80  
 Lys Lys Val Thr Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Val  
 85 90 95

Asp Glu Asn Asp Glu Val Leu Leu Ala Gly Phe Gly Arg Lys Gly Lys  
 100 105 110

Ala Lys Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser  
 115 120 125

Gly Val Ser Leu Leu Ala Leu Trp Lys Glu Lys Lys Glu Lys Pro Arg  
 130 135 140

Ser  
 145

<210> 115  
 <211> 1733  
 <212> DNA  
 <213> *Candida albicans*

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 caccgtctgt ggttgtaaag ttactgacac ttttttttct agaaagttcc ggaaaattgc 180  
 gacactcggg ggagctcgag agttgtatcc agttttcttg ttcggcgata ttccgaacca 240  
 ggtcgggttg ggctaacagc cgcccaggat ggaagaatta agaatttcat agaagccttc 300  
 agttcttggc gaagtaaagt ggcaaaacaa atggaagatc tattgcatta catatataaa 360  
 agcattagaa caatcttttc tcattgacag gtattctcat tgctctatat atattttctt 420  
 cttcttgaaa gaaatatcag tattacaatc ataacaacaa ccaaaagaaa ataactaata 480  
 gaccccatata caatatagaa atgtttttcca tattcaattc accatgtgtt tttgaacagc 540  
 tgccatcttt tagtcagccc ctacattcgc gttattttga ttgcagttct ccagtgaagt 600  
 attatccaga atgtaaaagg aggaaagcaa taaaagctaa cctaagagct ccaaaaaaaa 660  
 gcgatgcaaa ttgttcagaa cctttgaggt atgcacttgc tgaaacacca aatgggtata 720  
 cattaagctt gtctaagcgg attccatatg aacttttttc aaagtacgtt aatgagaaat 780  
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<210> 116  
 <211> 410  
 <212> PRT  
 <213> *Candida albicans*

&lt;400&gt; 116

Met Phe Ser Ile Phe Asn Ser Pro Cys Val Phe Glu Gln Leu Pro Ser  
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Phe Ser Gln Pro Leu His Ser Arg Tyr Phe Asp Cys Ser Ser Pro Val  
 20 25 30

Ser Tyr Tyr Pro Glu Cys Lys Arg Arg Lys Ala Ile Lys Ala Asn Leu  
 35 40 45

Arg Ala Pro Lys Lys Ser Asp Ala Asn Cys Ser Glu Pro Leu Arg Tyr  
 50 55 60

Ala Leu Ala Glu Thr Pro Asn Gly Tyr Thr Leu Ser Leu Ser Lys Arg  
 65 70 75 80

Ile Pro Tyr Glu Leu Phe Ser Lys Tyr Val Asn Glu Lys Leu Gly Glu  
 85 90 95

Leu Lys Glu Asn His Tyr Arg Pro Thr Tyr His Val Val Gln Asp Phe  
 100 105 110

Phe Gly Asn Gln Tyr Tyr Val Glu Asp Glu Ala Asp Glu Asp Ala Leu  
 115 120 125

Leu Arg Ser Ala Leu Lys Asp Leu Asp Phe Arg Ala Ile Gly Lys Lys  
 130 135 140

Ile Ala Lys Asp Leu Phe Gln Asp Tyr Glu Ile Glu Leu Asn His Arg  
 145 150 155 160

Gly Asp Glu Leu Ser Ile Leu Ser Lys Lys Asp Lys Ile Phe Lys Glu  
 165 170 175

Phe Ser Leu Asp Gln Val Phe Glu Asp Val Phe Val Ile Gly Cys Gly  
 180 185 190

Val Glu Asn Ile Asp Asp Gly Ser Arg Glu Lys Tyr Ala Leu Leu Lys  
 195 200 205

Ile Gly Leu Val Lys His Glu Glu Glu Ile Ser Glu Gly Gly Ile Asn  
 210 215 220

Glu Pro Lys Met Pro Ile Ile Glu Ser Lys Ile Asp Glu Ser His Asp  
 225 230 235 240

Asp Val Asn Met Ser Glu Ser Leu Lys Glu Glu Glu Ala Glu Lys Ala  
 245 250 255

Lys Glu Pro Leu Thr Lys Glu Asp Gln Ile Lys Lys Trp Ile Glu Glu  
 260 265 270

Glu Arg Leu Met Gln Glu Glu Ser Arg Lys Ser Glu Gln Glu Lys Ala  
 275 280 285

Ala Lys Glu Asp Glu Glu Arg Gln Lys Lys Glu Lys Glu Ala Arg Leu  
 290 295 300

Lys Ala Arg Lys Glu Ser Leu Ile Asn Lys Gln Lys Thr Lys Arg Ser  
305 310 315 320

Gln Gln Lys Lys Leu Gln Asn Ser Lys Ser Leu Pro Ile Ser Glu Ile  
325 330 335

Glu Ala Ser Asn Lys Asn Asn Asn Ser Asn Ser Gly Ser Ala Glu Ser  
340 345 350

Asp Asn Glu Ser Ile Asn Ser Asp Ser Asp Thr Thr Leu Asp Phe Ser  
355 360 365

Val Ser Gly Asn Thr Leu Lys Lys His Ala Ser Pro Leu Leu Glu Asp  
370 375 380

Val Glu Asp Glu Glu Val Asp Arg Tyr Asn Glu Ser Leu Ser Arg Ser  
385 390 395 400

Pro Lys Gly Asn Ser Ile Ile Glu Glu Ile  
405 410

<210> 117

<211> 890

<212> DNA

<213> Candida albicans

<400> 117

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ccatacatac attttgataa agatataatg ttatatcttct tttcgtaatt ttgttttact 180
tcggtttgct ctatagattt catcagccgc accgaaaagg gagatcaata aggtaccctt 240
taaaagggat aagaagccta catcacccca ataaatggag taatggccag cattggatga 300
agagaagaat tacgggatac tgggataaca ctgttaaaaa atgcttcgcg acgtgagggg 360
cttcttcata taaattgaac tgccaaatct ctttcacatt atccaggata gtttggaatg 420
tgtgttactg aaggatcaga atcaataaat acaatcaata caaatattta gcgcataaaa 480
ttcaaacaaa gtttactgaa atgaagttag attcaggaat atactcagag gcacaaagag 540
ttgtgagaac tccaaagttt agatatatta tggttagggct ggtgggcgct gctgtggtac 600
cgaccgcata catgaggaga ggctatacgg ttccctgcaca tagcttagac aacatcaacg 660
gcgtagacac aactaaggcg tctgttatgg gtacagaaca gagagcagct atgacgaagg 720
gtaagagttt acaagagatg atggatgatg atgaagtaac gtatttgatg ttcctcttca 780
atcatgtaag ggaatttgta cttgggtccc tgcatttatg ttctttgcat tttgttttcg 840
catttaatca tagtacgaca aacggggaag gggattgtga ttttacataa 890
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<210> 118

<211> 129

<212> PRT

<213> Candida albicans

<400> 118

Met Lys Leu Asp Ser Gly Ile Tyr Ser Glu Ala Gln Arg Val Val Arg  
1 5 10 15

Thr Pro Lys Phe Arg Tyr Ile Met Leu Gly Leu Val Gly Ala Ala Val



20	25	30
Val Pro Thr Ala Tyr Met Arg Arg Gly Tyr Thr Val Pro Ala His Ser		
35	40	45
Leu Asp Asn Ile Asn Gly Val Asp Thr Thr Lys Ala Ser Val Met Gly		
50	55	60
Thr Glu Gln Arg Ala Ala Met Thr Lys Gly Lys Ser Leu Gln Glu Met		
65	70	75
Met Asp Asp Asp Glu Val Thr Tyr Leu Met Phe Leu Phe Asn His Val		
85	90	95
Arg Glu Phe Val Leu Gly Ser Leu His Leu Cys Ser Leu His Phe Val		
100	105	110
Phe Ala Phe Asn His Ser Thr Thr Asn Gly Glu Gly Asp Cys Asp Phe		
115	120	125
Thr		

<210> 119  
 <211> 1418  
 <212> DNA  
 <213> Candida albicans

<400> 119

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tgccattctg	t	tttggtcaga	gtaaaatcca	caacattttt	acaaattatg	ttgcggccaa	180
taagtata	t	gacttgaaat	aagtctctgt	gcgattcctg	taagttgtcc	attgttaa	240
tggatatt	t	gggtgaaacg	tgtgacctta	tcatttccca	gttttctctc	tgaaatttaa	300
tgtcttcac	t	ctgtatggta	gcggtagaca	tgctggtttg	tagccttttt	attccttttt	360
aggtttctta	t	ctcacatgc	caaaataaat	atcagtgtaa	tataattttt	caagagtacg	420
taatggaaaa	a	agataaaaa	aaggaccgtc	ataaaaagag	acgtgattaa	acctaaaaat	480
ctaaagtaaa	a	gaagtgtgag	atggttgagg	aaaattccag	agttttgatt	gttcttctct	540
atacaccgcc	c	tagtgctact	ttgcagagga	ttatagggca	aactattccg	ttcttaagag	600
aatgtcaaag	a	tcaactagac	atcgtgattg	tacctgaatt	caaaacctca	ttccagttgg	660
attctgcgct	t	aggggaagatg	tacagtatta	ccagggatgt	ccttttgggc	tatggaatga	720
tcaacagcgg	c	aatcaacatc	atattcaaca	atattcattt	cgtcgagagt	aatttgcaat	780
ggaaagtgg	t	tttattgcca	caggaatcca	cttttgaaac	ttggaagcta	gagttgggac	840
aaggacaata	a	ccatagtata	gaacattatg	cattacacga	taatataatg	gaagagatag	900
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cttatgatac	a	acgatgcagg	cacgtacatc	aattcatcaa	gttggttaaaa	ccggatctct	1140
ccgtagaact	a	agttccctta	agggacgtgt	gcggccccac	agggaaagta	cccagatag	1200
aatgtttagt	a	tgtgagtaga	gaaaccgtca	gtggggcaga	gactgtgaat	aagactagga	1260
ttgaaaaagg	a	catgagccca	ttggcagtac	atgtgggttaa	tgtacttgga	ggaagggagg	1320
aagacggctg	a	gagcgagaag	ttaagcagca	cggaaatcag	acgcctactt	aagtcctctg	1380
cttcgccaac	a	gtgcactcca	caaaaccctt	gcgtataa			1418

<210> 120  
 <211> 305  
 <212> PRT  
 <213> Candida albicans

<400> 120  
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 Pro Ser Ala Thr Leu Gln Arg Ile Ile Gly Gln Thr Ile Pro Phe Leu  
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 Arg Glu Cys Gln Ser Gln Leu Asp Ile Val Ile Val Pro Glu Phe Lys  
 35 40 45  
 Thr Ser Phe Gln Leu Asp Ser Ala Leu Gly Lys Met Tyr Ser Ile Thr  
 50 55 60  
 Arg Asp Val Leu Leu Gly Tyr Gly Met Ile Asn Ser Gly Ile Asn Ile  
 65 70 75 80  
 Ile Phe Asn Asn Ile His Phe Val Glu Ser Asn Leu Gln Trp Lys Val  
 85 90 95  
 Val Leu Leu Pro Gln Glu Ser Thr Phe Glu Thr Trp Lys Leu Glu Leu  
 100 105 110  
 Gly Gln Gly Gln Tyr His Ser Ile Glu His Tyr Ala Leu His Asp Asn  
 115 120 125  
 Ile Met Glu Glu Ile Glu Gly Pro Lys Asp Ala Asn Lys Phe His Val  
 130 135 140  
 Thr Ala Leu Gly Gly Thr Phe Asp His Ile His Asp Gly His Lys Ile  
 145 150 155 160  
 Leu Leu Ser Val Ser Thr Phe Ile Thr Ser Gln Arg Leu Ile Cys Gly  
 165 170 175  
 Ile Thr Cys Asp Glu Leu Leu Gln Asn Lys Lys Tyr Lys Glu Leu Ile  
 180 185 190  
 Glu Pro Tyr Asp Thr Arg Cys Arg His Val His Gln Phe Ile Lys Leu  
 195 200 205  
 Leu Lys Pro Asp Leu Ser Val Glu Leu Val Pro Leu Arg Asp Val Cys  
 210 215 220  
 Gly Pro Thr Gly Lys Val Pro Glu Ile Glu Cys Leu Val Val Ser Arg  
 225 230 235 240  
 Glu Thr Val Ser Gly Ala Glu Thr Val Asn Lys Thr Arg Ile Glu Lys  
 245 250 255  
 Gly Met Ser Pro Leu Ala Val His Val Val Asn Val Leu Gly Gly Arg  
 260 265 270

Glu Glu Asp Gly Trp Ser Glu Lys Leu Ser Ser Thr Glu Ile Arg Arg  
 275 280 285

Leu Leu Lys Ser Ser Ala Ser Pro Thr Cys Thr Pro Gln Asn Pro Cys  
 290 295 300

Val  
 305

<210> 121  
 <211> 1433  
 <212> DNA  
 <213> Candida albicans

<400> 121  
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 ccacgattga cgaacaagtt ggtttgatcg ttgacagttt gaatgacgaa gagttagtgt 120  
 ccaccgccga taagatcaag gccaatgctg ctgggtgccaa ggaagttttg aaggaatctg 180  
 caaagactat tgtcgattct ggcaaaactac catccagctt gttgtcctac ttcgtgtgaa 240  
 taccgtaaga aatggaatag aatatatacg aatgtatacg aatattatag agaacgttct 300  
 cttttatttc tataatgaat aggttcgggt aacgggtccc tttttaggta tttctagaag 360  
 atgagagaag aggggaataat gagaaaggcg aaaaataaag gacaccttta acgaaagatc 420  
 aaaggtgtcc ttatttactt acaatagctg caattagtag gactcaaaaa aagtgaatac 480  
 aaaactgaaa ggatagatca atgtcttaca gaggacctat tggaaatttt ggcggtatgc 540  
 caatgtcatc atcgcaagga ccatactctg gcggtgcaca attcagatca aaccagaacc 600  
 aatccacttc tggcatctta aagcaatgga agcattcttt tgaaaagttt gcctccagaa 660  
 ttgaggggct cactgacaat gcagttgttt ataaattgaa gccttacatt ccaagtttgt 720  
 caagattttt cattgtggcc accttttatg aagattcggt taggatctta tcacaatggt 780  
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 tactaacttt ttacaatatc acgctaaaca actactgggt ttataacaat actaagagag 1320  
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<210> 122  
 <211> 310  
 <212> PRT  
 <213> Candida albicans

<400> 122  
 Met Ser Tyr Arg Gly Pro Ile Gly Asn Phe Gly Gly Met Pro Met Ser  
 , 1 5 10 15  
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 20 25 30  
 Asn Gln Ser Thr Ser Gly Ile Leu Lys Gln Trp Lys His Ser Phe Glu  
 35 40 45

Lys Phe Ala Ser Arg Ile Glu Gly Leu Thr Asp Asn Ala Val Val Tyr  
     50                    55                    60  
 Lys Leu Lys Pro Tyr Ile Pro Ser Leu Ser Arg Phe Phe Ile Val Ala  
     65                    70                    75                    80  
 Thr Phe Tyr Glu Asp Ser Phe Arg Ile Leu Ser Gln Trp Ser Asp Gln  
                     85                    90                    95  
 Ile Phe Tyr Leu Asn Lys Trp Lys His Tyr Pro Tyr Phe Phe Val Val  
                     100                    105                    110  
 Val Phe Leu Val Val Val Thr Val Ser Met Leu Ile Gly Ala Ser Leu  
                     115                    120                    125  
 Leu Val Leu Arg Lys Gln Thr Asn Tyr Ala Thr Gly Val Leu Cys Ala  
     130                    135                    140  
 Cys Val Ile Ser Gln Ala Leu Val Tyr Gly Leu Phe Thr Gly Ser Ser  
     145                    150                    155                    160  
 Phe Val Leu Arg Asn Phe Ser Val Ile Gly Gly Leu Leu Ile Ala Phe  
                     165                    170                    175  
 Ser Asp Ser Ile Val Gln Asn Lys Thr Thr Phe Gly Met Leu Pro Glu  
                     180                    185                    190  
 Leu Asn Ser Lys Asn Asp Lys Ala Lys Gly Tyr Leu Leu Phe Ala Gly  
                     195                    200                    205  
 Arg Ile Leu Ile Val Leu Met Phe Ile Ala Phe Thr Phe Ser Lys Ser  
     210                    215                    220  
 Trp Phe Thr Val Val Leu Thr Ile Ile Gly Thr Ile Cys Phe Ala Ile  
     225                    230                    235                    240  
 Gly Tyr Lys Thr Lys Phe Ala Ser Ile Met Leu Gly Leu Ile Leu Thr  
                     245                    250                    255  
 Phe Tyr Asn Ile Thr Leu Asn Asn Tyr Trp Phe Tyr Asn Asn Thr Lys  
                     260                    265                    270  
 Arg Asp Phe Leu Lys Tyr Glu Phe Tyr Gln Asn Leu Ser Ile Ile Gly  
                     275                    280                    285  
 Gly Leu Leu Leu Val Thr Asn Thr Gly Ala Gly Glu Leu Ser Val Asp  
     290                    295                    300  
 Glu Lys Lys Lys Ile Tyr  
     305                    310

&lt;210&gt; 123

&lt;211&gt; 1802

&lt;212&gt; DNA



Ala	Asp	Glu	Asp	Leu 85	Leu	Thr	His	Asp	Ala 90	Arg	Asp	Trp	Lys	Thr	Ala
Asp	Leu	Tyr	Ala 100	Ala	Met	Gly	Leu	Ser 105	Lys	Leu	Arg	Phe	Arg 110	Ala	Thr
Glu	Ser	Gln 115	Ile	Ile	Lys	Ala	His 120	Arg	Lys	Gln	Val	Val 125	Lys	Tyr	His
Pro	Asp 130	Lys	Gln	Ser	Ala	Ala 135	Gly	Gly	Ser	Leu	Asp 140	Gln	Asp	Gly	Phe
Phe 145	Lys	Ile	Ile	Gln 150	Lys	Ala	Phe	Glu	Thr 155	Leu	Thr	Asp	Ser	Asn 160	Lys
Arg	Ala	Gln	Tyr	Asp 165	Ser	Cys	Asp	Phe 170	Val	Ala	Asp	Val	Pro 175	Pro	Pro
Lys	Lys	Gly	Thr 180	Asp	Tyr	Asp	Phe	Tyr 185	Glu	Ala	Trp	Gly	Pro 190	Val	Phe
Glu	Ala	Glu 195	Ala	Arg	Phe	Ser	Lys 200	Lys	Thr	Pro	Ile	Pro 205	Ser	Leu	Gly
Asn 210	Lys	Asp	Ser	Ser	Lys	Lys 215	Glu	Val	Glu	Gln	Phe 220	Tyr	Ala	Phe	Trp
His 225	Arg	Phe	Asp	Ser 230	Trp	Arg	Thr	Phe	Glu 235	Phe	Leu	Asp	Glu	Asp 240	Val
Pro	Asp	Asp	Ser	Ser 245	Asn	Arg	Asp	His	Lys 250	Arg	Tyr	Ile	Glu	Arg 255	Lys
Asn	Lys	Ala 260	Ala	Arg	Asp	Lys	Lys 265	Lys	Thr	Ala	Asp	Asn 270	Ala	Arg	Leu
Val	Lys	Leu 275	Val	Glu	Arg	Ala	Val 280	Ser	Glu	Asp	Pro	Arg 285	Ile	Lys	Met
Phe 290	Lys	Glu	Glu	Glu	Lys	Lys 295	Glu	Lys	Glu	Arg	Arg 300	Lys	Trp	Glu	Arg
Glu 305	Ala	Gly	Ala	Arg	Ala 310	Glu	Ala	Glu	Ala	Lys 315	Ala	Lys	Ala	Glu	Ala
Glu	Ala	Lys	Ala	Lys 325	Ala	Glu	Ser	Glu	Ala 330	Lys	Ala	Asn	Ala 335	Ser	Ala
Lys	Ala	Asp	Lys 340	Lys	Lys	Ala	Lys	Glu 345	Ala	Ala	Lys	Ala 350	Ala	Lys	Lys
Lys	Asn 355	Lys	Arg	Ala	Ile	Arg	Asn 360	Ser	Ala	Lys	Glu	Ala 365	Asp	Tyr	Phe
Gly 370	Asp	Ala	Asp	Lys	Ala	Thr 375	Thr	Ile	Asp	Glu	Gln 380	Val	Gly	Leu	Ile

Val Asp Ser Leu Asn Asp Glu Glu Leu Val Ser Thr Ala Asp Lys Ile  
385 390 395 400

Lys Ala Asn Ala Ala Gly Ala Lys Glu Val Leu Lys Glu Ser Ala Lys  
405 410 415

Thr Ile Val Asp Ser Gly Lys Leu Pro Ser Ser Leu Leu Ser Tyr Phe  
420 425 430

Val

<210> 125

<211> 1472

<212> DNA

<213> Candida albicans

<400> 125

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cacctacact gttttttttt ttttcacett atgagtcctg tatttcttga aagagccgat 180
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tagatgttga agctttcaaa tccgttggtt ctactgaaac tttcgaacaa ccttcccaac 1380
gtgaagaagc taagaaagtc gtcaagaagg ctttcgaaga aagacaccaa gctggtaaga 1440
accaatgggt cttctctaag ttgagatttt aa 1472

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<210> 126

<211> 136

<212> PRT

<213> Candida albicans

<400> 126

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1 5 10 15

Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly

20	25	30
Ser Lys Ser His Pro Phe Gly His Ala Leu Val Ala Gly Ile Glu Arg		
35	40	45
Tyr Pro Leu Lys Val Thr Lys Lys His Gly Ala Lys Lys Val Ala Lys		
50	55	60
Arg Thr Lys Ile Lys Pro Phe Ile Lys Val Val Asn Tyr Asn His Leu		
65	70	75
Leu Pro Thr Arg Tyr Thr Leu Asp Val Glu Ala Phe Lys Ser Val Val		
85	90	95
Ser Thr Glu Thr Phe Glu Gln Pro Ser Gln Arg Glu Glu Ala Lys Lys		
100	105	110
Val Val Lys Lys Ala Phe Glu Glu Arg His Gln Ala Gly Lys Asn Gln		
115	120	125
Trp Phe Phe Ser Lys Leu Arg Phe		
130	135	

&lt;210&gt; 127

&lt;211&gt; 1299

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 127

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&lt;210&gt; 128

&lt;211&gt; 82



&lt;212&gt; PRT



127

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 50 55 60  
 Thr His Thr Pro His Thr Thr Leu Ser Asn Leu Ser Leu Asn Leu Pro  
 65 70 75 80  
 Ser His Tyr Pro Thr Ser Pro Leu Val Thr Leu Pro His Ser Thr Ile  
 85 90 95  
 Pro Leu Pro Thr Thr Ile His Leu Ser Thr Tyr Tyr Tyr His Pro Pro  
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 <213> Candida albicans

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&lt;210&gt; 134

&lt;211&gt; 1083

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 134

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 225 230 235 240  
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 245 250 255  
 Ile Asp Asp Ser Lys Asn Ile Ala Leu Ser Ser Ser Leu Phe Arg Gly  
 260 265 270  
 Gly Ser Ser Pro Val Lys Glu Thr Asn Asn Asn Leu Ser Asn Met Asn  
 275 280 285  
 Ser Ser Pro Ala Gln Asn Pro Lys Arg Gly Ser Val Ser Arg Ser Asn  
 290 295 300  
 Asp Ser Asn Lys Ser Ser His Ile Ala Val Ser Lys Arg Pro Lys Gln  
 305 310 315 320  
 Lys Lys Gly Ile Tyr Arg Asp Ser Gly Gly Arg Thr Arg Leu Gln Ile  
 325 330 335

Ala Cys Asp Lys Gly Lys Tyr Asp Val Val Lys Lys Met Ile Glu Glu  
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 Gly Gly Tyr Asp Ile Asn Asp Gln Asp Asn Ala Gly Asn Thr Ala Leu  
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 Glu Asn Gly Ala Asp Val Asn Ile Lys Ser Ile Glu Met Phe Gly Asp  
 385 390 395 400  
 Thr Pro Leu Ile Asp Ala Ser Ala Asn Gly His Leu Asp Val Val Lys  
 405 410 415  
 Tyr Leu Leu Lys Asn Gly Ala Asp Pro Thr Ile Arg Asn Ala Lys Gly  
 420 425 430  
 Leu Thr Ala Phe Glu Ser Val Asp Asp Glu Ser Glu Phe Asp Asp Glu  
 435 440 445  
 Glu Asp Gln Lys Ile Leu Arg Glu Ile Lys Lys Arg Leu Ser Ile Ala  
 450 455 460  
 Ala Lys Lys Trp Thr Asn Arg Ala Gly Ile His Asn Asp Lys Ser Lys  
 465 470 475 480  
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 485 490 495  
 Thr Lys Ala Lys Asn Glu Lys Ala Ala Asp Ser Pro Ser Met Ala Ser  
 500 505 510  
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 His Leu Pro Tyr Val Gly Thr Tyr Val Glu Asn Gly Gly Lys Ile Asp  
 545 550 555 560  
 Leu Arg Ser Phe Phe Glu Ser Val Lys Cys Gly His Glu Asp Ile Thr  
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 Ser Ile Phe Leu Ala Phe Gly Phe Pro Val Asn Gln Thr Ser Arg Asp  
 580 585 590  
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 625 630 635 640

Ile Thr Asn Ser Glu Glu Ile Gln Leu Ile Glu Asn Ala Ile Asn Asn  
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 Tyr Leu Lys Lys His Ser Glu Asp Asn Asn Asp Asp Asp Asp Asp Asp  
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 Asp Asn Asn Asn Glu Thr Tyr Lys His Glu Lys Lys Arg Glu Lys Thr  
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 725 730 735  
 Arg Leu Asp Asp Asn Glu Asn Val Gly Thr Gln Tyr Ser Leu Asp Trp  
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 850 855 860  
 Glu Met Glu Glu Ile Ser Tyr Arg Arg Ala Val Arg Asp Leu Tyr Pro  
 865 870 875 880  
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 885 890 895  
 Phe Leu Pro Leu Tyr Tyr Phe Val Asp Glu Lys Asn Asp Lys Phe Val  
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 930 935 940

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 965 970 975  
 Asn Phe Asp Gly Val Asp Leu Asp Thr Lys Ile Gly Tyr Glu Leu Leu  
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 Glu Tyr Lys Lys Phe Val Ser Leu Pro Met Ala Trp Ile Lys Trp Asp  
 995 1000 1005  
 Asn Val Val Ile Glu Asn His Ala Lys Arg Lys Glu Ile Glu Gly Asn  
 1010 1015 1020  
 Met Ile Gln Ile Ser Ile Asn Glu Phe Ala Arg Trp Arg Asn Asp Lys  
 1025 1030 1035 1040  
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 agagatttga cgataatcca ttagtggtgaa aactagctaa agaattctct gcacgtgacg 4680



Val Ser Tyr Asp Gln Lys Met Tyr Ile Ile Lys His Ile Asp Gly Ser  
 245 250 255  
 Ala Ser Phe Gln Glu Thr Phe Asp Ile Thr Pro Pro Phe Gly Gln Ile  
 260 265 270  
 Val Arg Phe Pro Tyr Met Tyr Lys Val Thr Leu Ser Gly Leu Ile Glu  
 275 280 285  
 Pro Asp Ala Asn Val Asn Val Leu Ala Ser Ser Cys Ser Ser Glu Val  
 290 295 300  
 Ser Ile Trp Asp Ser Lys Gln Val Ile Glu Pro Ser Gln Asp Ser Glu  
 305 310 315 320  
 Arg Ala Val Leu Pro Ile Ser Glu Glu Thr Asp Lys Asp Thr Asn Pro  
 325 330 335  
 Ile Gly Val Ala Val Asp Val Val Thr Ser Gly Thr Ile Leu Glu Pro  
 340 345 350  
 Cys Ser Gly Val Asp Thr Ile Glu Arg Leu Pro Leu Val Tyr Ile Leu  
 355 360 365  
 Asn Asn Glu Gly Ser Leu Gln Ile Val Gly Leu Phe His Val Ala Ala  
 370 375 380  
 Ile Lys Ser Gly His Tyr Ser Ile Asn Leu Glu Ser Leu Glu His Glu  
 385 390 395 400  
 Lys Ser Leu Ser Pro Thr Ser Glu Lys Ile Pro Ile Ala Gly Gln Glu  
 405 410 415  
 Gln Glu Glu Lys Lys Lys Asn Asn Glu Ser Ser Lys Ala Leu Ser Glu  
 420 425 430  
 Asn Pro Phe Thr Ser Ala Asn Thr Ser Gly Phe Thr Phe Leu Lys Thr  
 435 440 445  
 Gln Pro Ala Ala Ala Asn Ser Leu Gln Ser Gln Ser Ser Ser Thr Phe  
 450 455 460  
 Gly Ala Pro Ser Phe Gly Ser Ser Ala Phe Lys Ile Asp Leu Pro Ser  
 465 470 475 480  
 Val Ser Ser Thr Ser Thr Gly Val Ala Ser Ser Glu Gln Asp Ala Thr  
 485 490 495  
 Asp Pro Ala Ser Ala Lys Pro Val Phe Gly Lys Pro Ala Phe Gly Ala  
 500 505 510  
 Ile Ala Lys Glu Pro Ser Thr Ser Glu Tyr Ala Phe Gly Lys Pro Ser  
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 Phe Gly Ala Pro Ser Phe Gly Ser Gly Lys Ser Ser Val Glu Ser Pro  
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Ala	Ser	Gly	Ser	Ala	Phe	Gly	Lys	Pro	Ser	Phe	Gly	Thr	Pro	Ser	Phe
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Gly	Ser	Gly	Asn	Ser	Ser	Val	Glu	Pro	Pro	Ala	Ser	Gly	Ser	Ala	Phe
				565					570					575	
Gly	Lys	Pro	Ser	Phe	Gly	Thr	Pro	Ser	Phe	Gly	Ser	Gly	Asn	Ser	Ser
			580					585					590		
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Ser	Pro	Lys	Glu	Val	Asp	Ser	Thr	Ser	Pro	Phe	Pro	Ser	Ser	Gly	Asp
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Gln	Ser	Glu	Asp	Glu	Ser	Lys	Ser	Asp	Val	Asp	Ser	Ser	Ser	Thr	Pro
		675					680					685			
Phe	Gly	Thr	Lys	Pro	Asn	Thr	Ser	Thr	Lys	Pro	Lys	Thr	Asn	Ala	Phe
	690					695					700				
Asp	Phe	Gly	Ser	Ser	Ser	Phe	Gly	Ser	Gly	Phe	Ser	Lys	Ala	Leu	Glu
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Ser	Val	Gly	Ser	Asp	Thr	Thr	Phe	Lys	Phe	Gly	Thr	Gln	Ala	Ser	Pro
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		755					760					765			
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		770				775					780				
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785					790					795					800
Pro	Glu	Thr	Pro	Ser	Asp	Glu	Asp	Gly	Glu	Val	Val	Glu	Glu	Glu	Ala
				805					810					815	
Gln	Lys	Ser	Pro	Ile	Gly	Lys	Leu	Thr	Glu	Thr	Ile	Lys	Lys	Ser	Ala
			820					825					830		
Asn	Ile	Asp	Met	Ala	Gly	Leu	Lys	Asn	Pro	Val	Phe	Gly	Asn	His	Val
		835					840					845			

Lys	Ala	Lys	Ser	Glu	Ser	Pro	Phe	Ser	Ala	Phe	Ala	Thr	Asn	Ile	Thr
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Lys	Pro	Ser	Ser	Thr	Thr	Pro	Ala	Phe	Ser	Phe	Gly	Asn	Ser	Thr	Met
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Asn	Lys	Ser	Asn	Thr	Ser	Thr	Val	Ser	Pro	Met	Glu	Glu	Ala	Asp	Thr
				885					890					895	
Lys	Glu	Thr	Ser	Glu	Lys	Gly	Pro	Ile	Thr	Leu	Lys	Ser	Val	Glu	Asn
			900					905					910		
Pro	Phe	Leu	Pro	Ala	Lys	Glu	Glu	Arg	Thr	Gly	Glu	Ser	Ser	Lys	Lys
		915					920					925			
Asp	His	Asn	Asp	Asp	Pro	Lys	Asp	Gly	Tyr	Val	Ser	Gly	Ser	Glu	Ile
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Ser	Val	Arg	Thr	Ser	Glu	Ser	Ala	Phe	Asp	Thr	Thr	Ala	Asn	Glu	Glu
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Ile	Pro	Lys	Ser	Gln	Asp	Val	Asn	Asn	His	Glu	Lys	Ser	Glu	Thr	Asp
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Pro	Lys	Tyr	Ser	Gln	His	Ala	Val	Val	Asp	His	Asp	Asn	Lys	Ser	Lys
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Glu	Met	Asn	Glu	Thr	Ser	Lys	Asn	Asn	Glu	Arg	Ser	Gly	Gln	Pro	Asn
		995					1000					1005			
His	Gly	Val	Gln	Gly	Asp	Gly	Ile	Ala	Leu	Lys	Lys	Asp	Asn	Glu	Lys
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Ser	Ser	Glu	Glu	Asp	Ala	Ser	Glu	Lys	Asp	Ser	Arg	Gln	Ser	Ser	Glu
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Val	Lys	Glu	Ser	Asp	Asp	Asn	Met	Ser	Leu	Asn	Ser	Asp	Arg	Asp	Glu
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Leu	Pro	His	Gly	Gly	Glu	Ala	Phe	Lys	Ala	Arg	Glu	Val	Ser	Ala	Ser
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Ala	Asp	Phe	Asp	Val	Gln	Thr	Ser	Leu	Glu	Asp	Asn	Tyr	Ala	Glu	Ser
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Gly	Ile	Gln	Thr	Asp	Leu	Ser	Glu	Ser	Ser	Lys	Glu	Asn	Glu	Val	Gln
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Thr	Asp	Ala	Ile	Pro	Val	Lys	His	Asn	Ser	Thr	Gln	Thr	Val	Lys	Lys
				1140				1145					1150		

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 Phe Ser Val Gln Thr Phe Glu Gly Asp Glu Asn Tyr Leu Ala Glu Gln  
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 Cys Lys Pro Lys Gln Leu Lys Glu Tyr Tyr Thr Ser Ala Lys Val Ser  
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 Thr Phe Gln Thr Val Glu Ala Glu Phe Thr Val Leu Met Glu Asn Ile  
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 Arg Asn Met Asp Thr Phe Phe Thr Asp Gln Ser Ser Ile Pro Leu Val  
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 Lys Arg Thr Val Arg Ser Ile Asn Asn Leu Tyr Thr Trp Arg Ile Pro  
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 Asp Tyr Val Arg Lys Asp Ile Ala Gln Ile Thr Glu Asp Val Ala Asn  
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 Ala Lys Glu Glu Tyr Leu Phe Leu Met His Phe Asp Asp Ala Ser Ser  
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 Gly Tyr Val Lys Asp Leu Ser Thr His Gln Phe Arg Met Gln Lys Thr  
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 Leu Arg Gln Lys Leu Phe Asp Val Ser Ala Lys Ile Asn His Thr Glu  
 1345 1350 1355 1360  
 Glu Leu Leu Asn Ile Leu Lys Leu Phe Thr Val Lys Asn Lys Arg Leu  
 1365 1370 1375  
 Asp Asp Asn Pro Leu Val Ala Lys Leu Ala Lys Glu Ser Leu Ala Arg  
 1380 1385 1390  
 Asp Gly Leu Leu Lys Glu Ile Lys Leu Leu Arg Glu Gln Val Ser Arg  
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 Leu Gln Leu Glu Glu Lys Gly Lys Lys Ala Ser Ser Phe Asp Ala Ser  
 1410 1415 1420  
 Ser Ser Ile Thr Lys Asp Met Lys Gly Phe Lys Val Val Glu Val Gly  
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 1445 1450 1455

Asn Met Ala Lys  
1460

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<211> 1321  
<212> DNA  
<213> *Candida albicans*

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gagacgacca agattcaaac atgcaaatgt atgcaccata tccattctaa acatagtttt 540  
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<210> 138  
<211> 128  
<212> PRT  
<213> *Candida albicans*

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Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ile Ile Glu Pro  
65 70 75 80

Ser Leu Lys Ala Leu Ala Ser Lys Tyr Asn Cys Asp Lys Ser Val Cys  
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Arg Lys Cys Tyr Ala Arg Leu Pro Pro Arg Ala Thr Asn Cys Arg Lys  
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Arg Lys Cys Gly His Thr Asn Gln Leu Arg Pro Lys Lys Lys Leu Lys  
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<210> 139  
<211> 2216  
<212> DNA  
<213> Candida albicans

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gatcaagctt ccaacgagtg atgtaatatt aaacaatgta attatataaa tatgaaacat 240  
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ccgtactagt agttaagtat gaacaaattt tgggtttatt tgccattttt tttcacgcgg 360  
gtttcttggg tgcgcaaacc caccttttct aacaccacta agaaatatca actttatagg 420  
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agcacttggt tcgtggagaa atgaatgatc ctctgaaat tttagcgggt gatccgtaca 540  
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&lt;210&gt; 140

&lt;211&gt; 571

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 140

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Thr Ser Asp Glu Glu Asp Glu Gln Ala Ile Ala Arg Glu Leu Glu Phe  
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Met Glu Arg Lys Arg Gln Ala Leu Val Glu Arg Leu Lys Arg Lys Gln  
 35 40 45

Glu Phe Lys Lys Pro Gln Asp Pro Asn Phe Glu Ala Ile Glu Val Pro  
 50 55 60

Gln Ser Pro Thr Lys Asn Arg Val Lys Val Gly Ser His Asn Ala Thr  
 65 70 75 80

Gln Gln Gly Thr Lys Phe Glu Gly Ser Asn Ile Asn Glu Val Arg Leu  
 85 90 95

Ser Gln Leu Gln Gln Gln Pro Lys Pro Pro Ala Ser Thr Thr Thr Tyr  
 100 105 110

Phe Met Glu Lys Phe Gln Asn Ala Lys Lys Asn Glu Asp Lys Gln Ile  
 115 120 125

Ala Lys Phe Glu Ser Met Met Asn Ala Arg Val His Thr Phe Ser Thr  
 130 135 140

Asp Glu Lys Lys Tyr Val Pro Ile Ile Thr Asn Glu Leu Glu Ser Phe  
 145 150 155 160

Ser Asn Leu Trp Val Lys Lys Arg Tyr Ile Pro Glu Asp Asp Leu Lys  
 165 170 175

Arg Ala Leu His Glu Ile Lys Ile Leu Arg Leu Gly Lys Leu Phe Ala  
 180 185 190

Lys Ile Arg Pro Pro Lys Phe Gln Glu Pro Glu Tyr Ala Asn Trp Ala  
 195 200 205

Thr Val Gly Leu Ile Ser His Lys Ser Asp Ile Lys Phe Thr Ser Ser  
 210 215 220

Glu Lys Pro Val Lys Phe Phe Met Phe Thr Ile Thr Asp Phe Gln His  
 225 230 235 240

Thr Leu Asp Val Tyr Ile Phe Gly Lys Lys Gly Val Glu Arg Tyr Tyr  
 245 250 255

Asn Leu Arg Leu Gly Asp Val Ile Ala Ile Leu Asn Pro Glu Val Leu

260					265					270					
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Arg	Ile	Ser	His	Asp	Phe	Lys	Cys	Ile	Leu	Glu	Ile	Gly	Ser	Ser	Arg
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Tyr	Lys	Ala	Lys	Gly	Glu	Asn	Gly	Phe	Asn	Ile	Ile	Lys	Gly	Thr	Arg
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Phe	Thr	Asn	Ser	Asn	Ser	Ala	Lys	Ala	Phe	Phe	Asp	Glu	Lys	Phe	Gln
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Asn	Pro	Asp	Met	Leu	Ala	Asn	Leu	Asp	Asn	Lys	Arg	Arg	Lys	Ile	Ile
			420					425					430		
Glu	Thr	Lys	Lys	Ser	Thr	Ala	Leu	Ser	Arg	Glu	Leu	Gly	Lys	Ile	Met
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Gln	Lys	Met	Lys	Arg	Thr	Thr	Glu	Ser	Ala	Leu	Gln	Thr	Gly	Leu	Ile
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Gln	Arg	Leu	Gly	Phe	Asp	Pro	Thr	His	Gly	Lys	Ile	Ser	Gln	Val	Leu
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Lys	Ser	Ser	Val	Ser	Gly	Ser	Glu	Pro	Lys	Asn	Asn	Leu	Leu	Gly	Lys
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Ile	Leu	Ala	Pro	Ser	Lys	Asn	Glu	Trp	Phe	Lys	Lys	Arg	Ser	His	Arg
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Ser	Asp	Gly	Ser	Ala	Ser	Asp	Leu	Glu	Ile	Ile					

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Ile Ile Glu Gln Leu Lys Glu Asn Asp Ile Ser Leu Pro Arg Val Lys
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Ala Leu Val Cys Ser Val Gly Gly Gly Gly Leu Phe Ser Gly Ile Ile
  50                      55                      60

Lys Gly Leu Asp Arg Asn Gln Leu Ala Glu Lys Ile Pro Val Val Ala
  65                      70                      75                      80

Val Glu Thr Ala Gly Cys Asp Val Leu Asn Lys Ser Leu Lys Lys Gly
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Ser Pro Val Thr Leu Glu Lys Leu Thr Ser Val Ala Thr Ser Leu Ala
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Ser Pro Tyr Ile Ala Ser Phe Ala Phe Glu Ser Phe Asn Lys Tyr Gly  
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Cys Lys Ser Val Val Leu Ser Asp Gln Asp Val Leu Ala Thr Cys Leu  
130 135 140

Arg Tyr Ala Asp Asp Tyr Asn Phe Ile Val Glu Pro Ala Cys Gly Ala  
145 150 155 160

Ser Leu His Leu Cys Tyr His Pro Glu Ile Leu Glu Asp Ile Leu Glu  
165 170 175

Gln Lys Ile Tyr Glu Asp Asp Ile Val Ile Ile Ile Ala Cys Gly Gly  
180 185 190

Ser Cys Met Thr Tyr Glu Asp Leu Val Lys Ala Ser Ser Thr Leu Asn  
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Val Ser  
210

<210> 143

<211> 2549

<212> DNA

<213> Candida albicans

<400> 143

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&lt;211&gt; 1253

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&lt;213&gt; Candida albicans

&lt;400&gt; 145

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<213> *Candida albicans*

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Gly Gly Asn Gly Thr Val Leu Ser Val Asn His Asp Thr Cys Thr Leu  
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Ala Phe Ile Glu Thr Phe Gly Asp Asp Tyr Arg Thr Cys Phe Ala Asn  
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Lys Val Asp Leu Ser Ser Asn Ser Val Asp Trp Asp Leu Ile Asp Ser  
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<213> Candida albicans

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<211> 888
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Thr Asp Leu Cys Glu Leu Ser Arg Thr Ser Val Leu Ser Ser Gly Tyr  
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 Glu Gly Trp Tyr Lys Ala His Trp Ile Gly Val Gly Val Lys Lys Ala  
 820 825 830  
 Pro Tyr Phe Glu Glu Asn Val Gly Gly Ile Asp Asn Trp Tyr Asp Thr  
 835 840 845  
 Ala Lys Asp Thr Ser Ile Lys His Asn Val Pro Met Ile Arg Arg Arg  
 850 855 860  
 Tyr Arg Lys Glu Thr Leu Asp Gln Glu Trp Asn Phe Val Arg Asp His  
 865 870 875 880  
 Phe Gly Val Ile Asn Ser Ile Trp  
 885

&lt;210&gt; 149

&lt;211&gt; 3146

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 149

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&lt;210&gt; 150

&lt;211&gt; 881

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 150

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Lys Ala Gln Thr Thr Phe Pro Asn Phe Glu Ser Asp Val Leu Asn Glu
      20             25             30

His Asn Lys Phe Arg Ala Leu His Val Asp Thr Ala Pro Leu Thr Trp
      35             40             45

Ser Asp Thr Leu Ala Thr Tyr Ala Gln Asn Tyr Ala Asp Gln Tyr Asp
      50             55             60

Cys Ser Gly Val Leu Thr His Ser Asp Gly Pro Tyr Gly Glu Asn Leu
      65             70             75             80

Ala Leu Gly Tyr Thr Asp Thr Gly Ala Val Asp Ala Trp Tyr Gly Glu
      85             90             95

Ile Ser Lys Tyr Asn Tyr Ser Asn Pro Gly Phe Ser Glu Ser Thr Gly
      100            105            110

His Phe Thr Gln Val Val Trp Lys Ser Thr Ala Glu Ile Gly Cys Gly
      115            120            125

Tyr Lys Tyr Cys Gly Thr Thr Trp Asn Asn Tyr Ile Val Cys Ser Tyr
      130            135            140

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Asn	Pro	Pro	Gly	Asn	Tyr	Leu	Gly	Glu	Phe	Ala	Glu	Glu	Val	Glu	Pro	145	150	155	160
Leu	Ile	Ser	Thr	Val	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Ser	165	170	175	
Thr	Thr	Ser	Asp	Thr	Val	Ser	Thr	Ile	Ser	Ser	Ser	Ile	Met	Pro	Ala	180	185	190	
Val	Ala	Gln	Gly	Tyr	Thr	Thr	Thr	Val	Ser	Ser	Ala	Ala	Ser	Ser	Ser	195	200	205	
Ser	Leu	Lys	Ser	Thr	Thr	Ile	Asn	Pro	Ala	Lys	Thr	Ala	Thr	Leu	Thr	210	215	220	
Ala	Ser	Ser	Ser	Thr	Val	Ile	Thr	Ser	Ser	Thr	Glu	Ser	Val	Gly	Ser	225	230	235	240
Ser	Thr	Val	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Val	Thr	Thr	Ser	Tyr	Ala	245	250	255	
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Thr	Thr	Ser	Ser	Val	Ala	Thr	Ser	Ser	Ser	Thr	Thr	Ser	Ser	Asp	Pro	275	280	285	
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Ala	Ala	Ala	Ser	Ser	Ser	Ala	Ser	Thr	Glu	Asn	Ala	Ala	Ser	Ser	Ser	305	310	315	320
Ser	Ala	Ile	Ser	Ser	Ser	Ser	Ser	Met	Val	Ser	Ala	Pro	Leu	Ser	Ser	325	330	335	
Thr	Leu	Thr	Thr	Ser	Thr	Ala	Ser	Ser	Arg	Ser	Val	Thr	Ser	Asn	Ser	340	345	350	
Val	Asn	Ser	Val	Lys	Phe	Ala	Asn	Thr	Thr	Val	Phe	Ser	Ala	Gln	Thr	355	360	365	
Thr	Ser	Ser	Val	Ser	Ala	Ser	Leu	Ser	Ser	Ser	Val	Ala	Ala	Asp	Asp	370	375	380	
Ile	Gln	Gly	Ser	Thr	Ser	Lys	Glu	Ala	Thr	Ser	Ser	Val	Ser	Glu	His	385	390	395	400
Thr	Ser	Ile	Val	Thr	Ser	Ala	Thr	Asn	Ala	Ala	Gln	Tyr	Ala	Thr	Arg	405	410	415	
Leu	Gly	Ser	Ser	Ser	Arg	Ser	Ser	Ser	Gly	Ala	Val	Ser	Ser	Ser	Ala	420	425	430	
Val	Ser	Gln	Ser	Val	Leu	Asn	Ser	Val	Ile	Ala	Val	Asn	Thr	Asp	Val	435	440	445	

Ser Val Thr Ser Val Ser Ser Thr Ala His Thr Thr Lys Asp Thr Ala  
 450 455 460  
 Thr Thr Ser Val Thr Ala Ser Glu Ser Ile Thr Ser Glu Thr Ala Gln  
 465 470 475 480  
 Ala Ser Ser Ser Thr Glu Lys Asn Ile Ser Asn Ser Ala Ala Thr Ser  
 485 490 495  
 Ser Ser Ile Tyr Ser Asn Ser Ala Ser Val Ser Gly His Gly Val Thr  
 500 505 510  
 Tyr Ala Ala Glu Tyr Ala Ile Thr Ser Glu Gln Ser Ser Ala Leu Ala  
 515 520 525  
 Thr Ser Val Pro Ala Thr Asn Cys Ser Ser Ile Val Lys Thr Thr Thr  
 530 535 540  
 Leu Glu Asn Ser Ser Thr Thr Thr Ile Thr Ala Ile Thr Lys Ser Thr  
 545 550 555 560  
 Thr Thr Leu Ala Thr Thr Ala Asn Asn Ser Thr Arg Ala Ala Thr Ala  
 565 570 575  
 Val Thr Ile Asp Pro Thr Leu Asp Pro Thr Asp Asn Ser Ala Ser Pro  
 580 585 590  
 Thr Asp Asn Ala Lys His Thr Ser Thr Tyr Gly Ser Ser Ser Thr Gly  
 595 600 605  
 Ala Ser Leu Asp Ser Leu Arg Thr Thr Thr Ser Ile Ser Val Ser Ser  
 610 615 620  
 Asn Thr Thr Gln Leu Val Ser Thr Cys Thr Ser Glu Ser Asp Tyr Ser  
 625 630 635 640  
 Asp Ser Pro Ser Phe Ala Ile Ser Thr Ala Thr Thr Thr Glu Ser Asn  
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 660 665 670  
 Pro Thr Ser Ala Ala Ser Ser Thr Asp Glu Thr Ala Phe Thr Arg Thr  
 675 680 685  
 Ile Ser Thr Ser Cys Ser Thr Leu Asn Gly Ala Ser Thr Gln Thr Ser  
 690 695 700  
 Glu Leu Thr Thr Ser Pro Met Lys Thr Asn Thr Val Val Pro Ala Ser  
 705 710 715 720  
 Ser Phe Pro Ser Thr Thr Thr Thr Cys Leu Glu Asn Asp Asp Thr Ala  
 725 730 735  
 Phe Ser Ser Ile Tyr Thr Glu Val Asn Ala Ala Thr Ile Ile Asn Pro  
 740 745 750





<400> 152

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Thr Gln Leu Asp Met Val Asn Gln Gln Leu Ala Tyr Leu Asp Arg Gln  
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Glu Lys Leu Ala Glu Leu Thr Lys Lys Glu Leu Glu Ser Tyr Pro Thr  
35 40 45

Asp Lys Val Trp Arg Ser Cys Gly Lys Ser Phe Ile Leu Gln Asp Lys  
50 55 60

Ser Lys Tyr Val Asn Asp Leu Ser His Ala Glu Thr Val Leu Leu Asp  
65 70 75 80

Gln Arg Lys Thr Leu Lys Ile Lys Lys Asn Tyr Leu Glu Thr Thr Val  
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Glu Lys Thr Ile Asp Asn Leu Lys Ala Leu Met Lys Asn  
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<210> 153

<211> 1478

<212> DNA

<213> Candida albicans

<400> 153

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&lt;210&gt; 154

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 154

Met Leu Pro Ser Leu Arg Lys Gly Cys Phe Ile Val Asn Ser Ile Arg  
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Leu Lys Leu Pro Arg Phe Tyr Ser Leu Asn Ala Gln Pro Leu Gly Thr  
 20 25 30

Asp Asn Thr Ile Glu Asn Asn Thr Pro Thr Glu Thr Asn Arg Leu Ser  
 35 40 45

Lys Thr Ser Gln Lys Phe Trp Glu Lys Val Ser Leu Asn Arg Asp Val  
 50 55 60

Glu Lys Gly Lys Ile Ala Leu Gln Leu Asp Gly Arg Thr Ile Lys Thr  
 65 70 75 80

Pro Leu Gly Asn Gly Ile Ile Val Asp Asn Ala Lys Ser Leu Leu Ala  
 85 90 95

Tyr Leu Leu Lys Leu Glu Trp Ser Ser Leu Ser Ser Leu Ser Ile Lys  
 100 105 110

Thr His Ser Leu Pro Leu Thr Ser Leu Val Ala Arg Cys Ile Asp Leu  
 115 120 125

Gln Met Thr Asn Glu Pro Gly Cys Asp Pro Gln Leu Val Ala Lys Ile  
 130 135 140

Gly Gly Asn Ser Asp Val Ile Lys Asn Gln Leu Leu Arg Tyr Leu Asp  
 145 150 155 160

Thr Asp Thr Leu Leu Val Phe Ser Pro Met Asn Glu Phe Glu Gly Arg  
 165 170 175

Leu Arg Asn Ala Gln Asn Glu Leu Tyr Ile Pro Ile Ile Lys Gly Met  
 180 185 190

Glu Glu Phe Leu Arg Asn Phe Ser Ser Glu Ser Asn Ile Arg Leu Gln  
 195 200 205

Ile Leu Asp Ala Asp Ile His Gly Leu Arg Gly Asn Gln Gln Ser Asp  
 210 215 220

Ile Val Lys Asn Ala Ala Lys Lys Tyr Met Ser Ser Leu Ser Pro Trp  
 225 230 235 240

Asp Leu Ala Ile Leu Glu Lys Thr Val Leu Thr Thr Lys Ser Phe Ile  
 245 250 255

Cys Gly Val Leu Leu Leu Glu Asn Lys Lys Asp Thr Ala Asn Leu Ile  
 260 265 270

Pro Ala Leu Lys Thr Asp Met Asp Asn Ile Val Arg Ala Ala Thr Leu  
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Glu Thr Ile Phe Gln Val Glu Lys Trp Gly Glu Val Glu Asp Thr His  
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Asp Val Asp Lys Arg Asp Ile Arg Arg Lys Ile His Thr Ala Ala Ile  
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Ala Ala Phe Lys Gln  
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<210> 155

<211> 2336

<212> DNA

<213> Candida albicans

<400> 155

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<210> 156

<211> 611

<212> PRT

<213> Candida albicans

<400> 156

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 His Lys Ser Lys Thr Lys Ile Ile Asn Ala Ala Lys Leu Ile Ile Glu  
 35 40 45  
 Thr His Leu Ser Tyr Tyr Thr Ile Leu Asn Asn Ile Ser Asp Ile Gln  
 50 55 60  
 Ala Tyr Leu Ser Thr Trp Leu Arg Asp Leu Gly Thr Thr Gly Pro Tyr  
 65 70 75 80  
 Gln Thr Ile Leu Ser Glu Ser Ile Ser Leu Met Phe Asp Arg Thr Val  
 85 90 95  
 Ser Ile Phe Arg Lys Cys Thr Ile Glu Gly Gly Phe Pro His Leu Ile  
 100 105 110  
 Ala Arg Leu Tyr Leu Arg Leu Lys Ser Tyr Gln Lys Leu Leu Asn Asp  
 115 120 125  
 Ala Gly Leu Lys Asn Phe Phe Ser Ser Tyr Asp Tyr Ala Phe Gly Val  
 130 135 140  
 Ala Tyr Asn Leu Val Asn Cys Ser Glu Tyr Arg Tyr Asp Glu Val His  
 145 150 155 160  
 Tyr Ile Ser Asn Gly Thr Tyr Ser Leu Val Ala Ser Met Lys Ile Asp  
 165 170 175  
 Pro Ala Glu Val Ile Lys Arg Glu His Phe Arg Leu Thr Ile Pro Lys  
 180 185 190  
 Phe Asn Ile Ser Asn Ile Leu Ile Glu Ile Phe His Leu Leu Asp Gly  
 195 200 205  
 Leu Ala Phe Phe Lys Val Asn Pro Asp Ser Leu Ser Ile Ser Thr Ala  
 210 215 220  
 Ser Ala Glu Thr Ile Phe Arg Ser Ile Ser Glu Gly Asn His Gln Val  
 225 230 235 240  
 Leu Glu Leu Gly Arg Ser Leu Met Phe Pro Leu Leu Arg Thr Gly Asp  
 245 250 255

Phe	Glu	Ile	Cys	Arg	Ile	Asp	Asp	Ala	Gly	Ala	Val	Ile	Thr	Phe	Thr
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Glu	Ala	Lys	Asp	Val	Lys	Leu	Glu	Ile	Ile	Ser	Leu	Asp	Glu	Val	Ser
		275					280					285			
Trp	Val	Met	Gln	Trp	Lys	Ser	Cys	Leu	Gln	Asn	Tyr	Glu	Arg	Arg	Ala
	290					295					300				
Ala	Asn	Asp	Ser	Ser	Phe	Ile	Lys	Thr	His	Leu	Gln	Phe	Lys	Lys	Ala
305					310					315					320
Asn	Asn	Phe	Asn	Glu	Asp	Asn	Asn	Gly	Leu	Gly	Leu	Ile	Val	Asp	Arg
			325					330						335	
Asn	Ile	Pro	Thr	Asp	Asp	Phe	Thr	Leu	Ala	Ser	Thr	Asn	Arg	Gln	Ser
		340						345					350		
Pro	Pro	Pro	Ser	Asn	Thr	Gly	Cys	Ser	Leu	His	Arg	Ser	Lys	Pro	Leu
		355					360					365			
His	Ile	Pro	Leu	Ser	Ser	Val	Ile	Arg	Glu	Asp	Phe	Tyr	Asp	Ser	Ser
	370					375					380				
Leu	Asn	Glu	Arg	Ile	Ser	Lys	Asp	Gly	Asp	Ser	Ser	Cys	Glu	Ser	Phe
385					390					395					400
Ser	Gly	Ala	Glu	Ser	Ile	Leu	Ser	Asp	Tyr	Asp	Phe	His	Asp	Asn	Glu
			405						410					415	
Phe	Phe	Asn	Asn	Gln	Ser	Pro	His	Tyr	Phe	Ser	Glu	His	Ile	Asp	Asn
		420						425					430		
Asn	Ser	Arg	Glu	Val	Val	Ile	Thr	Asp	Glu	Asn	Thr	Ile	Ile	Ser	Leu
		435					440					445			
Glu	Asn	Thr	Gln	Val	Ser	Arg	Trp	Ser	Asn	Tyr	Ser	Trp	Gln	Lys	Ile
	450					455					460				
Ser	Pro	His	Gln	Leu	Gln	Val	Ser	Ile	Ile	Gln	Leu	Arg	Met	Gly	Asn
465					470					475					480
Phe	Ile	Val	Ala	Tyr	Asp	Ser	Asp	Tyr	Asn	Leu	His	Gln	Phe	Lys	Ile
			485						490					495	
Arg	Leu	Cys	Asp	Asp	Ile	Lys	Cys	Ile	Gln	Ser	Thr	Glu	Gln	Asp	Ile
		500						505					510		
Gln	Ile	Arg	Val	Pro	Leu	Gly	Ala	Ile	Met	Cys	Ser	Val	Thr	Gly	Ile
		515					520					525			
Leu	Asn	Ile	Arg	Thr	Lys	Asp	Ala	Asp	Lys	Leu	Leu	Arg	Val	Leu	Ser
	530					535					540				
Phe	Tyr	Thr	Thr	Asp	His	Thr	Glu	Ala	Val	Ser	His	Ser	Asn	Asn	Gln
545					550					555					560

Asp Ala Thr Ala Ser Pro Leu Ser Ser Val Ser Ser Ala Met Asp Leu  
 565 570 575

Lys His Ser Leu Gln Lys Cys Ser Ser Thr Ile Met Pro Gln Glu Leu  
 580 585 590

Thr Gln Asp Val Ile Gly Ser Lys Ser Asp Leu Ile Ser Asn Ile Arg  
 595 600 605

Gln Lys Ile  
 610

<210> 157

<211> 2960

<212> DNA

<213> Candida albicans

<400> 157

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gtaagccttt	ctaacattct	tgtgggtcacg	tgatgtgtat	gtttcttttt	tttattcctc	180
cgggtgataa	cgacgcgaaa	aatatTTTTT	catttttctt	ttaaccatca	caatttgcga	240
cgcgacgcga	aaaaaatgca	gagaagtaaa	agaatgctgg	ataagaaatc	aacaacacag	300
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cggacgagaa	tttcccacct	ccaatcataa	tatcaagtca	tcattcaact	agaaagaacc	1560
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tcagttcctg	gaagtttcaa	aattcatact	atattatgac	agaattgtgc	gaaaatggta	2100
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gaatttggaa aatcatcgtg gaattaagcc tggctttacg attcatccat gattcttgtc 2220
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tagagcccaa ttatgagaga aggccacagg caaatcaaat cttacaaact gaggaatgcc 2880
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agccaaaatt ttttatatga 2960

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<210> 158

<211> 819

<212> PRT

<213> Candida albicans

<400> 158

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Met Ser Ser Leu Asp Glu Asp Glu Glu Asp Phe Glu Met Leu Asp Thr
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Glu Asn Leu Gln Phe Met Gly Lys Lys Met Phe Gly Lys Gln Ala Gly
      20             25             30

Glu Asp Glu Ser Asp Asp Phe Ala Ile Gly Gly Ser Thr Pro Thr Asn
  35             40             45

Lys Leu Lys Phe Tyr Pro Tyr Ser Asn Asn Lys Leu Thr Arg Ser Thr
  50             55             60

Gly Thr Leu Asn Leu Ser Leu Ser Asn Thr Ala Leu Ser Glu Ala Asn
  65             70             75             80

Ser Lys Phe Leu Gly Lys Ile Glu Glu Glu Glu Glu Glu Glu Glu
      85             90             95

Gly Lys Asp Glu Glu Ser Val Asp Ser Arg Ile Lys Arg Trp Ser Pro
  100            105            110

Phe His Glu Asn Glu Ser Val Thr Thr Pro Ile Thr Lys Arg Ser Ala
  115            120            125

Glu Lys Thr Asn Ser Pro Ile Ser Leu Lys Gln Trp Asn Gln Arg Trp
  130            135            140

Phe Pro Lys Asn Asp Ala Arg Thr Glu Asn Thr Ser Ser Ser Ser
  145            150            155            160

Tyr Ser Val Ala Lys Pro Asn Gln Ser Ala Phe Thr Ser Ser Gly Leu
      165            170            175

Val Ser Lys Met Ser Met Asp Thr Ser Leu Tyr Pro Ala Lys Leu Arg
      180            185            190

```



Ile	Pro	Glu	Thr	Pro	Val	Lys	Lys	Ser	Pro	Leu	Val	Glu	Gly	Arg	Asp
		195					200					205			
His	Lys	His	Val	His	Leu	Ser	Ser	Ser	Lys	Asn	Ala	Ser	Ser	Ser	Leu
	210					215					220				
Ser	Val	Ser	Pro	Leu	Asn	Phe	Val	Glu	Asp	Asn	Asn	Leu	Gln	Glu	Asp
225					230					235					240
Leu	Leu	Phe	Ser	Asp	Ser	Pro	Ser	Ser	Lys	Ala	Leu	Pro	Ser	Ile	His
				245					250					255	
Val	Pro	Thr	Ile	Asp	Ser	Ser	Pro	Leu	Ser	Glu	Ala	Lys	Tyr	His	Ala
			260					265					270		
His	Asp	Arg	His	Asn	Asn	Gln	Thr	Asn	Ile	Leu	Ser	Pro	Thr	Asn	Ser
		275					280					285			
Leu	Val	Thr	Asn	Ser	Ser	Pro	Gln	Thr	Leu	His	Ser	Asn	Lys	Phe	Lys
	290					295					300				
Lys	Ile	Lys	Arg	Ala	Arg	Asn	Ser	Val	Ile	Leu	Lys	Asn	Arg	Glu	Leu
305					310					315					320
Thr	Asn	Ser	Leu	Gln	Gln	Phe	Lys	Asp	Asp	Leu	Tyr	Gly	Thr	Asp	Glu
				325					330					335	
Asn	Phe	Pro	Pro	Pro	Ile	Ile	Ile	Ser	Ser	His	His	Ser	Thr	Arg	Lys
			340					345					350		
Asn	Pro	Gln	Pro	Tyr	Gln	Phe	Arg	Gly	Arg	Tyr	Asp	Asn	Asp	Thr	Asp
		355					360					365			
Glu	Glu	Ile	Ser	Thr	Pro	Thr	Arg	Arg	Lys	Ser	Ile	Ile	Gly	Ala	Thr
	370					375					380				
Ser	Gln	Thr	His	Arg	Glu	Ser	Arg	Pro	Leu	Ser	Leu	Ser	Ser	Ala	Ile
385					390					395					400
Val	Thr	Asn	Thr	Thr	Ser	Ala	Glu	Thr	His	Ser	Ile	Ser	Ser	Thr	Asp
				405					410					415	
Ser	Ser	Pro	Leu	Asn	Ser	Lys	Arg	Arg	Leu	Ile	Ser	Ser	Asn	Lys	Leu
			420				425						430		
Ser	Ala	Asn	Pro	Asp	Ser	His	Leu	Phe	Glu	Lys	Phe	Thr	Asn	Val	His
		435					440					445			
Ser	Ile	Gly	Lys	Gly	Gln	Phe	Ser	Thr	Val	Tyr	Gln	Val	Thr	Phe	Ala
	450					455					460				
Gln	Thr	Asn	Lys	Lys	Tyr	Ala	Ile	Lys	Ala	Ile	Lys	Pro	Asn	Lys	Tyr
465					470					475					480
Asn	Ser	Leu	Lys	Arg	Ile	Leu	Leu	Glu	Ile	Lys	Ile	Leu	Asn	Glu	Val
				485					490					495	





<400> 163  
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170

```

ctaccaaaaca aatacaactt tggaatacac cagatattct gctaattcac cttaaaaggt 3540
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atttggatct gtcgaggtac gttgtctata aagatgatcc cagagggtta atctatgacc 3660
tgtatgcagt agataaccac tatgggtggtt tgggtggtgg gcactatacc gcgtacgtaa 3720
agaattttgc cgacaataaa tgggtactatt ttgatgattc tcgagtaact gaaactgcgc 3780
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gcaatggatt aggcagctct aaactacagg aaataatcca aaagtcacgc cacggatatg 3900
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acgaggagga agatgtttct gatgatatga tagaatgtaa tgaagatgtg caggcccctg 4020
aatatagtaa tcgtagtttg gaggttgggc atattgaaac tcaggactgc aacgacgaag 4080
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aagtctacaa gaataattca ggcttggggt catcgagtac gtctgaaata tctgagggat 4200
gcccagaaaa cgaagtcgct gatttgaatt taaaaaatgg tgtgacacta gaatcgccag 4260
aataa 4265

```

&lt;210&gt; 166

&lt;211&gt; 1254

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 166

```

Met Gly Ser Ser Asp Val Ser Ser Arg Glu Cys Ser Leu Val Tyr Asn
  1             5             10             15

```

```

Glu Asp Pro Asp Phe Thr Asp Gly Thr Thr Pro Cys Asp Arg Leu Gly
          20             25             30

```

```

Val Asp Leu Met Asn Val Leu Asp Asp Lys Asp Glu Ile Lys Gln Glu
      35             40             45

```

```

Ser Val Pro Val Ser Asp Arg Glu Ile Glu Asp Thr Glu Ser Asp Ala
      50             55             60

```

```

Ser Ala Val Ser Ser Phe Ala Ser Ala Asn Glu Leu Ile Ala Glu Pro
      65             70             75             80

```

```

His Ala Ala Ser Glu Thr Asn Leu Gly Thr Asn Gly Gln Asp Gly Arg
          85             90             95

```

```

Asn Val Leu Glu Gln Gln Arg Asp Val Val Ala Arg Leu Ile Glu Glu
      100             105             110

```

```

Asn Lys Glu Thr Gln Lys Glu Gly Asp Lys Val Cys Ile Val Pro Lys
      115             120             125

```

```

Val Trp Tyr Asp Lys Phe Phe Asp Pro Asp Val Thr Asp Pro Glu Asp
      130             135             140

```

```

Ile Gly Pro Ile Asn Thr Arg Met Ile Cys Arg Asp Phe Glu Asn Phe
      145             150             155             160

```

```

Val Leu Glu Asp Tyr Asn Arg Cys Pro Tyr Leu Ser Ile Ala Glu Pro
          165             170             175

```

```

Val Phe Asn Phe Leu Ser Glu Ile Tyr Gly Met Thr Ser Gly Ser Tyr
          180             185             190

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Pro Val Val Thr Asn Leu Val Ile Asn Gln Thr Thr Gly Glu Leu Glu  
 195 200 205  
 Thr Glu Tyr Asn Lys Trp Phe Phe Arg Leu His Tyr Leu Thr Glu Lys  
 210 215 220  
 Gln Asp Gly Arg Lys Arg Arg His Gly Gln Asp Asp Ser Ile Met Tyr  
 225 230 235 240  
 Leu Ser Met Ser Ala Leu Asn Leu Val Arg Asp Leu Val Glu Lys Ser  
 245 250 255  
 Met Asn Leu Phe Phe Glu Lys Ala Asp His Leu Asp Val Asn Ala Val  
 260 265 270  
 Asp Phe Lys Ile Trp Phe Val Ser Glu Gly Ser Asp Ile Ala Thr Asp  
 275 280 285  
 Ser Asn Val Ser Thr Phe Leu Asn Ser Ser Tyr Glu Ile Thr Pro Leu  
 290 295 300  
 Gln Phe Leu Glu Leu Pro Ile Lys Lys Leu Leu Ile Pro Asp Met Phe  
 305 310 315 320  
 Glu Asn Arg Leu Asp Lys Ile Thr Ser Asn Pro Ser Asp Leu Val Ile  
 325 330 335  
 Glu Ile Lys Pro Ile Glu Gly Asn His His Trp Pro Ser Asn Tyr Phe  
 340 345 350  
 Ala Tyr Asn Lys Leu Glu Pro Ala Ser Gly Thr Thr Gly Leu Val Asn  
 355 360 365  
 Leu Gly Asn Thr Cys Tyr Met Asn Ser Ala Leu Gln Cys Leu Val His  
 370 375 380  
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 385 390 395 400  
 Ile Asn Glu Glu Asn Pro Leu Gly Tyr His Gly Tyr Val Ala Arg Ala  
 405 410 415  
 Phe Ser Asp Leu Val Gln Lys Leu Phe Gln Asn Arg Met Ser Ile Met  
 420 425 430  
 Gln Arg Asn Ala Ala Phe Pro Pro Ser Met Phe Lys Ser Thr Ile Gly  
 435 440 445  
 His Phe Asn Ser Met Phe Ser Gly Tyr Met Gln Gln Asp Ser Gln Glu  
 450 455 460  
 Phe Leu Ala Phe Leu Leu Asp Ser Leu His Glu Asp Leu Asn Arg Ile  
 465 470 475 480  
 Ile Lys Lys Glu Tyr Thr Glu Lys Pro Ser Leu Ser Pro Gly Asp Asp  
 485 490 495



Val Asn Asp Trp Asn Val Val Lys Lys Leu Ala Asp Asp Thr Trp Glu  
500 505 510

Met His Leu Lys Arg Asn Cys Ser Val Ile Thr Asp Leu Phe Val Gly  
515 520 525

Met Tyr Lys Ser Thr Leu Tyr Cys Pro Glu Cys Gln Asn Val Ser Ile  
530 535 540

Thr Phe Asp Pro Tyr Asn Asp Val Thr Leu Pro Leu Pro Val Asp Thr  
545 550 555 560

Val Trp Asp Lys Thr Ile Lys Ile Phe Pro Met Asn Ser Pro Pro Leu  
565 570 575

Leu Leu Glu Val Glu Leu Ser Lys Ser Ser Thr Tyr Met Asp Leu Lys  
580 585 590

Asn Tyr Val Gly Lys Met Ser Gly Leu Asp Pro Asn Thr Leu Phe Gly  
595 600 605

Cys Glu Ile Phe Ser Asn Gln Ile Tyr Val Asn Tyr Glu Ser Thr Glu  
610 615 620

Ser Asn Ala Gln Phe Leu Thr Leu Gln Glu Leu Ile Lys Pro Ala Asp  
625 630 635 640

Asp Val Ile Phe Tyr Glu Leu Pro Val Thr Asn Asp Asn Glu Val Ile  
645 650 655

Val Pro Val Leu Asn Thr Arg Ile Glu Lys Gly Tyr Lys Asn Ala Met  
660 665 670

Leu Phe Gly Val Pro Phe Phe Ile Thr Leu Lys Glu Asp Glu Leu Asn  
675 680 685

Asn Pro Gly Ala Ile Arg Met Lys Leu Gln Asn Arg Phe Val His Leu  
690 695 700

Ser Gly Gly Tyr Ile Pro Phe Pro Glu Pro Val Gly Asn Arg Thr Asp  
705 710 715 720

Phe Ala Asp Ala Phe Pro Leu Leu Val Glu Lys Tyr Pro Asp Val Glu  
725 730 735

Phe Glu Gln Tyr Lys Asp Ile Leu Gln Tyr Thr Ser Ile Lys Val Thr  
740 745 750

Asp Lys Asp Lys Ser Phe Phe Ser Ile Lys Ile Leu Ser Val Glu Lys  
755 760 765

Glu Gln Gln Phe Ala Ser Asn Asn Arg Thr Gly Pro Asn Phe Trp Thr  
770 775 780

Pro Ile Ser Gln Leu Asn Leu Asp Lys Ala Thr Asp Ile Asp Asp Lys  
785 790 795 800

Leu	Glu	Asp	Val	Val	Lys	Asp	Ile	Tyr	Asn	Tyr	Ser	Ser	Leu	Val	Asp	
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Cys	Ala	Glu	Gly	Val	Leu	Met	Gln	Val	Asp	Asp	Glu	Gly	Asp	Thr	Glu	
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Gly	Ser	Glu	Ala	Lys	Asn	Phe	Ser	Lys	Pro	Phe	Gln	Ser	Gly	Asp	Asp	
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Glu	Glu	Asn	Lys	Glu	Thr	Val	Thr	Asn	Asn	Glu	Asn	Val	Asn	Asn	Thr	
	850					855					860					
Asn	Asp	Arg	Asp	Glu	Asp	Met	Glu	Leu	Thr	Asp	Asp	Val	Glu	Glu	Asp	
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Ala	Ser	Thr	Glu	Pro	Glu	Leu	Thr	Asp	Lys	Pro	Glu	Ala	Leu	Asp	Lys	
				885					890					895		
Ile	Lys	Asp	Ser	Leu	Thr	Ser	Thr	Pro	Phe	Ala	Ile	Leu	Ser	Met	Asn	
			900					905					910			
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		915					920					925				
Ser	Asp	Asp	Lys	Ile	Tyr	Asn	Trp	Glu	Asn	Pro	Ala	Thr	Leu	Pro	Asn	
	930					935					940					
Lys	Glu	Leu	Glu	Asn	Ala	Lys	Leu	Glu	Arg	Ser	Asn	Ala	Lys	Glu	Arg	
945				950						955					960	
Thr	Ile	Thr	Leu	Asp	Asp	Cys	Leu	Gln	Leu	Phe	Ser	Lys	Pro	Glu	Ile	
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Leu	Gly	Leu	Thr	Asp	Ser	Trp	Tyr	Cys	Pro	Thr	Cys	Lys	Glu	His	Arg	
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Gln	Ala	Thr	Lys	Gln	Ile	Gln	Leu	Trp	Asn	Thr	Pro	Asp	Ile	Leu	Leu	
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Ile	His	Leu	Lys	Arg	Phe	Glu	Ser	Gln	Arg	Ser	Phe	Ser	Asp	Lys	Ile	
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Asp	Ala	Thr	Val	Asn	Phe	Pro	Ile	Thr	Asp	Leu	Asp	Leu	Ser	Arg	Tyr	
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Val	Val	Tyr	Lys	Asp	Asp	Pro	Arg	Gly	Leu	Ile	Tyr	Asp	Leu	Tyr	Ala	
				1045					1050					1055		
Val	Asp	Asn	His	Tyr	Gly	Gly	Leu	Gly	Gly	Gly	His	Tyr	Thr	Ala	Tyr	
			1060				1065						1070			
Val	Lys	Asn	Phe	Ala	Asp	Asn	Lys	Trp	Tyr	Tyr	Phe	Asp	Asp	Ser	Arg	
		1075					1080					1085				
Val	Thr	Glu	Thr	Ala	Pro	Glu	Asn	Ser	Ile	Ala	Gly	Ser	Ala	Tyr	Leu	
	1090					1095					1100					

Leu Phe Tyr Ile Arg Arg His Lys Asp Gly Asn Gly Leu Gly Ser Ser  
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 Lys Leu Gln Glu Ile Ile Gln Lys Ser Arg His Gly Tyr Asp Glu Arg  
 1125 1130 1135  
 Ile Lys Lys Ile Tyr Asp Glu Gln Met Lys Leu Tyr Glu Phe Asn Lys  
 1140 1145 1150  
 Thr Asp Glu Glu Glu Asp Val Ser Asp Asp Met Ile Glu Cys Asn Glu  
 1155 1160 1165  
 Asp Val Gln Ala Pro Glu Tyr Ser Asn Arg Ser Leu Glu Val Gly His  
 1170 1175 1180  
 Ile Glu Thr Gln Asp Cys Asn Asp Glu Asp Asp Asn Asp Asp Gly Glu  
 1185 1190 1195 1200  
 Arg Thr Asn Ser Gly Arg Arg Lys Leu Arg Leu Leu Lys Lys Val Tyr  
 1205 1210 1215  
 Lys Asn Asn Ser Gly Leu Gly Ser Ser Ser Thr Ser Glu Ile Ser Glu  
 1220 1225 1230  
 Gly Cys Pro Glu Asn Glu Val Ala Asp Leu Asn Leu Lys Asn Gly Val  
 1235 1240 1245  
 Thr Leu Glu Ser Pro Glu  
 1250

<210> 167  
 <211> 3146  
 <212> DNA  
 <213> Candida albicans

<400> 167  
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 gcagcctggc aagcagcgaa ggccatctgt gctgcatttc cacactcctt gtatgactgc 180  
 atacgcataa agaggtgcct tgctgtaggc gtatatgata ctaagcaaca gagaaaccac 240  
 ggttctcttc tcttcttatt tcgttattgt cttccctttt tactatgggt aaagtcgccc 300  
 taaagcgggg cgctcacaat atcgccgcag ctacagccgt tttttttttt tttgtttttt 360  
 tttgcgtgctg ttctcgaaga atgaatggct cactgaaaaa ttttgattca tcgatataaa 420  
 gaacactggt cacttcgatg tcatccggcc aataaagttg tttttaggat aaacgagtaa 480  
 gtggttagctg gtacaggatc atgagatttt cacacttctt gaagtacaat gctgtcccag 540  
 aatggcaaaa ccattatatg gactacagcg agctgaaaaa tcttatttac acgctacaaa 600  
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&lt;210&gt; 168

&lt;211&gt; 881

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 168

```

Met Arg Phe Ser His Phe Leu Lys Tyr Asn Ala Val Pro Glu Trp Gln
  1             5             10             15

```

```

Asn His Tyr Met Asp Tyr Ser Glu Leu Lys Asn Leu Ile Tyr Thr Leu
      20             25             30

```

```

Gln Thr Asp Glu Leu Gln Val Gly Asp Asn Glu Glu Gly Phe Gly Ala
    35             40             45

```

```

Gly Lys Ser Ser Asn Ile Thr Asp Arg Phe Lys Asn Lys Phe Ser Phe
    50             55             60

```

```

Lys Asn Ala Lys Glu Asp Thr Ser Ser Gly Met Asn Lys Asp Ala Gly
    65             70             75             80

```



Tyr	Arg	Trp	Pro	Leu	Pro	Arg	Pro	Ile	Asn	Leu	Lys	Phe	Thr	Ser	Ile	385	390	395	400
Asn	Asn	Val	Ala	Leu	Pro	Lys	Leu	Phe	Phe	Thr	Lys	Lys	Ala	Tyr	Lys	405	410	415	
Ile	Tyr	Phe	Ile	Ile	Leu	Val	Thr	Gly	Leu	Leu	Leu	Gly	Ile	Lys	Thr	420	425	430	
Phe	Asn	Asp	Ala	Ala	Gln	His	Arg	Cys	Met	Ala	Leu	Val	Glu	Cys	Val	435	440	445	
Ala	Phe	Leu	Trp	Ala	Ser	Glu	Ala	Ile	Pro	Leu	His	Ile	Thr	Ala	Phe	450	455	460	
Leu	Val	Pro	Leu	Leu	Val	Val	Leu	Phe	Lys	Val	Leu	Lys	Thr	Ser	Asp	465	470	475	480
Gly	Ala	Ile	Met	Ser	Ala	Ala	Ser	Ala	Ser	Ser	Glu	Ile	Leu	Ala	Ala	485	490	495	
Met	Trp	Ser	Ser	Thr	Ile	Met	Ile	Leu	Leu	Ala	Gly	Phe	Thr	Leu	Gly	500	505	510	
Glu	Val	Leu	Ala	Gln	Tyr	Asn	Ile	Ala	Lys	Val	Leu	Ala	Ser	Trp	Leu	515	520	525	
Leu	Ala	Phe	Ala	Gly	Cys	Lys	Pro	Arg	Asn	Val	Leu	Leu	Met	Ala	Met	530	535	540	
Cys	Val	Val	Phe	Phe	Leu	Ser	Met	Trp	Ile	Ser	Asn	Val	Ala	Ala	Pro	545	550	555	560
Val	Leu	Thr	Tyr	Ser	Leu	Leu	Ser	Pro	Leu	Leu	Asp	Ala	Met	Asp	Ala	565	570	575	
Asp	Ser	Pro	Phe	Ala	Gln	Ala	Leu	Val	Leu	Gly	Val	Ala	Leu	Ala	Ala	580	585	590	
Asn	Ile	Gly	Gly	Met	Ser	Ser	Pro	Ile	Ser	Ser	Pro	Gln	Asn	Ile	Ile	595	600	605	
Ser	Met	Ser	Tyr	Leu	Lys	Pro	Tyr	Gly	Ile	Gly	Trp	Gly	Gln	Phe	Phe	610	615	620	
Ala	Val	Ala	Leu	Pro	Ser	Gly	Ile	Leu	Ala	Met	Leu	Leu	Val	Trp	Ile	625	630	635	640
Leu	Leu	Phe	Thr	Thr	Phe	Lys	Met	Asn	Lys	Thr	Lys	Leu	Glu	Lys	Phe	645	650	655	
Lys	Pro	Ile	Lys	Thr	Lys	Phe	Thr	Val	Lys	Gln	Tyr	Tyr	Ile	Ile	Thr	660	665	670	
Val	Thr	Val	Ala	Thr	Ile	Leu	Leu	Trp	Cys	Val	Glu	Ser	Gln	Ile	Glu	675	680	685	

<400> 169						
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gtaccagaac	tgagttggcc	ttatctacat	ttctactcat	tttgaatgca	caggtatctg	300
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aaatgatcat	tgacatcgtg	atcgtaaaggc	aaaaaaaaat	acaataggct	ccctaaataa	480
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<400> 170																
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Glu	Asp	Gly	Arg	Asn	Asp	His	His	Asn	Asn	Asn	Asn	Asn	Leu	Met	Lys	
			20					25					30			
Lys	Ala	Met	Met	Asn	Asn	Glu	Gln	Ile	Asp	Arg	Thr	Gln	Asp	Ile	Asp	
		35					40					45				
Asn	Ala	Lys	Glu	Met	Leu	Arg	Lys	Ile	Ser	Ser	Glu	Ser	Ser	Ser	Arg	
	50					55					60					
Arg	Ser	Ser	Leu	Leu	Asn	Lys	Asp	Ser	Ser	Leu	Val	Asn	Gly	Asn	Ala	
65					70					75					80	
Asn	Ser	Gly	Gly	Gly	Thr	Ser	Ile	Asn	Gly	Thr	Arg	Gly	Ser	Ser	Lys	
				85					90					95		
Ser	Ser	Asn	Thr	His	Phe	Gln	Tyr	Ala	Ser	Thr	Ala	Tyr	Gly	Val	Arg	
			100					105					110			
Met	Leu	Ser	Lys	Asp	Ile	Ser	Asn	Thr	Lys	Val	Glu	Leu	Asp	Val	Glu	
		115					120					125				



Asn Leu Met Ile Val Thr Lys Leu Asn Asp Val Ser Leu Tyr Phe Leu  
 130 135 140  
 Thr Arg Glu Leu Val Glu Trp Val Leu Val His Phe Pro Arg Val Thr  
 145 150 155 160  
 Val Tyr Val Asp Ser Glu Leu Lys Asn Ser Lys Lys Phe Ala Ala Gly  
 165 170 175  
 Glu Leu Cys Glu Asp Ser Lys Cys Arg Glu Ser Arg Ile Lys Tyr Trp  
 180 185 190  
 Thr Lys Asp Phe Ile Arg Glu His Asp Val Phe Phe Asp Leu Val Val  
 195 200 205  
 Thr Leu Gly Gly Asp Gly Thr Val Leu Phe Val Ser Ser Ile Phe Gln  
 210 215 220  
 Arg His Val Pro Pro Val Met Ser Phe Ser Leu Gly Ser Leu Gly Phe  
 225 230 235 240  
 Leu Thr Asn Phe Lys Phe Glu His Phe Arg Glu Asp Leu Pro Arg Ile  
 245 250 255  
 Met Asn His Lys Ile Lys Thr Asn Leu Arg Leu Arg Leu Glu Cys Thr  
 260 265 270  
 Ile Tyr Arg Arg His Arg Pro Glu Val Asp Pro Asn Thr Gly Lys Lys  
 275 280 285  
 Ile Cys Val Val Glu Lys Leu Ser Thr His His Ile Leu Asn Glu Val  
 290 295 300  
 Thr Ile Asp Arg Gly Pro Ser Pro Phe Leu Ser Met Leu Glu Leu Tyr  
 305 310 315 320  
 Gly Asp Gly Ser Leu Met Thr Val Ala Gln Ala Asp Gly Leu Ile Ala  
 325 330 335  
 Ala Thr Pro Thr Gly Ser Thr Ala Tyr Ser Leu Ser Ala Gly Gly Ser  
 340 345 350  
 Leu Val Cys Pro Thr Val Asn Ala Ile Ala Leu Thr Pro Ile Cys Pro  
 355 360 365  
 His Ala Leu Ser Phe Arg Pro Ile Ile Leu Pro Glu Ser Ile Asn Leu  
 370 375 380  
 Lys Val Lys Val Ser Met Lys Ser Arg Ala Pro Ala Trp Ala Ala Phe  
 385 390 395 400  
 Asp Gly Lys Asp Arg Ile Glu Leu Gln Lys Gly Asp Phe Ile Thr Ile  
 405 410 415  
 Cys Ala Ser Pro Tyr Ala Phe Pro Thr Val Glu Ala Ser Pro Asp Glu  
 420 425 430



183

&lt;400&gt; 172

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
 1 5 10 15

Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp  
 20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
 35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
 50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ile Ile Glu Pro  
 65 70 75 80

Ser Leu Lys Ala Leu Ala Ser Lys Tyr Asn Cys Asp Lys Ser Val Cys  
 85 90 95

Arg Lys Cys Tyr Ala Arg Leu Pro Pro Arg Ala Thr Asn Cys Arg Lys  
 100 105 110

Arg Lys Cys Gly His Thr Asn Gln Leu Arg Pro Lys Lys Lys Leu Lys  
 115 120 125

&lt;210&gt; 173

&lt;211&gt; 1175

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 173

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&lt;212&gt; DNA

<213> *Candida albicans*

&lt;400&gt; 175

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&lt;210&gt; 176

&lt;211&gt; 252

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 176

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Met Ser Leu Pro Ala Thr Phe Asp Leu Thr Pro Glu Asp Ala Gln Leu
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Leu Leu Ala Ala Asn Thr His Leu Gly Ala Arg Asn Val Gln Val His
      20                      25                      30

Gln Glu Pro Tyr Val Phe Asn Ala Arg Pro Asp Gly Val His Val Ile
      35                      40                      45

Asn Val Gly Lys Thr Trp Glu Lys Leu Val Leu Ala Ala Arg Ile Ile
      50                      55                      60

Ala Ala Ile Pro Asn Pro Glu Asp Val Val Ala Ile Ser Ser Arg Thr
      65                      70                      75                      80

Tyr Gly Gln Arg Ala Val Leu Lys Phe Ala Ala His Thr Gly Ala Thr
      85                      90                      95

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190

<210> 180  
 <211> 114  
 <212> PRT  
 <213> Candida albicans

<400> 180  
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 Arg Ser Gly Val Lys Lys Leu Ile Ser Lys His His Trp Leu Pro Glu  
             20                    25                    30  
 Tyr Tyr Phe Ser Asp Leu Ser Phe Ser Val Val Gln Gln Trp Asp Ser  
             35                    40                    45  
 Arg Ala Ile Glu Lys Thr Thr Ile Ile Ser Cys Met Arg Pro Ala Asn  
             50                    55                    60  
 Gln Glu Ile Tyr Pro Leu Arg His Cys Glu Thr Leu Arg Ser Gln Pro  
             65                    70                    75                    80  
 Cys Ser Leu Phe Ser Ser Leu Tyr Ala Arg Ser Phe Gln Ser Ser Cys  
                     85                    90                    95  
 Thr Leu His Val Ala Glu Pro Ser Pro Gly Phe His Met Tyr Gly Cys  
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 His Thr

<210> 181  
 <211> 959  
 <212> DNA  
 <213> Candida albicans

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<210> 182











<211> 2471  
 <212> DNA  
 <213> *Candida albicans*

<400> 187  
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<210> 188  
 <211> 656  
 <212> PRT  
 <213> *Candida albicans*

<400> 188  
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20 25 30

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35 40 45

Arg Asn Gly Ala Asn Cys Glu Val Thr Met Thr Ser Val Ala Gly His  
50 55 60

Leu Thr Gly Ile Asp Phe Ser His Asp Ser His Gly Trp Gly Lys Cys  
65 70 75 80

Ala Ile Gln Glu Leu Phe Asp Ala Pro Leu Asn Glu Ile Met Asn Asn  
85 90 95

Asn Gln Lys Lys Ile Ala Ser Asn Ile Lys Arg Glu Ala Arg Asn Ala  
100 105 110

Asp Tyr Leu Met Ile Trp Thr Asp Cys Asp Arg Glu Gly Glu Tyr Ile  
115 120 125

Gly Trp Glu Ile Trp Gln Glu Ala Lys Arg Gly Asn Arg Leu Ile Gln  
130 135 140

Asn Asp Gln Val Tyr Arg Ala Val Phe Ser His Leu Glu Arg Gln His  
145 150 155 160

Ile Leu Asn Ala Ala Arg Asn Pro Ser Arg Leu Asp Met Lys Ser Val  
165 170 175

His Ala Val Gly Thr Arg Ile Glu Ile Asp Leu Arg Ala Gly Val Thr  
180 185 190

Phe Thr Arg Leu Leu Thr Glu Thr Leu Arg Asn Lys Leu Arg Asn Gln  
195 200 205

Ala Thr Met Thr Lys Asp Gly Ala Lys His Arg Gly Gly Asn Lys Asn  
210 215 220

Asp Ser Gln Val Val Ser Tyr Gly Thr Cys Gln Phe Pro Thr Leu Gly  
225 230 235 240

Phe Val Val Asp Arg Phe Glu Arg Ile Arg Asn Phe Val Pro Glu Glu  
245 250 255

Phe Trp Tyr Ile Gln Leu Val Val Glu Asn Lys Asp Asn Gly Gly Thr  
260 265 270

Thr Thr Phe Gln Trp Asp Arg Gly His Leu Phe Asp Arg Leu Ser Val  
275 280 285

Leu Thr Phe Tyr Glu Thr Cys Ile Glu Thr Ala Gly Asn Val Ala Gln  
290 295 300

Val Val Asp Leu Lys Ser Lys Pro Thr Thr Lys Tyr Arg Pro Leu Pro  
305 310 315 320

Leu Thr Thr Val Glu Leu Gln Lys Asn Cys Ala Arg Tyr Leu Arg Leu  
 325 330 335  
 Asn Ala Lys Gln Ser Leu Asp Ala Ala Glu Lys Leu Tyr Gln Lys Gly  
 340 345 350  
 Phe Ile Ser Tyr Pro Arg Thr Glu Thr Asp Thr Phe Pro His Ala Met  
 355 360 365  
 Asp Leu Lys Ser Leu Val Glu Lys Gln Ala Gln Leu Asp Gln Leu Ala  
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 Ala Gly Gly Arg Thr Ala Trp Ala Ser Tyr Ala Ala Ser Leu Leu Gln  
 385 390 395 400  
 Pro Glu Asn Thr Ser Asn Asn Asn Lys Phe Lys Phe Pro Arg Ser Gly  
 405 410 415  
 Ser His Asp Asp Lys Ala His Pro Pro Ile His Pro Ile Val Ser Leu  
 420 425 430  
 Gly Pro Glu Ala Asn Val Ser Pro Val Glu Arg Arg Val Tyr Glu Tyr  
 435 440 445  
 Val Ala Arg His Phe Leu Ala Cys Cys Ser Glu Asp Ala Lys Gly Gln  
 450 455 460  
 Ser Met Thr Leu Val Leu Asp Trp Ala Val Glu Arg Phe Ser Ala Ser  
 465 470 475 480  
 Gly Leu Val Val Leu Glu Arg Asn Phe Leu Asp Val Tyr Pro Trp Ala  
 485 490 495  
 Arg Trp Glu Thr Thr Lys Gln Leu Pro Arg Leu Glu Met Asn Ala Leu  
 500 505 510  
 Val Asp Ile Ala Lys Ala Glu Met Lys Ala Gly Thr Thr Ala Pro Pro  
 515 520 525  
 Lys Pro Met Thr Glu Ser Glu Leu Ile Leu Leu Met Asp Thr Asn Gly  
 530 535 540  
 Ile Gly Thr Asp Ala Thr Ile Ala Glu His Ile Asp Lys Ile Gln Val  
 545 550 555 560  
 Arg Asn Tyr Val Arg Ser Glu Lys Val Gly Lys Glu Thr Tyr Leu Gln  
 565 570 575  
 Pro Thr Thr Leu Gly Val Ser Leu Val His Gly Phe Glu Ala Ile Gly  
 580 585 590  
 Leu Glu Asp Ser Phe Ala Lys Pro Phe Gln Arg Arg Glu Met Glu Gln  
 595 600 605  
 Asp Leu Lys Lys Ile Cys Glu Gly His Ala Ser Lys Thr Asp Val Val  
 610 615 620

Lys Asp Ile Val Glu Lys Tyr Arg Lys Tyr Trp His Lys Thr Asn Ala  
625 630 635 640

Cys Lys Asn Thr Leu Leu Gln Val Tyr Asp Arg Val Lys Ala Ser Met  
645 650 655

<210> 189

<211> 1937

<212> DNA

<213> Candida albicans

<400> 189

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tccaatatat taaggggtaa ggactactat tattcgccct gaattgaaat cttttagaaa 240
gcacctgttc tctctctggt gttctttttt tctcatctat tatctaattt cttcaacctt 300
cgttatttgt tgttattccg taatcgtggt gctcaacttt tgaaatttca cttgtttacc 360
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tatagatata atcgaatcca atgactgggc ctggacctga aataaataag gaggagcacc 540
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tcctttcccc caactag 1937

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<210> 190

<211> 478

<212> PRT

<213> Candida albicans

&lt;400&gt; 190

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 20 25 30  
 Leu Ile Asp Gly Ser Thr Asn Ser Ser Lys Arg Pro Ile Glu Lys Tyr  
 35 40 45  
 Asp Lys Arg Ile Ala Asp Pro Thr Lys Ser Tyr Phe Pro His Ser Ile  
 50 55 60  
 Ser Arg Thr Pro Arg Arg Lys Tyr Thr Tyr Ile Leu Val Leu Thr Ser  
 65 70 75 80  
 Leu Asn Gly Thr Phe Glu Ser Lys His Val Val Ile Pro Phe Lys Pro  
 85 90 95  
 Asp Gly Leu Lys Leu Gly Arg Pro Val Ala Asn Ser Asn Ser Ser Ser  
 100 105 110  
 Ser Ser Ser Leu Arg Gly Gly Lys Arg Val Asp Ser His Thr Phe Ser  
 115 120 125  
 Gln Val Arg Ser Asp Asn Gly Asn Phe Asp Ser Arg Val Leu Ser Arg  
 130 135 140  
 Asn His Ala Leu Leu Ser Cys Asp Pro Leu Thr Gly Lys Val Tyr Ile  
 145 150 155 160  
 Arg Asp Leu Lys Ser Ser Asn Gly Thr Phe Ile Asn Gly Gln Arg Ile  
 165 170 175  
 Gly Ser Asn Asp Val Glu Ile Lys Val Gly Asp Val Ile Asp Leu Gly  
 180 185 190  
 Thr Asp Ile Asp Thr Lys Ile Glu His Arg Lys Ile Ser Ala Thr Val  
 195 200 205  
 Glu Glu Leu Phe Val Gln Pro Leu Leu Glu Ser Pro Ile Phe Glu Asn  
 210 215 220  
 Glu Asp Ser Asp Asp Cys His Thr Ile Thr Glu Lys Glu Glu Ala Ala  
 225 230 235 240  
 Ala Ile Thr Ser His Ile Tyr Gly Asp Ser Asn Asn Leu Glu Leu Glu  
 245 250 255  
 Glu Val Ile Leu Gly Ser Asp Thr Glu Ile Leu Ser Gly Ile Phe Ile  
 260 265 270  
 Asn Asn Cys Ile Gly Thr Ser Pro Thr Leu Ser Asn Ile Ile Lys Thr  
 275 280 285  
 Leu Ala Met Glu Ile Pro Phe Ser Lys Cys Asp Asn Phe Lys Leu Gln

201

290	295	300
Ser Met Glu Asn Phe Leu Ile Asn Tyr Thr Thr His Leu Glu Tyr Thr		
305	310	315 320
Asn Lys Leu Leu Val Glu Lys Asn Asp Gln Gln Leu Val Lys Leu Gln		
	325	330 335
Asn Gly Leu Arg Arg Lys Leu Ser Gly Lys Tyr Glu Lys Ile Ile Glu		
	340	345 350
Gln Asn Arg Asn Gln Val Lys Gln Leu Glu Arg Asp His Met Phe Phe		
	355	360 365
Lys Lys Ser Phe Glu Val Lys Lys Arg Arg Asn Asn Glu Lys Gln Lys		
	370	375 380
Ser Met Glu Arg Glu Ile Glu Asp Leu Lys Thr Arg Leu Glu Val Glu		
385	390	395 400
Arg Tyr Lys Asn Ser Gln Met Met Lys Lys Asn Lys Gln Lys Glu Gln		
	405	410 415
Glu Leu Ser Thr Ala Ser Lys Lys Lys Thr Thr Glu His Asp Thr Arg		
	420	425 430
Gly Val Pro Gly Met Asn Pro Lys Gly Thr Asp Lys Phe Ser Ile Lys		
	435	440 445
Asn Thr Leu Cys Asn His Phe Thr Leu Leu Thr Phe Gly Thr Ile Ser		
450	455	460
Ile Gly Ile Ile Ala Ile Val Phe Lys Ile Leu Ser Pro Asn		
465	470	475

&lt;210&gt; 191

&lt;211&gt; 2849

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 191

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gtgaattaga ggggtccgat ttggattga 2849

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&lt;210&gt; 192

&lt;211&gt; 782

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 192

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Met Thr Ser Tyr Ile Glu Arg Leu Lys Ser Ala Ala Ser Tyr Leu Asp
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Thr Val Pro Asp Glu His His Asp Phe Arg Lys Pro Thr Ala Lys Val
      20             25             30

Val Thr Thr Gln Leu Thr Ile Ala Thr Ser Leu Gly Ile Phe Ala Leu
      35             40             45

Leu Ser Phe Ser Ile Leu Leu Lys Lys Trp Pro Arg Leu Tyr Ala Ser
      50             55             60

Arg Arg Tyr Lys Asp Asp Gly Asn Leu Arg Leu Pro Ser Trp Asn Gln
      65             70             75             80

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Phe Val Thr Met Asp Ser Val Ala Asn Ala Gln Met Ala Ala Gln Ala  
 385 390 395 400  
 Val Leu Asp Pro Arg Val His Tyr Phe Ile Thr Arg Leu Ala Pro Ala  
 405 410 415  
 Pro His Asp Ile Lys Trp Asp His Val Cys Leu Ser Arg Lys Asp Arg  
 420 425 430  
 Leu Thr Lys Val Tyr Ser Thr Thr Val Phe Ile Gly Leu Ser Ser Leu  
 435 440 445  
 Phe Leu Val Ile Pro Val Ser Tyr Leu Ala Thr Leu Leu Asn Leu Lys  
 450 455 460  
 Thr Leu Ser Lys Phe Trp Pro Ser Val Gly Gln Leu Leu Lys Asp His  
 465 470 475 480  
 Gln Trp Ala Ala Asn Ile Val Thr Gly Leu Leu Pro Thr Tyr Leu Phe  
 485 490 495  
 Thr Leu Leu Asn Phe Gly Ile Pro Tyr Phe Tyr Glu Tyr Leu Thr Ser  
 500 505 510  
 Tyr Gln Gly Leu Val Ser Tyr Ser Glu Glu Glu Ile Ser Leu Val Ser  
 515 520 525  
 Lys Asn Phe Phe Tyr Ile Phe Val Asn Leu Phe Leu Val Phe Thr Leu  
 530 535 540  
 Ala Gly Thr Ala Ser Asn Tyr Trp Ala Tyr Leu Ser Asp Thr Thr Lys  
 545 550 555 560  
 Ile Ala Tyr Gln Leu Ala Thr Ser Val Lys Glu Phe Ser Leu Phe Tyr  
 565 570 575  
 Val Asp Leu Ile Ile Leu Gln Gly Ile Gly Met Phe Pro Phe Lys Leu  
 580 585 590  
 Leu Leu Val Gly Ser Leu Ile Gly Phe Pro Leu Val Lys Ile Lys Ala  
 595 600 605  
 Lys Thr Pro Arg Gln Arg Asn Glu Leu Tyr Asn Pro Pro Ile Phe Asn  
 610 615 620  
 Phe Gly Leu Gln Leu Pro Gln Pro Ile Leu Ile Leu Ile Ile Thr Leu  
 625 630 635 640  
 Ile Tyr Ser Val Met Ser Thr Lys Ile Leu Thr Ser Gly Leu Ala Tyr  
 645 650 655  
 Phe Ile Ile Gly Phe Tyr Val Tyr Lys Tyr Gln Leu Ile Phe Ala Thr  
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 Asp His Leu Pro His Ser Thr Gly Lys Val Trp Pro Leu Ile Phe Arg  
 675 680 685



<400>	193					
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<210> 194

<211> 426

<212> PRT

<213> Candida albicans

<400> 194

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Ala Gln Gln Thr Arg Gln His Lys Arg Ala Lys Val Val Asn Tyr Ala  
35 40 45

Glu Tyr Asp Asn Asp Leu Phe Asp Glu Phe Asn Met Asn Gly Ser Asn  
50 55 60

Phe Asn Asn Ala Asp Thr His Tyr Lys Asp Asn Ala Val Ser His Glu  
65 70 75 80

Asn Thr Pro Ala Leu Thr Asn Gly Val Thr Met Asp Gly Ser Glu Tyr  
85 90 95

Asn Val Leu Glu Asn Met Asn Gly Ala Asp Ser Ile Ile Ser Asn Asn  
100 105 110

Lys Tyr Asp Ala Gly Ser Asn Met Val Val Glu Ser Leu Ser Gly Leu  
115 120 125

Asn Ser Asn Asn Asn Ala Ser Asn Gly Pro Ser Asn Lys Ala Gln Ala  
130 135 140

Gln Asp Ile Gly Asn Ala Val Leu Pro Asp Leu Gln Asp Gln His His  
145 150 155 160

Asn Pro Phe Asn Ile Leu Arg Tyr Pro Lys Ile Arg Asp Thr Phe Ile  
165 170 175

Asn Gly Lys Val Val Ser Pro Tyr Arg Leu Asn Thr Asp Gln Glu Thr  
180 185 190

Lys Ala Asn Ala Asn Ser Gly Glu Ala Ile Met Ile Pro Ile Thr Leu  
195 200 205

Asp Ile Glu His Met Gly His Thr Ile Lys Asp Gln Phe Leu Trp Asn  
210 215 220

Tyr Asn Asp Asp Ser Ile Ser Pro Glu Glu Phe Ala Ser Ile Tyr Cys  
225 230 235 240

Lys Asp Leu Asp Met Thr Ser Ala Thr Leu Gln Thr Gln Ile Ala Asn  
245 250 255

Ile Ile Lys Glu Gln Leu Lys Asp Leu Glu Asn Ile Ala Ala Thr Glu  
260 265 270

Ile Met Ser Asp Leu His Val Ile Ile Asn Leu Thr Cys Asn Leu Gln  
           275                                  280                                  285  
 Asp Arg Phe Phe Glu Asp Asn Phe Gln Trp Asn Leu Asn Asp Lys Ser  
           290                                  295                                  300  
 Leu Thr Pro Glu Arg Phe Ala Thr Ser Ile Val Gln Asp Leu Gly Leu  
 305                                  310                                  315                                  320  
 Thr Arg Glu Phe Ile Pro Leu Ile Ser Gln Ser Leu His Glu Thr Ile  
                                   325                                  330                                  335  
 Leu Lys Ile Lys Lys Asp Trp Val Asp Gly His Leu Ile Gln Asp His  
                                   340                                  345                                  350  
 Val Pro Asn Asp Ala Ala Phe Gly Tyr Leu Ser Gly Ile Arg Leu Asp  
                                   355                                  360                                  365  
 Ile Asp Glu Leu Gly Ser Asn Trp Cys Pro Arg Val Glu Ile Leu Thr  
           370                                  375                                  380  
 Lys Glu Glu Ile Gln Lys Arg Glu Ile Glu Lys Glu Arg Asn Leu Arg  
 385                                  390                                  395                                  400  
 Arg Leu Lys Arg Glu Thr Asp Arg Leu Ser Arg Arg Gly Arg Arg Arg  
                                   405                                  410                                  415  
 Leu Asp Asp Leu Glu Thr Thr Met Arg Met  
                                   420                                  425

<210> 195  
 <211> 815  
 <212> DNA  
 <213> Candida albicans

<400> 195  
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 attggtatca tgattgcctc tccagaattg gcgtttgctc tcgtttcttg atcagtgttg 180  
 agtctatatg gagacaccac ttttcggtta atgaaagtat ctcttatttt agggatatctc 240  
 aatatgttga aggggttggt gtgttggtct tgcagatccg gtagaacggc gtttccaata 300  
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 tcagctccat tcatgttctc taggacattg tattcggaac cgtccatggt aacaccattt 480  
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 ttgaccactt tagccctttt atgctgcctt gtttggttag ccattgtaaa gatggggata 660  
 ccatcatctt cgtttgtaaa tctgttatga aagttagaaa tataagcttg tggaataagc 720  
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<210> 196  
 <211> 104

208

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 196

Met Arg His Cys Ile Ile Phe Ile Val Cys Ile Ser Ile Val Glu Ile  
 1 5 10 15

Arg Thr Val His Ile Glu Phe Ile Lys Glu Ile Val Val Ile Phe Arg  
 20 25 30

Ile Val Asp His Phe Ser Pro Phe Met Leu Pro Cys Leu Leu Ser His  
 35 40 45

Cys Lys Asp Gly Asp Thr Ile Ile Phe Val Cys Gln Ser Val Met Lys  
 50 55 60

Val Arg Asn Ile Ser Leu Trp Asn Lys Leu Val Leu Val Arg His Cys  
 65 70 75 80

Val Leu Leu Cys Ala Phe Leu Leu Ser Phe Phe Asn Val Leu His Ser  
 85 90 95

Ile Ile Ser Ile Cys Arg Ile Phe  
 100

&lt;210&gt; 197

&lt;211&gt; 737

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 197

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 acaaaacagg gcatctcaca tattcgcgta ctggtgttct tttagctcat tccgatatpa 180  
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 tgaccagaag agctgacggt aagaccgcca ctgttaagat taacaaaaaa ttgaacaagg 600  
 ccggttaagcc attcagacaa accaagttca aggttagagg ctcttcttct ttgtacactt 660  
 tggttatcaa cgatgctggt aaggctaaga aattgatcca atctttgcca ccaactttga 720  
 aggttaacag attataa 737

&lt;210&gt; 198

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 198

Met Ala Arg Glu Ile Thr Asp Ile Lys Gln Phe Leu Glu Leu Thr Arg  
 1 5 10 15

<400> 200  
Met Ala Lys Gln Ser Leu Asp Val Ser Ser Asp Arg Arg Lys Ala Arg  
1 5 10 15  
Lys Ala Tyr Phe Thr Ala Pro Ser Ser Gln Arg Arg Val Leu Leu Ser  
20 25 30

210

Ala Pro Leu Ser Lys Glu Leu Arg Ala Gln Tyr Gly Ile Lys Ala Leu  
           35                          40                          45

Pro Ile Arg Arg Asp Asp Glu Val Leu Val Val Arg Gly Ser Lys Lys  
           50                          55                          60

Gly Gln Glu Gly Lys Ile Ser Ser Val Tyr Arg Leu Lys Phe Ala Val  
       65                          70                          75                          80

Gln Val Asp Lys Val Thr Lys Glu Lys Val Asn Gly Ala Ser Val Pro  
                           85                          90                          95

Ile Asn Leu His Pro Ser Lys Leu Val Ile Thr Lys Leu His Leu Asp  
                           100                          105                          110

Lys Asp Arg Lys Ala Leu Ile Gln Arg Lys Gly Gly Lys Leu Glu  
           115                          120                          125

&lt;210&gt; 201

&lt;211&gt; 1376

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 201

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 agggattgct taagaatcaa agtagcttaa ctctaaagta ttattttcct cagttgtggg 120  
 cccatgtggt ggaggggaagg aatatattga aatgtaaatg ttcttaagtt cggttgaact 180  
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 gattcaaagg cgaagtgcgt aggattgtaa ctctatatac tttaggatac ttacaatttt 360  
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 tattgccagc cagacaattc ggttacgtta ttttgactac ttctgcgggt attatggacc 1320  
 atgaggaagc tagaagaaag cacgtttccg gtaaaatctt gggttttgtc tattaa 1376

&lt;210&gt; 202

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 202

211

Met Thr Arg Ser Ser Val Leu Ala Asp Ala Leu Asn Ala Ile Asn Asn  
 1 5 10 15  
 Ala Glu Lys Thr Gly Lys Arg Gln Val Leu Leu Arg Pro Ser Ser Lys  
 20 25 30  
 Val Ile Ile Lys Phe Leu Gln Val Met Gln Lys His Gly Tyr Ile Gly  
 35 40 45  
 Glu Phe Glu Tyr Ile Asp Asp His Arg Ser Gly Lys Ile Val Val Gln  
 50 55 60  
 Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asn  
 65 70 75 80  
 Val Lys Ile Gly Asp Ile Glu Lys Trp Thr Ala Asn Leu Leu Pro Ala  
 85 90 95  
 Arg Gln Phe Gly Tyr Val Ile Leu Thr Thr Ser Ala Gly Ile Met Asp  
 100 105 110  
 His Glu Glu Ala Arg Arg Lys His Val Ser Gly Lys Ile Leu Gly Phe  
 115 120 125  
 Val Tyr  
 130

&lt;210&gt; 203

&lt;211&gt; 1340

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 203

ccctcaaccc gcatttttgcT gagaattttc accaaggccc taggtgatat tagattccac 60  
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 ccaaatactc ccagggggaa tctttgaggg atatgTTtg ttcggaaaag acaaaccaca 720  
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 tgagtagttc atacttccaa ggaatcgtag acgataacaa aaaaactgac tacttgactg 1020  
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1340

<213> Candida albicans

Asn Val Phe Ser Gly Tyr Val Phe Leu Val Asp Gln Gln Leu Lys Ile  
245 250 255



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<400> 206
Met Asn Glu Ala Asp Val Thr Lys Phe Val Asn Asn Ala Arg Lys Thr
  1          5          10          15

Leu Thr Asp Ala Gln Leu Leu Cys Ser Ser Ala Asn Leu Arg Ile Val
      20          25          30

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Asp	Ile	Lys	Lys	Leu	Ser	Ser	Trp	Gln	Leu	Ser	Ile	Ser	Lys	Leu	
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Asn	Phe	Leu	Ile	Val	Gly	Leu	Arg	Gln	Gln	Gly	Lys	Phe	Leu	Tyr	Thr
	50					55					60				
Ile	Leu	Lys	Glu	Gly	Ile	Gly	Thr	Lys	Leu	Ile	Gln	Lys	Gln	Trp	Asn
65					70					75					80
Gln	Ala	Val	Leu	Val	Val	Leu	Val	Asp	Glu	Met	Lys	Tyr	Trp	Gln	Tyr
				85					90					95	
Glu	Ile	Thr	Ser	Lys	Val	Gln	Arg	Leu	Asp	Gly	Ile	Val	Asn	Glu	Leu
			100					105					110		
Ser	Ile	Ser	Glu	Lys	Asp	Asp	Thr	Asp	Pro	Ser	Lys	Leu	Gly	Asp	Tyr
		115					120					125			
Ile	Ser	Arg	Asp	Asn	Val	Asn	Leu	Leu	Asn	Asp	Lys	Leu	Lys	Glu	Val
	130					135					140				
Pro	Val	Ile	Glu	Arg	Gln	Ile	Glu	Asn	Ile	Lys	Leu	Gln	Tyr	Glu	Asn
145					150					155					160
Met	Val	Arg	Lys	Val	Asn	Lys	Glu	Leu	Ile	Asp	Thr	Lys	Leu	Thr	Asp
				165					170					175	
Val	Thr	Gln	Lys	Phe	Gln	Ser	Lys	Phe	Gly	Ile	Asp	Asn	Leu	Met	Glu
			180					185					190		
Thr	Asn	Val	Ala	Glu	Gln	Phe	Ser	Arg	Glu	Leu	Thr	Asp	Leu	Glu	Lys
		195					200					205			
Asp	Leu	Ala	Glu	Ile	Met	Asn	Ser	Leu	Thr	Gln	His	Phe	Asp	Lys	Thr
	210					215					220				
Leu	Leu	Leu	Gln	Asp	Lys	Lys	Ile	Asp	Asn	Asp	Glu	Arg	Glu	Glu	Leu
225					230					235					240
Phe	Lys	Val	Val	Gln	Gly	Asp	Asp	Lys	Glu	Leu	Tyr	Asn	Ile	Phe	Lys
				245					250					255	
Thr	Leu	His	Glu	Val	Ile	Asp	Asp	Val	Asp	Lys	Thr	Ile	Leu	Asn	Leu
			260					265					270		
Gly	Gln	Phe	Leu	Gln	Ala	Lys	Ile	Lys	Glu	Lys	Thr	Glu	Leu	His	Ser
		275					280					285			
Glu	Val	Ser	Glu	Ile	Ile	Asn	Asp	Phe	Asn	Arg	Asn	Leu	Glu	Tyr	Leu
	290					295					300				
Leu	Ile	Phe	Lys	Asp	Ile	Ser	Asn	Leu	Ile	Asp	Ser	Phe	Lys	Asn	Ser
305					310					315					320
Cys	Thr	Gln	Asp	Ile	Gln	Thr	Thr	Lys	Glu	Leu	Cys	Glu	Phe	Tyr	Asp
				325					330					335	

Asn Phe Glu Glu Ser Tyr Gly Asn Leu Val Leu Glu Ala Lys Arg Arg  
 340 345 350  
 Lys Asp Val Ala Asn Arg Met Lys Thr Ile Leu Lys Asp Cys Glu Lys  
 355 360 365  
 Gln Leu Gln Asn Leu Asp Ala Gln Asp Gln Glu Glu Arg Gln Asn Phe  
 370 375 380  
 Ile Ala Glu Asn Gly Thr Tyr Leu Pro Glu Thr Ile Trp Pro Gly Lys  
 385 390 395 400  
 Ile Asp Asp Phe Ser Ser Leu Tyr Thr Leu Asn Tyr Asn Val Lys Asn  
 405 410 415

Pro

<210> 207  
 <211> 1342  
 <212> DNA  
 <213> Candida albicans

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<210> 208  
 <211> 146  
 <212> PRT  
 <213> Candida albicans

216

&lt;400&gt; 208

Met Ser Leu Val Val Gln Glu Gln Gly Ser Phe Gln His Ile Leu Arg  
 1 5 10 15

Leu Leu Asn Thr Asn Val Asp Gly Asn Ile Lys Ile Val Tyr Ala Leu  
 20 25 30

Thr Thr Ile Lys Gly Val Gly Arg Arg Tyr Ser Asn Leu Val Cys Lys  
 35 40 45

Lys Ala Asp Val Asp Leu His Lys Arg Ala Gly Glu Leu Thr Gln Glu  
 50 55 60

Glu Leu Glu Arg Ile Val Gln Ile Met Gln Asn Pro Thr His Tyr Lys  
 65 70 75 80

Ile Pro Ala Trp Phe Leu Asn Arg Gln Asn Asp Ile Thr Asp Gly Lys  
 85 90 95

Asp Tyr His Thr Leu Ala Asn Asn Val Glu Ser Lys Leu Arg Asp Asp  
 100 105 110

Leu Glu Arg Leu Lys Lys Ile Arg Ala His Arg Gly Ile Arg His Phe  
 115 120 125

Trp Gly Leu Arg Val Arg Gly Gln His Thr Lys Thr Thr Gly Arg Arg  
 130 135 140

Arg Ala  
 145

&lt;210&gt; 209

&lt;211&gt; 1268

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 209

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 cttacgctca atcttcccac atcagagcta tcagaaaagt tatttctgaa atcttgacca 1020  
 gagaagttca aaactctact ttggctcaat tgacctccaa attgattcca gaagttatca 1080

Val	Gly	Ala	Leu	Met	Ala	Leu	His	Gly	Glu	Gly	Ser	Gly	Glu	Glu	Lys
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Gly Lys Lys Val Ser Gly Phe Lys Asp Glu Val Leu Glu Thr Val  
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<210> 211  
 <211> 2042  
 <212> DNA  
 <213> Candida albicans

<400> 211  
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 ctttatttcc acttctttac aagctttctg cttttctcta tgacgtcttt cccaaaacac 180  
 tacctcttga cagcacttgt tgttttcggt tttctctaag aatatcacta ttttcaacttt 240  
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 gggaagaata agggatcttt ggaactgaag gaaaataagg gagagggagg aaacaaggag 360  
 gcggtgaaaag gggatcgaca gggatatttaa agccactcat ggagtcgtat tcctagcatg 420  
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<210> 212  
 <211> 513  
 <212> PRT  
 <213> Candida albicans

<400> 212  
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325 330 335

Leu Val Gly Leu Asp Ser Trp Pro Lys Asp Lys Leu Lys Met Phe Leu  
340 345 350

Asp Ala Arg Gly Ile Lys Tyr Ser Met Leu Ser Thr Glu His Gln Leu  
355 360 365

Arg Glu Leu Val Lys Lys Ser Arg Asn Glu Lys Leu Lys Ile Leu Pro  
370 375 380

Lys Asp Tyr Gln Lys Tyr Phe Asp Asn Ser Asn Trp Ser Leu Asp Asp  
385 390 395 400

Ile Lys Gly Trp Phe Ala Asp Lys Lys Asp Asp Phe Gln Asp Ser Gln  
405 410 415

Thr Tyr Ser Thr Ile Met Gln Asp Phe Asp Lys Val Ser Lys Asn Thr  
420 425 430

Asn Asp Ala Lys Asp Gln Ile Ala Lys Thr Trp Ser Asn Thr Phe Gln  
435 440 445

Ser Trp Ser Gln Glu Asp Leu Leu Gln Tyr Leu Lys Ser Phe Gly Val  
450 455 460

Pro Val Lys Gln Thr Ser Thr Lys Asp Asp Leu Ile Asn Leu Ala Lys  
465 470 475 480

Gln Asn Thr Gln Trp Leu Phe Gly Thr Val Lys Glu Pro Ala Tyr Lys  
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Arg Tyr Leu His Asn Val Lys Asn Trp Ser Lys Ser Ile Leu Gly Phe  
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Asn

<210> 213

<211> 2192

<212> DNA

<213> Candida albicans

<400> 213

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cacaaagaga agactgttct aattaaacaa ataattattga gctacctgct aagtatgtcc 240  
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ggctttgggc gttagtaaga acaaaaagaa aagaagagaa caaaaaagaa acgatacgga 360  
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&lt;210&gt; 214

&lt;211&gt; 563

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 214

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  1                      5                      10                      15

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Ser Ala Thr Ser Asn Asn Ser Tyr Ile Ala Thr Asp Gln Thr Gln Asn
      20                      25                      30

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Ala Phe Asn Asp Thr His Phe Cys Lys Val Asp Arg Asn Asp His Val
      35                      40                      45

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Ser Pro Ser Cys Asn Val Thr Phe Asn Glu Leu Asn Ala Ile Asn Glu
      50                      55                      60

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Asn Ile Arg Asp Asp Leu Ser Ala Leu Leu Lys Ser Asp Phe Phe Lys
      65                      70                      75                      80

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Tyr Phe Arg Leu Asp Leu Tyr Lys Gln Cys Ser Phe Trp Asp Ala Asn
      85                      90                      95

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Asp Gly Leu Cys Leu Asn Arg Ala Cys Ser Val Asp Val Val Glu Asp
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Trp Asp Thr Leu Pro Glu Tyr Trp Gln Pro Glu Ile Leu Gly Ser Phe

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115					120					125					
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130					135					140					
Phe	Leu	Asp	Gln	Leu	Cys	Gln	Thr	Ser	Lys	Lys	Pro	Val	Asp	Ile	Glu
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Val	Leu	Ile	Asp	Leu	Thr	Ala	Asn	Pro	Glu	Arg	Phe	Thr	Gly	Tyr	Gly
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225					230					235					240
Glu	Tyr	Leu	Asn	Thr	Lys	Thr	Gly	Lys	Trp	Glu	Pro	Asn	Leu	Asp	Leu
				245					250					255	
Phe	Met	Ala	Arg	Ile	Gly	Asn	Phe	Pro	Asp	Arg	Val	Thr	Asn	Met	Tyr
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Leu	Pro	Glu	Phe	Ser	Phe	Cys	Asp	Leu	Val	Asn	Lys	Glu	Ile	Lys	Asn
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305					310					315					320
Asp	Leu	Val	Phe	Ala	Asn	Asp	Leu	Ser	Leu	Thr	Leu	Lys	Asp	Glu	Phe
				325					330					335	
Arg	Ser	Arg	Phe	Lys	Asn	Val	Thr	Lys	Ile	Met	Asp	Cys	Val	Gln	Cys
			340					345					350		
Asp	Arg	Cys	Arg	Leu	Trp	Gly	Lys	Ile	Gln	Thr	Thr	Gly	Tyr	Ala	Thr
	355					360						365			
Ala	Leu	Lys	Ile	Leu	Phe	Glu	Ile	Asn	Asp	Ala	Asp	Glu	Phe	Thr	Lys
	370					375					380				
Gln	His	Ile	Val	Gly	Lys	Leu	Thr	Lys	Tyr	Glu	Leu	Ile	Ala	Leu	Leu
385					390					395					400
Gln	Thr	Phe	Gly	Arg	Leu	Ser	Glu	Ser	Ile	Glu	Ser	Val	Asn	Met	Phe
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<210> 216



[illegible]

<210> 219  
 <211> 1121  
 <212> DNA  
 <213> Candida albicans

<400> 219  
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 gttctgcaga atgatgtttg atagtatcga taatggagtg agatcaagag aaaaaaaatg 240  
 aatatgtcag ccaaccaagt tctgagtagg cagtaaatga gtacgcatag tgtattttatc 300  
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 tcactcatca gatgtccaag attttcgaaa aataaatatt ctcatttttc tctcaatgaa 660  
 ataattgtta ctaacattga atttcctcgt aactaattgc attacttctt tagacttttg 720  
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<210> 220  
 <211> 143  
 <212> PRT  
 <213> Candida albicans

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 Gly Ser Pro Ile Thr Leu Val Glu Pro Glu Ile Leu Arg Phe Lys Val  
 35 40 45  
 Tyr Glu Pro Leu Leu Leu Val Gly Leu Asp Lys Phe Ser Asn Ile Asp  
 50 55 60  
 Ile Arg Val Arg Val Thr Gly Gly Gly His Val Ser Gln Val Tyr Ala  
 65 70 75 80  
 Ile Arg Gln Ala Ile Ala Lys Gly Leu Val Ala Tyr His Gln Lys Tyr  
 85 90 95  
 Val Asp Glu Gln Ser Lys Asn Glu Leu Lys Lys Ala Phe Thr Ser Tyr  
 100 105 110  
 Asp Arg Thr Leu Leu Ile Ala Asp Ser Arg Arg Pro Glu Pro Lys Lys  
 115 120 125

Phe Gly Gly Lys Gly Ala Arg Ser Arg Phe Gln Lys Ser Tyr Arg  
 130 135 140

<210> 221  
 <211> 707  
 <212> DNA  
 <213> Candida albicans

<400> 221  
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 gtaaatacag aaggttaaga gatagttgtc ttaaaggggt accgaaagca tttaggggag 240  
 gcttaaggga ggggtgccgat cctatgaagt attaatacgt aatgccaaaa ggaattgttg 300  
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 gctcaaagga aaaattgcag ggcgatgcaa aggtagttag tgacgctttt aagaaaatgg 600  
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 aagagcaata caacaagctc aaaggggcgg ggcataagaa ggagtag 707

<210> 222  
 <211> 68  
 <212> PRT  
 <213> Candida albicans

<400> 222  
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 Met Ala Ser Gln Asp Lys Asp Gly Lys Thr Thr Asp Ala Asp Glu Ser  
 35 40 45  
 Glu Lys His Asn Tyr Gln Glu Gln Tyr Asn Lys Leu Lys Gly Ala Gly  
 50 55 60  
 His Lys Lys Glu  
 65

<210> 223  
 <211> 1877  
 <212> DNA  
 <213> Candida albicans

<400> 223  
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 gttgtttcgt agcagtattc gttgggtccag atgcaggaat gctgggttata aagtttgttg 180

Leu Arg Met Ser Arg Val His Leu Arg Gln Ile Thr Lys Ser Leu Asp  
100 105 110



Arg Thr Leu Ile Ser Leu Ser His Gly Asn Phe Ser His Gln Tyr Asn  
 115 120 125  
 Arg Asn Ile Phe Val Thr Trp Trp Lys Ser Leu Phe Glu Ala Ser Thr  
 130 135 140  
 Ala Phe Arg Arg Ala Ser Gly Leu Thr Val Ser Pro Leu Thr Arg Arg  
 145 150 155 160  
 Gly Ile Ala Arg Phe Asp His Phe Arg Pro Val Pro Asn Val Ser Lys  
 165 170 175  
 Phe Ala Ser Phe Pro Arg Val Pro Lys Gly Ala Pro Arg Gly Leu Phe  
 180 185 190  
 Thr Asn Trp Asn Met Thr Thr Ser Lys Arg Leu Leu Gly Gln Arg Ala  
 195 200 205  
 Tyr Ser Thr Ser Ser Ile Lys Phe Thr Gln Glu Ala Val Asn Asn Met  
 210 215 220  
 Thr Ile Ser Leu Arg Cys Phe Phe Asn Ser Leu Gly Gly Leu Asn Gln  
 225 230 235 240  
 Cys Ser His Ser Asn Ser Cys Lys Ala Tyr Gln Asn Ala Ser Asn Val  
 245 250 255  
 Thr Ser Lys Gln Asp His Val Gln Pro Val Ala Leu Lys Lys Leu Ser  
 260 265 270  
 Gln Lys Asp Ile Asn Phe Ile Arg Asn Leu Glu Leu Phe Lys Ile Met  
 275 280 285  
 Lys Thr Gln Asn Glu Val Val Asp Glu Thr Ser Ala Tyr Tyr Met Glu  
 290 295 300  
 Lys Pro Gly Ser Tyr Ile Glu Phe Thr Ile Ser Glu Phe Asn Val Asn  
 305 310 315 320  
 Gly Thr Phe Ser Ala Pro Leu Ser Phe Leu Asp Pro Ser Leu Leu Ala  
 325 330 335  
 Asp Leu Asp Glu Met Ile Arg Asn Tyr Lys Tyr Glu Leu Lys Ser Ile  
 340 345 350  
 Tyr Ser Ser Val Asp Met Ile Leu Gln Asn Tyr Gly Ser Leu Pro Ile  
 355 360 365  
 Thr Phe His Arg Asn Lys Ile Arg Ile His Phe Pro Asn Ser Thr Val  
 370 375 380  
 Val Glu Thr Glu Lys Leu Ile Ala Gly Leu Asn Ile Ala Thr Gly Val  
 385 390 395 400  
 Ile Tyr Ala Asp Thr Ser Pro Asp Ile Ser Leu Glu Gly Thr Asn Leu  
 405 410 415

Leu Thr Ser Lys Gly Tyr Val Lys Thr Gln Phe Ser Trp Gln Tyr Tyr

50

55

60

Tyr Tyr Thr Leu Thr Glu Glu Gly Val Glu Tyr Leu Arg Glu Tyr Leu  
65 70 75 80

Asn Leu Pro Glu His Ile Val Pro Gly Thr Tyr Ile Gln Glu Arg Asn  
85 90 95

Pro Ser Gln Arg Pro Gln Arg Arg Tyr  
100 105

&lt;210&gt; 227

&lt;211&gt; 3998

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 227

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			20					25					30			
Ala	Pro	Asn	Pro	Ser	Ile	Pro	Ser	Ala	Ser	Thr	Ser	Thr	Ser	Pro	Leu	
		35					40					45				
His	Arg	Glu	Ile	Val	Asp	Asp	Ser	Val	Ala	Thr	Ala	Asn	Thr	Thr	Ser	
	50					55					60					
Asn	Val	Val	Gln	His	Asn	Leu	Pro	Thr	Ile	Asp	Asn	Asn	Leu	Met	Asp	
65					70					75					80	
Ser	Asp	Ala	Thr	Ser	His	Asn	Gln	Asp	His	Trp	His	Ser	Asp	Ile	Asn	
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Arg	Ala	Gly	Thr	Ser	Met	Ser	Thr	Ser	Asp	Ile	Pro	Thr	Asp	Leu	His	
			100					105					110			



Glu	Ser	Asn	Ser	Glu	Lys	Pro	Thr	Lys	Ala	Asp	Phe	Phe	Ala	Arg					
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Leu	Ala	Thr	Ala	Val	Gly	Glu	Asn	Glu	Ile	Ser	Asp	Ser	Glu	Glu	Thr				
435								440				445							
Phe	Val	Tyr	Glu	Ser	Ala	Ala	Asn	Ser	Thr	Lys	Asn	Leu	Ile	Phe	Pro				
450								455				460							
Asp	Ser	Ser	Ser	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Lys	Gln				
465								470				475			480				
Gln	Gln	Gln	Gln	Gln	Asn	His	Gly	Ile	Thr	Ser	Lys	Ile	Ser	Ala	Pro				
				485								490				495			
Leu	Leu	Asn	Asn	Asn	Lys	Lys	Leu	Leu	Ser	Arg	Leu	Lys	Asn	Ser	Arg				
				500								505				510			
His	Ile	Ser	Thr	Gly	Ala	Ile	Leu	Asn	Asn	Thr	Ile	Ala	Thr	Ile	Ser				
				515								520				525			
Thr	Asn	Pro	Asn	Leu	Asn	Ser	Asn	Val	Met	Gln	Asn	Asn	Asn	Asn	Leu				
				530								535				540			
Met	Ser	Gly	His	Asn	His	Leu	Asp	Glu	Leu	Ser	Ser	Ile	Lys	Gln	Glu				
545												550				555		560	
Pro	Pro	His	Gln	Leu	Gln	Gln	Gln	Gln	Pro	Pro	Met	Asp	Val	Gln	Ser				
				565								570				575			
Val	Asp	Ser	Tyr	Thr	Ser	Asp	Asn	Pro	Asp	Ser	Asn	Val	Ile	Ala	Lys				
				580								585				590			
Ser	Pro	Asp	Lys	Arg	Ser	Ser	Leu	Val	Ser	Leu	Ser	Lys	Val	Ser	Pro				
				595								600				605			
His	Leu	Leu	Ser	Ser	Thr	Ser	Ser	Asn	Gly	Asn	Thr	Ile	Ser	Cys	Pro				
610								615								620			
Asn	Val	Ala	Thr	Asn	Ser	Gln	Glu	Leu	Glu	Pro	Asn	Asn	Asp	Ile	Ser				
625								630								635		640	
Thr	Lys	Lys	Ser	Leu	Ser	Asn	Ser	Thr	Leu	Arg	His	Ser	Ser	Ala	Asn				
				645								650				655			
Arg	Asn	Ser	Asn	Tyr	Gly	Asp	Asn	Lys	Arg	Pro	Leu	Arg	Thr	Thr	Val				
				660								665				670			
Ser	Lys	Ile	Phe	Asp	Ser	Asn	Pro	Asn	Gly	Ala	Pro	Leu	Arg	Arg	Tyr				
				675								680				685			
Ser	Gly	Val	Pro	Asp	His	Val	Asn	Leu	Glu	Asp	Tyr	Ile	Glu	Gln	Pro				
690								695								700			
His	Asn	Tyr	Pro	Thr	Met	Gln	Asn	Ser	Val	Lys	Lys	Asp	Glu	Phe	Tyr				
705								710								715		720	

Asn	Ser	Arg	Asn	Asn	Lys	Phe	Pro	His	Gly	Leu	Asn	Phe	Tyr	Gly	Asp	725	730	735
Asn	Asn	Val	Ile	Glu	Glu	Glu	Asn	Asn	Gly	Asp	Ser	Ser	Asn	Val	Asn	740	745	750
Arg	Pro	Gln	His	Thr	Asn	Leu	Gln	His	Glu	Phe	Ile	Pro	Glu	Asp	Asn	755	760	765
Glu	Ser	Asp	Glu	Asn	Asp	Ile	His	Ser	Met	Phe	Tyr	Tyr	Asn	His	Lys	770	775	780
Asn	Asp	Leu	Glu	Thr	Lys	Pro	Leu	Ile	Ser	Asp	Tyr	Gly	Glu	Asp	Glu	785	790	800
Asp	Val	Asp	Asp	Tyr	Asp	Arg	Pro	Asn	Ala	Thr	Phe	Asn	Ser	Tyr	Tyr	805	810	815
Gly	Ser	Ala	Ser	Asn	Thr	His	Glu	Leu	Pro	Leu	His	Gly	Arg	Met	Pro	820	825	830
Ser	Arg	Ser	Asn	Asn	Asp	Tyr	Tyr	Asp	Phe	Met	Val	Gly	Asn	Asn	Thr	835	840	845
Gly	Asn	Asn	Asn	Gln	Leu	Asn	Glu	Tyr	Thr	Pro	Leu	Arg	Met	Lys	Arg	850	855	860
Gly	Gln	Arg	His	Leu	Ser	Arg	Thr	Asn	Asn	Ser	Ile	Met	Asn	Gly	Ser	865	870	875
Ile	His	Met	Asn	Gly	Asn	Asp	Asp	Val	Thr	His	Ser	Asn	Ile	Asn	Asn	885	890	895
Asn	Asp	Ile	Val	Gly	Tyr	Ser	Pro	His	Asn	Phe	Tyr	Ser	Arg	Lys	Ser	900	905	910
Pro	Phe	Val	Lys	Val	Lys	Asn	Phe	Leu	Tyr	Leu	Ala	Phe	Val	Ile	Ser	915	920	925
Ser	Leu	Leu	Met	Thr	Gly	Phe	Ile	Leu	Gly	Phe	Leu	Leu	Ala	Thr	Asn	930	935	940
Lys	Glu	Leu	Gln	Asp	Val	Asp	Val	Val	Val	Met	Asp	Asn	Val	Ile	Ser	945	950	955
Ser	Ser	Asp	Glu	Leu	Ile	Phe	Asp	Ile	Thr	Val	Ser	Ala	Phe	Asn	Pro	965	970	975
Gly	Phe	Phe	Ser	Ile	Ser	Val	Ser	Gln	Val	Asp	Leu	Asp	Ile	Phe	Ala	980	985	990
Lys	Ser	Ser	Tyr	Leu	Lys	Cys	Asp	Ser	Asn	Gly	Asp	Cys	Thr	Val	Met	995	1000	1005
Glu	Gln	Glu	Arg	Lys	Ile	Leu	Gln	Ile	Thr	Thr	Asn	Leu	Ser	Leu	Val	1010	1015	1020

$\langle 210 \rangle \quad 230$



<211> 191  
 <212> PRT  
 <213> Candida albicans

<400> 230

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Met Lys Tyr Ile Gln Thr Glu Gln Gln Ile Glu Ile Pro Glu Gly Val
 1             5             10             15

Thr Val Ser Ile Lys Ser Arg Ile Val Lys Val Val Gly Pro Arg Gly
      20             25             30

Thr Leu Thr Lys Asn Leu Lys His Ile Asp Val Thr Phe Thr Lys Val
      35             40             45

Asn Asn Gln Leu Ile Lys Val Ala Val His Asn Gly Asp Arg Lys His
      50             55             60

Val Ala Ala Leu Arg Thr Val Lys Ser Leu Val Asp Asn Met Ile Thr
      65             70             75             80

Gly Val Thr Lys Gly Tyr Lys Tyr Lys Met Arg Tyr Val Tyr Ala His
      85             90             95

Phe Pro Ile Asn Val Asn Ile Val Glu Lys Asp Gly Ala Lys Phe Ile
      100            105            110

Glu Val Arg Asn Phe Leu Gly Asp Lys Lys Ile Arg Asn Val Pro Val
      115            120            125

Arg Asp Gly Val Thr Ile Glu Phe Ser Thr Asn Val Lys Asp Glu Ile
      130            135            140

Val Leu Ser Gly Asn Ser Val Glu Asp Val Ser Gln Asn Ala Ala Asp
      145            150            155            160

Leu Gln Gln Ile Cys Arg Val Arg Asn Lys Asp Ile Arg Lys Phe Leu
      165            170            175

Asp Gly Ile Tyr Val Ser His Lys Gly Phe Ile Val Glu Asp Met
      180            185            190

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<210> 231  
 <211> 1373  
 <212> DNA  
 <213> Candida albicans

<400> 231

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tctgaggaag aaaagatggt acgtacaata tcacggccttg acaatacgag tattgcaaac 120
agtaatggaa atggtaatga tgacacctct aatcagagaa cggaagcact ggggcgtaag 180
acgagtaatg gagggcgaat atgattacta agttaaataa atcagataca gtatttaaag 240
ttctttcaaa aaaagataat gtcatatatt ttactatcta cgcagtgaaa gagttccttc 300
taatgacaca ctattcactt cgggtaacgg atattgtgta ctgaaaaata taaaaaattt 360
tatcccgga atgcgatgag atgaaaatgc atgaagtagc gtatatattg attgcatgag 420
gttggaacttg aaagggcata tatactcggg tttatcattg attcaagtgt tcccataaat 480

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<400> 232																
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Ala	Gln	Glu	Leu	Gln	Asp	Ser	Gln	Leu	Gln	Gln	Lys	Arg	Gln	Ile	Ile	
			20					25					30			
Lys	Gln	Ala	Leu	Ala	Gln	Gly	Lys	Pro	Leu	Pro	Lys	Glu	Leu	Ala	Glu	
		35					40					45				
Asp	Glu	Ser	Leu	Gln	Lys	Asp	Phe	Arg	Tyr	Asp	Gln	Ser	Leu	Lys	Glu	
	50					55					60					
Ser	Glu	Glu	Ala	Asp	Asp	Leu	Gln	Val	Asp	Asp	Glu	Tyr	Ala	Ala	Thr	
65					70					75					80	
Ser	Gly	Ile	Met	Asp	Pro	Arg	Ile	Ile	Val	Thr	Thr	Ser	Arg	Asp	Pro	
				85					90					95		
Ser	Thr	Arg	Leu	Ser	Gln	Phe	Ala	Lys	Glu	Ile	Lys	Leu	Leu	Phe	Pro	
			100					105					110			
Asn	Ala	Val	Arg	Leu	Asn	Arg	Gly	Asn	Tyr	Val	Met	Pro	Asn	Leu	Val	
		115					120					125				
Asp	Ala	Cys	Lys	Lys	Ser	Gly	Thr	Thr	Asp	Leu	Val	Val	Leu	His	Glu	
	130					135					140					
His	Arg	Gly	Val	Pro	Thr	Ser	Leu	Thr	Ile	Ser	His	Phe	Pro	His	Gly	
145					150					155					160	
Pro	Thr	Ala	Gln	Phe	Ser	Leu	His	Asn	Val	Val	Met	Arg	His	Asp	Ile	
				165					170					175		
Ile	Asn	Ala	Gly	Asn	Gln	Ser	Glu	Val	Asn	Pro	His	Leu	Ile	Phe	Asp	

<400>	233						
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tagtagttac	gaaaggcaca	gaaaataaca	aaaaaaaaaa	aaaagtcaat	tttctacggt	180	
ctccatccgt	acctctttaa	atccgtacat	tattgttttg	cttaatttca	atatttcgga	240	
aaaagcgagc	gccctggtaa	aatgtggttc	aaagcctgca	gcctttgtgt	ggtaactcac	300	
caaatgcaat	tcagtcacgt	tccacacagt	ttgggtttcc	agcctggctt	tagggaagaa	360	
tgggctcact	aggcgttcat	aatacgcgga	gggggaaata	ccaaatgcta	ttgattatgg	420	
ttaaaatatg	tgttatttga	ctttgtatat	acaaacagaa	gagaaaccaa	cacactaaag	480	
actagacaca	taactgacca	atgtcctctg	tccaatccaa	gatcttatcc	caagctccaa	540	
gtgagttgga	attacaagtc	gccaaagacct	tcatcgatct	agaaagctcc	tctccagaac	600	
taaaggctga	cttgagacca	ttgcaaatca	aatctatcag	agaagtatgt	taaaagttat	660	
ataatttgga	agcagcaaca	ttgtgatttc	ttctaaaggg	gttcttttga	gtaatttttt	720	
caaaaaagag	tgatttttag	cagtatctgt	atgaaatttt	catgtgtctg	agaaaaatag	780	
taatttcgag	agctgtcaat	accatgaacg	ttgcgatgag	cctttgaact	ataaaggcct	840	
ccttggctcag	taccaatatc	gatgaataaa	atagaagcac	gcgaaaaaga	ccttacccca	900	
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ttcaacgctg	cttgattctt	attgttttag	ttgatgtcac	cggtggttaag	aaagcactag	1020	
tcctttttgt	cccagttcca	gctttgtctg	cataccataa	ggtccaaacc	aaattgacct	1080	
gtgaattgga	aaagaaattc	cctgaccgtc	atgttatatt	cttggctgaa	agaagaatct	1140	
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tgatttagata	tttggttcgt	ggtaacaaga	tccaaaagg	tttgttagac	tccaaggatg	1320	
ttcaacaat	cgactacaag	ttggaatcct	tccaagctgt	ctacaacaag	ttgactggca	1380	
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<210> 234
<211> 190
<212> PRT
<213> Candida albicans
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<210> 235
<211> 1333
<212> DNA
<213> Candida albicans
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<400> 235							
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gagatcttac	atccttacat	ctaaagtaaa	acctagacat	ttacttcgag	ttatactttt	180	
tttttattta	tctatttttt	ctcttgcgga	catttaaacac	ctgaattccg	cctaacgcc	240	
ggactgatcc	tgccagggaa	gggagctttg	tctagtgcga	ataggccgga	ccagtaggaa	300	
ggttacagca	gctggcccg	agatgtattg	ggtcacagga	aatagcgcaa	ctcttctttt	360	
tqccccgqaa	aqcgcggttca	atctaccttc	qaagggtctag	tacatgagcg	cgaaggaggc	420	

<400> 237  
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Ala Arg Ala Lys Ala Met Lys Phe Ala Asp Gly Phe Leu Ile His Ser  
145 150 155 160

Gly Gln Pro Val Asn Asp Phe Ile Asp Thr Ala Thr Arg His Val Leu  
                           165                          170                          175

Met Arg Gln Gly Val Leu Gly Ile Lys Val Lys Ile Met Arg Asp Pro  
                           180                          185                          190

Ala Lys Ser Arg Thr Gly Pro Lys Ala Leu Pro Asp Ala Val Thr Ile  
                           195                          200                          205

Ile Glu Pro Lys Glu Glu Glu Pro Ile Leu Ala Pro Ser Val Lys Asp  
           210  215                          220

Tyr Arg Pro Ala Glu Glu Thr Glu Ala Gln Ala Glu Pro Val Glu Ala  
 225  230                          235                          240

&lt;210&gt; 239

&lt;211&gt; 2168

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 239

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agcatgtacg ctatacatTT acgtgctgag ctccctaggaa agctcatgag cagccactgt 120
atcgtggagc ataactacaa caaagaatac acagcgtcac atagagggtt tttgagagga 180
gaagttgaaa taggacttga tcttggggga gaggggattt gaaagcacc attcaggagt 240
atgtgtctgt aattgaagtg ttagcgcgcg attcacctgt aataagagtg atgatttgat 300
agcgccattc tacatcatat ggcaaatgtt gaaaaactgt acgcgcgaac taaaattttt 360
ttttacatcc cactaaatga aaatttttaa tccgatgccc ttccaaatat gcttattcga 420
aggacggctc tgacaagggc atatgcgtta agattgattg ttcaatattc ataaaacagg 480
atctttcaag ggacgataaa atggatgagc aagttatttt tacaacaaat acctcaggaa 540
caatagcttc tgtacactca tttgaacaga taaatttgag gcaatgctcc actcaatcaa 600
gaaatagctg tgttcaagta ggaaataaat acctttttat tgctcaagca caaaaagcat 660
taatcaatgt ctacaatctg tcaggttctt tcaaaagaga atctgttgaa cagcgcttac 720
cattacctga aatcctaata tgtctggaag tagttgaaaa tgatggtgtg cagtatgata 780
gaattcaagg tgtcaatcat aatttaccag acttcaatct tccgtacctt ttacttggct 840
ccaccgaatc gggtaaatgt tacatatggg agttaaattc agggatttta ttgaacgtga 900
agcctatggc tcattaccaa agtatcacca agattaagtc cattttaaac ggcaagtata 960
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aagtgaccaa tctcttaacc aacccttaca gactcgaacg tggaaattta ctttttgaag 1740
gagaatccaa aggcaaacaa cctagtaata ataatggtca caattttatg aagataccaa 1800

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acttacaaag agttatcttt gatggtaaaa acaaaggcca ttacacgat atttggtatc 1860  
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 atgcctatatt ggagcaggtc aaaacgcaag aatcgatatt ttcacatatc ggtaagggtgt 1980  
 caagcaatgt aaaagtgtt gacaataaaa tcgacgccac ttcattcttta gacagcaatg 2040  
 ccgctaaaga tgaggaaatt acagaactta agaccaacat agaagcatta actcatgcct 2100  
 acaaggagtt acgtgacatg cacgaaaagc tgtacgagga acaccaacag atgcttgaca 2160  
 agcaataa 2168

<210> 240

<211> 555

<212> PRT

<213> Candida albicans

<400> 240

Met Asp Glu Gln Val Ile Phe Thr Thr Asn Thr Ser Gly Thr Ile Ala  
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 Ser Val His Ser Phe Glu Gln Ile Asn Leu Arg Gln Cys Ser Thr Gln  
 20 25 30  
 Ser Arg Asn Ser Cys Val Gln Val Gly Asn Lys Tyr Leu Phe Ile Ala  
 35 40 45  
 Gln Ala Gln Lys Ala Leu Ile Asn Val Tyr Asn Leu Ser Gly Ser Phe  
 50 55 60  
 Lys Arg Glu Ser Val Glu Gln Arg Leu Pro Leu Pro Glu Ile Leu Lys  
 65 70 75 80  
 Cys Leu Glu Val Val Glu Asn Asp Gly Val Gln Tyr Asp Arg Ile Gln  
 85 90 95  
 Gly Val Asn His Asn Leu Pro Asp Phe Asn Leu Pro Tyr Leu Leu Leu  
 100 105 110  
 Gly Ser Thr Glu Ser Gly Lys Leu Tyr Ile Trp Glu Leu Asn Ser Gly  
 115 120 125  
 Ile Leu Leu Asn Val Lys Pro Met Ala His Tyr Gln Ser Ile Thr Lys  
 130 135 140  
 Ile Lys Ser Ile Leu Asn Gly Lys Tyr Ile Ile Thr Ser Gly Asn Asp  
 145 150 155 160  
 Ser Arg Val Ile Ile Trp Gln Thr Val Asp Leu Val Ser Ala Ser Asn  
 165 170 175  
 Asp Asp Pro Lys Pro Leu Cys Ile Leu His Asp His Thr Leu Pro Val  
 180 185 190  
 Thr Asp Phe Gln Val Ser Ser Ser Gln Gly Lys Phe Leu Ser Cys Thr  
 195 200 205  
 Asp Thr Lys Leu Phe Thr Val Ser Gln Asp Ala Thr Ile Arg Cys Tyr  
 210 215 220











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acactatata tattttgtgc ctggttgagg tggatctcct caatctggta tttaccgaca 780
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tgacaaacca agaaatttta cctcaaaaact caacagtggc agaactgcaa aagagcacta 1020
ataaagtaca gacaaatggg ccgcaacggc acgatttcat agtcactcta gaaataaaaac 1080
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aaaggaacca ccctgaatct gttcaacaaa caatactaata ttcgggtgac ttataactcaa 1260
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<210> 246

<211> 270

<212> PRT

<213> Candida albicans

<400> 246

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Val Lys Leu Leu Glu Glu Leu Gln Glu Gly Lys Gln Phe Asn Asn Lys
      20              25              30

Asn Ile Phe Pro Glu Lys Ala Leu Tyr Leu Lys Leu Ala Leu Asp Tyr
      35              40              45

Ser Phe Phe Arg Lys Asn Leu Leu Glu Phe Cys Val His Leu Asp Lys
      50              55              60

Ile Lys Gly Val Ile Arg Pro Asn Tyr Asp Thr Ile Tyr Ile Leu Cys
      65              70              75              80

Leu Leu Glu Val Asp Leu Leu Asn Leu Val Phe Thr Asp Asn Ile Leu
      85              90              95

Glu Ile Cys Leu Pro Arg Phe Val Ser Arg Glu Asp Leu Arg Val Phe
      100              105              110

Asn Asn Thr Phe Tyr Thr Tyr His Asp Asn Arg Leu Arg Ile Leu Gln
      115              120              125

Glu Asp Phe Ser Gln Leu Phe Lys Lys Ile Lys Thr Lys Ala Ser Val
      130              135              140

Leu Cys Phe Thr Val Glu Glu Ile Phe Leu Thr Asn Gln Glu Ile Leu
      145              150              155              160

Pro Gln Asn Ser Thr Val Ala Glu Leu Gln Lys Ser Thr Asn Lys Val
      165              170              175

Gln Thr Asn Gly Pro Gln Arg His Asp Phe Ile Val Thr Leu Glu Ile
      180              185              190

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250

Lys Leu Asn Lys Thr Gln Ile Thr Phe Leu Ile Gly Ala Lys Gly Thr  
 195 200 205  
 Arg Ile Glu Ser Leu Arg Glu Lys Ser Gly Ala Ser Ile Lys Ile Ile  
 210 215 220  
 Pro Ile Ser Asp Lys Met Thr Ala His Glu Arg Asn His Pro Glu Ser  
 225 230 235 240  
 Val Gln Gln Thr Ile Leu Ile Ser Gly Asp Leu Tyr Ser Ile Ala Leu  
 245 250 255  
 Ala Val Thr Ser Ile Glu Ser Ala Leu Ile Thr Leu Asp Leu  
 260 265 270

<210> 247  
 <211> 1766  
 <212> DNA  
 <213> Candida albicans

<400> 247  
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 gaccttagaa aaggcattac tgaggctact gactaaagcg cgttacataa atgcatagta 180  
 tatttcttgt tgtatacgca gcggccaact agtggcagca agaatgtaat gaacgattca 240  
 tctgcagggt tggaggccgc aactagatca aaacgtaaat agcgggtgaa gtgttctgga 300  
 cgttagaagt aacgtccgca gatcgaagct aaacacgaga ttagatttcg ggtaacggaa 360  
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 cgaaattagt ggcgagtaca atattgcatt catccataca ctcagtgcc a tctggaggcg 600  
 aaatcatatc tgcagaagat cttaaagaac ttgaaatttc agggaattcg atctgcgttg 660  
 ataatcgttg ctatcctaag atatttgaac caagacacga ttggcagccc atactgccag 720  
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 caaaactaaa tgatgagaag aatgtcgggtg ataatggtag ccatgagtta attgtatctt 840  
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<210> 248  
 <211> 421

251

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 248

Met Val Arg Ile Leu Pro Ile Ile Leu Ser Ala Leu Ser Ser Lys Leu  
 1 5 10 15

Val Ala Ser Thr Ile Leu His Ser Ser Ile His Ser Val Pro Ser Gly  
 20 25 30

Gly Glu Ile Ile Ser Ala Glu Asp Leu Lys Glu Leu Glu Ile Ser Gly  
 35 40 45

Asn Ser Ile Cys Val Asp Asn Arg Cys Tyr Pro Lys Ile Phe Glu Pro  
 50 55 60

Arg His Asp Trp Gln Pro Ile Leu Pro Gly Gln Glu Leu Pro Gly Gly  
 65 70 75 80

Leu Asp Ile Arg Ile Asn Met Asp Thr Gly Leu Lys Glu Ala Lys Leu  
 85 90 95

Asn Asp Glu Lys Asn Val Gly Asp Asn Gly Ser His Glu Leu Ile Val  
 100 105 110

Ser Ser Glu Asp Met Lys Ala Ser Pro Gly Asp Tyr Glu Phe Ser Ser  
 115 120 125

Asp Phe Lys Glu Met Arg Asn Ile Ile Asp Ser Asn Pro Thr Leu Ser  
 130 135 140

Ser Gln Asp Ile Ala Arg Leu Glu Asp Ser Phe Asp Arg Ile Met Glu  
 145 150 155 160

Phe Ala His Asp Tyr Lys His Gly Tyr Lys Ile Ile Thr His Glu Phe  
 165 170 175

Ala Leu Leu Ala Asn Leu Ser Leu Asn Glu Asn Leu Pro Leu Thr Leu  
 180 185 190

Arg Glu Leu Ser Thr Arg Val Ile Thr Ser Cys Leu Arg Asn Asn Pro  
 195 200 205

Pro Val Val Glu Phe Ile Asn Glu Ser Phe Pro Asn Phe Lys Ser Lys  
 210 215 220

Ile Met Ala Ala Leu Ser Asn Leu Asn Asp Ser Asn His Arg Ser Ser  
 225 230 235 240

Asn Ile Leu Ile Lys Arg Tyr Leu Ser Ile Leu Asn Glu Leu Pro Val  
 245 250 255

Thr Ser Glu Asp Leu Pro Ile Tyr Ser Thr Val Val Leu Gln Asn Val  
 260 265 270

Tyr Glu Arg Asn Asn Lys Asp Lys Gln Leu Gln Ile Lys Val Leu Glu  
 275 280 285





253

&lt;400&gt; 250

Met Phe Phe Lys Val Ser Asn Phe Thr Ser Leu Thr Leu Leu Ser Leu  
 1 5 10 15

Ile Pro Ile Val Gly Pro Ile Leu Ala Asn Gln Leu Met Ala Pro Lys  
 20 25 30

Arg Thr Phe Thr Tyr Leu Gln Arg Tyr Phe Leu Leu Lys Gly Phe Ser  
 35 40 45

Lys Lys Gln Ala Lys Asp Phe Gln Tyr Glu His Tyr Ala Ser Phe Ile  
 50 55 60

Cys Phe Gly Met Ser Ala Gly Leu Leu Glu Leu Ile Pro Phe Phe Thr  
 65 70 75 80

Ile Val Thr Ile Ser Ser Asn Thr Val Gly Ala Ala Lys Trp Cys Thr  
 85 90 95

Ser Leu Leu Lys Gly Glu Arg Lys Lys Glu  
 100 105

&lt;210&gt; 251

&lt;211&gt; 1256

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 251

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 aggtcgagg gaatccttga aagccaagag ttttttttcc gtaatgatct cccaaagcaa 240  
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&lt;210&gt; 252

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

<400> 252

Met Ala Tyr Ile Lys Ile Ala Leu Leu Ala Ala Ile Ala Ala Leu Ala  
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 20 25 30  
 Asp Val Lys Ser Asn Leu Gln Glu Tyr Ile Ser Leu Ala Glu Asp Ser  
 35 40 45  
 Ser Ser Gly Phe Ser Leu Ser Ser Leu Pro Ser Gly Val Leu Asp Ile  
 50 55 60  
 Gly Leu Ala Leu Ala Ser Ala Thr Asp Asp Ser Tyr Thr Thr Leu Tyr  
 65 70 75 80  
 Ser Glu Val Asp Phe Ala Ala Val Ser Lys Met Leu Thr Met Val Pro  
 85 90 95  
 Trp Tyr Ser Ser Arg Leu Leu Pro Glu Leu Glu Ser Leu Leu Gly Thr  
 100 105 110  
 Ser Thr Thr Ala Ala Ser Ser Thr Glu Ala Ser Ser Ala Ala Thr Ser  
 115 120 125  
 Ser Ala Val Ala Ser Ser Ser Glu Thr Thr Ser Ser Ala Val Ala Ser  
 130 135 140  
 Ser Ser Glu Ala Thr Ser Ser Ala Val Ala Ser Ser Ser Glu Ala Ser  
 145 150 155 160  
 Ser Ser Ala Ala Thr Ser Ser Ala Val Ala Ser Ser Ser Glu Ala Thr  
 165 170 175  
 Ser Ser Thr Val Ala Ser Ser Thr Lys Ala Ala Ser Ser Thr Lys Ala  
 180 185 190  
 Ser Ser Ser Ala Val Ser Ser Ala Val Ala Ser Ser Thr Lys Ala Ser  
 195 200 205  
 Ala Ile Ser Gln Ile Ser Asp Gly Gln Val Gln Ala Thr Ser Thr Val  
 210 215 220  
 Ser Glu Gln Thr Glu Asn Gly Ala Ala Lys Ala Val Ile Gly Met Gly  
 225 230 235 240  
 Ala Gly Val Met Ala Ala Ala Ala Met Leu Leu  
 245 250

<210> 253

<211> 2693

<212> DNA

<213> Candida albicans

&lt;400&gt; 253

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&lt;210&gt; 254

&lt;211&gt; 730

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 254

Met Ile Ser Val Cys Pro Gln Asn Asp Leu Gln Lys Cys Tyr Arg Ser  
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Leu	Thr	Phe	Asp	Val	Pro	Gly	Gln	Phe	Glu	Glu	Arg	Asn	Glu	Gln	
			20					25					30		
Asn	Leu	Lys	Lys	Arg	Ala	Lys	Lys	Lys	Gly	Ser	Phe	Gln	Pro	Ser	Val
		35					40					45			
Ala	Phe	Asp	Thr	Val	Pro	Ser	Thr	Ala	Gly	Tyr	Ser	Ser	Ile	Asp	Asp
	50					55					60				
Ser	Arg	Glu	Gly	Phe	Lys	Gly	Val	Pro	Val	Pro	Asn	Tyr	Tyr	Thr	Met
	65				70					75					80
Glu	Glu	Cys	Tyr	Asp	Asp	Glu	Thr	Asp	Ser	Phe	Ser	Pro	Asn	Leu	Gln
				85					90					95	
Tyr	Tyr	Leu	Arg	Asp	Thr	Phe	Gln	Ser	Ser	Pro	Phe	Leu	Asn	Thr	Arg
			100				105						110		
Lys	Glu	Asn	Lys	Ser	Glu	Ser	Ser	Ser	Phe	Pro	Met	Arg	Ser	Ser	Lys
		115					120					125			
Leu	Leu	Glu	Lys	Asn	Ser	Asp	Ile	Lys	Lys	Tyr	Phe	Leu	Val	Ser	Lys
	130					135					140				
Asn	Gly	Lys	Ile	Val	Arg	Arg	Asp	Tyr	Pro	Ser	Thr	Pro	Val	Ile	Val
145					150					155					160
Asn	Glu	Thr	Leu	Met	Ile	Asn	Arg	Phe	Glu	Lys	Asn	Trp	Ile	Lys	Leu
				165					170					175	
Trp	Arg	Gln	Arg	Lys	Leu	Gln	Ile	Asn	Glu	Arg	Leu	Asn	Asp	Lys	Lys
			180					185					190		
Lys	Trp	Phe	Thr	Tyr	Pro	Glu	Leu	Ile	Phe	Ser	Glu	Glu	Arg	Ile	Lys
		195					200					205			
Pro	Leu	Tyr	Arg	Gly	Asp	Asp	Ser	Ala	Pro	Cys	Thr	Lys	Glu	Gln	Lys
	210					215					220				
Arg	Lys	His	Lys	Ile	Leu	Gln	Gln	Lys	Val	Gly	Tyr	Pro	Asn	Asn	Pro
225					230					235					240
Lys	Thr	Ile	Val	Cys	His	Ile	Asn	Gly	Lys	Lys	His	Thr	Trp	Val	Ala
				245					250					255	
Leu	Asp	Trp	Thr	Val	Tyr	Lys	Phe	Ala	Arg	Asn	Leu	Asp	His	Ile	Val
			260					265					270		
Val	Ile	Thr	Thr	Leu	Pro	Lys	Met	Ile	Ser	Asn	Arg	Lys	Lys	Thr	Ala
		275					280					285			
Lys	Asp	Asp	Thr	Glu	Trp	Ala	Pro	Gly	Tyr	Gln	Lys	Glu	Val	Ile	Asp
	290					295					300				
Gln	Lys	Leu	Asn	Asp	Ile	Phe	Asp	Tyr	Ile	Leu	Gln	Leu	Val	Lys	Val
305					310						315				320

Val Lys Ile Ser Val Lys Ile Thr Leu Glu Ile Ile Val Gly Lys Ile  
 325 330 335  
 Lys Lys Ser Leu Val Asp Val Ile Asn Val His Thr Pro Asp Phe Leu  
 340 345 350  
 Val Leu Ala Thr Leu Lys His Glu Arg Asn Glu Asn Leu Ile Thr Tyr  
 355 360 365  
 Lys Ser Lys Lys Leu Thr Asp Val Phe Pro Val Ser Tyr Pro Ile Pro  
 370 375 380  
 Thr Phe Val Val Pro Ser Lys Arg Met Tyr Ser Phe Glu Leu Asn Leu  
 385 390 395 400  
 Gln Arg Glu Val Asn Glu His Tyr Val Ser Lys Asn His Met Lys His  
 405 410 415  
 Glu His Thr Asp Val Glu Ser Met Ser Ser Ser Met Phe Lys Lys Asn  
 420 425 430  
 Thr Ile Ser Asp Ile Ser Ser His Ile Ser Val Asp Ser Tyr Ala Glu  
 435 440 445  
 Asp Phe Lys Arg Gln Gly Tyr Ile Lys Lys Gln Phe Asn Thr Ser Asn  
 450 455 460  
 Asp Ser Ile Pro Arg Lys Leu Thr Gly Leu Ala Gln His Ser Arg Arg  
 465 470 475 480  
 Lys Ile Thr Gly Asp Ile Glu Lys Leu Gln Asp Asp Glu Lys Asp Arg  
 485 490 495  
 Glu Cys Thr Lys Glu Lys Leu Leu Leu Lys Lys Ile Asp Ile Ile Ile  
 500 505 510  
 Arg Glu Ser Leu Lys Ser Ser Leu Ala Ile Glu Thr Leu Pro Gly Lys  
 515 520 525  
 Asn Val Ser Gln Ser Ser His Gly Asp Gln Ile Ser Ser Phe Lys Asn  
 530 535 540  
 Ala Leu Ile Gly Asn Gly Ser Lys Asn Thr Lys Phe Arg Lys Ser Leu  
 545 550 555 560  
 Ile Pro Tyr Ser Ser Ser Glu Glu Gln Asn Thr Thr Thr Thr Ile Lys  
 565 570 575  
 Leu Ser Ser Ser Pro Thr Ser Gln Ile Lys Phe Ala Thr Ser Val Lys  
 580 585 590  
 His Lys Asp Gly Arg Ala Ala Leu Gly Lys Ala Arg Asn Leu Pro Asp  
 595 600 605  
 Ile Arg His Ser Ile Ser Phe Asp Lys Glu Asn Ser Phe Asp Pro Ser  
 610 615 620

Asp Lys Ser Ser Ser Val Asp Asn Ser Ile Pro Leu Arg Lys Val Lys  
 625 630 635 640  
 Ser Ala Gly Ala Leu Arg Lys Val Lys Thr Asn Asp Ser Ser Ser Ser  
 645 650 655  
 Ala Gly Ser Lys Lys Ser Ser Ser Ser Phe Ser Thr Val Asn Thr Phe  
 660 665 670  
 Thr Gly Gly Gly Val Gly Ile Phe Lys Val Phe Lys Ser Gly Ser Ser  
 675 680 685  
 Ser Gly Asn Lys Ser Ser Ser Arg Arg Asn Ser Ser Ser Gly Asp Val  
 690 695 700  
 Phe Glu Ser Asp Asp Arg Asn Asp Lys Lys Lys Lys Lys Lys Lys Lys  
 705 710 715 720  
 Lys Lys Ser Leu Phe Leu Phe Gly Lys Ile  
 725 730

&lt;210&gt; 255

&lt;211&gt; 2270

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 255

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<210> 256

<211> 589

&lt;212&gt; PRT

<213> Candida albicans

<400> 256

Met Ser Leu Thr Ala Asp Glu Tyr Lys Gln Gln Gly Asn Ala Ala Phe  
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Thr Ala Lys Asp Tyr Asp Lys Ala Ile Glu Leu Phe Thr Lys Ala Ile  
20 25 30

Glu Val Ser Glu Thr Pro Asn His Val Leu Tyr Ser Asn Arg Ser Ala  
35 40 45

Cys Tyr Thr Ser Leu Lys Lys Phe Ser Asp Ala Leu Asn Asp Ala Asn  
50 55 60

Glu Cys Val Lys Ile Asn Pro Ser Trp Ser Lys Gly Tyr Asn Arg Leu  
65 70 75 80

Gly Ala Ala His Leu Gly Leu Gly Asp Leu Asp Glu Ala Glu Ser Asn  
85 90 95

Tyr Lys Lys Ala Leu Glu Leu Asp Ala Ser Asn Lys Ala Ala Lys Glu  
100 105 110

Gly Leu Asp Gln Val His Arg Thr Gln Gln Ala Arg Gln Ala Gln Pro  
115 120 125

Asp Leu Gly Leu Thr Gln Leu Phe Ala Asp Pro Asn Leu Ile Glu Asn  
130 135 140

Leu Lys Lys Asn Pro Lys Thr Ser Glu Met Met Lys Asp Pro Gln Leu  
145 150 155 160

Val Ala Lys Leu Ile Gly Tyr Lys Gln Asn Pro Gln Ala Ile Gly Gln  
165 170 175

Asp Leu Phe Thr Asp Pro Arg Leu Met Thr Ile Met Ala Thr Leu Met  
180 185 190

Gly Val Asp Leu Asn Met Asp Asp Ile Asn Gln Ser Asn Ser Met Pro  
195 200 205





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<400> 258
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Cys Lys Cys Asp His Ser Thr Gly Ser Pro Gln Cys Lys Ser Cys Gly
      35                40                45
Glu Lys Cys Lys Cys Glu Thr Thr Cys Thr Cys Glu Lys Ser Lys Cys
  50                55                60
Asn Cys Glu Lys Cys
  65

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Leu Glu Lys Lys Phe Gln Asp Arg His Val Ile Phe Leu Ala Glu Arg  
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 Arg Ile Leu Pro Lys Pro Ser Arg Thr Ser Arg Gln Val Gln Lys Arg  
                     100                    105                    110  
 Pro Arg Ser Arg Thr Leu Thr Ala Val His Asp Lys Ile Leu Glu Asp  
                     115                    120                    125  
 Leu Val Phe Pro Thr Glu Ile Val Gly Lys Arg Val Arg Tyr Leu Val  
                     130                    135                    140  
 Gly Gly Asn Lys Ile Gln Lys Val Leu Leu Asp Ser Lys Asp Val Gln  
                     145                    150                    155                    160  
 Gln Ile Asp Tyr Lys Leu Glu Ser Phe Gln Ala Val Tyr Asn Lys Leu  
                     165                    170                    175  
 Thr Gly Lys Gln Ile Val Phe Glu Ile Pro Ser Glu Thr His  
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 <211> 803  
 <212> DNA  
 <213> Candida albicans

<400> 261  
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 <213> Candida albicans

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265

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 Leu Thr Ser Lys Gly Tyr Val Lys Thr Gln Phe Ser Trp Gln Tyr Tyr  
           50                          55                          60  
 Tyr Tyr Thr Leu Thr Glu Glu Gly Val Glu Tyr Leu Arg Glu Tyr Leu  
           65                          70                          75                          80  
 Asn Leu Pro Glu His Ile Val Pro Gly Thr Tyr Ile Gln Glu Arg Asn  
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 Pro Thr Gln Arg Pro Gln Arg Arg Tyr  
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 <213> Candida albicans

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&lt;210&gt; 272

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 272

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Gly Gln Glu Val Asp Gly Glu Ala Val Gly Asp Glu Phe Lys Gly Tyr
      35              40              45

Val Phe Lys Ile Ser Gly Gly Asn Asp Lys Gln Gly Phe Pro Met Lys
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Gln Gly Val Leu Leu Pro Thr Arg Ile Lys Leu Leu Leu Thr Lys Asn
      65              70              75              80

Val Ser Cys Tyr Arg Pro Arg Arg Asp Gly Glu Arg Lys Arg Lys Ser
      85              90              95

Val Arg Gly Ala Ile Val Gly Pro Asp Leu Ala Val Leu Ala Leu Val
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Ile Val Lys Lys Gly Glu Gln Glu Leu Glu Gly Leu Thr Asp Thr Thr
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Val Pro Lys Arg Leu Gly Pro Lys Arg Ala Asn Asn Ile Arg Lys Phe
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Phe Gly Leu Ser Lys Glu Asp Asp Val Arg Asp Phe Val Ile Arg Arg
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Glu Val Thr Lys Gly Glu Lys Thr Tyr Thr Lys Ala Pro Lys Ile Gln
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Arg Leu Val Thr Pro Gln Arg Leu Gln Arg Lys Arg His Gln Arg Ala
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Leu Lys Val Arg Asn Ala Gln Ala Gln Arg Glu Ala Ala Ala Glu Tyr
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Ala Gln Leu Leu Ala Lys Arg Leu Ser Glu Arg Lys Ala Glu Lys Ala
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Glu Ile Arg Lys Arg Arg Ala Ser Ser Leu Lys Ala

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<212> PRT

<213> Candida albicans

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Ser Lys Arg Lys Lys Gly Ser Lys Lys Ala Ala Tyr His Arg Gln Pro  
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Ser Pro Trp Ile Ser Ser Ala Thr Gly Leu Glu Phe Phe Ser Glu Trp  
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Glu Asn Ile Pro Ser Glu Leu Leu Lys Asn Leu Lys Pro Phe His Pro  
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Pro Lys Glu Lys Ser Met Asn Thr Asn Glu Leu Ile His Val Ser Ala  
195 200 205

Lys Arg Asn Thr Leu Val Asp Asn Lys Thr Ser Glu Thr Leu Gln Arg  
210 215 220

Lys Met Asp Glu Phe Ser Lys Arg Arg Gly Lys Gly Arg Lys Lys Ser  
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Val Val Thr Leu Leu Gln Met Lys Lys Lys Leu Glu Gly  
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<212> DNA

<213> Candida albicans

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agacatccgt ttctgacctt gttcaagcaa caaataaagc tatcaatata ataagaagta 1620  
aagcttttga cacttctctt tttcatgata gcgtgtctaa aatgtacgac tggatggagc 1680  
tagccaaaag gacagtagag atatatacta atatattctc tacttcttcc gctgatgata 1740  
aagattggat gaaaatggta gcaaatcttt acaaaagaga tggaaatctgg gctaaacatc 1800  
tttatctggt atgtggaatt gtagagtaca tgcttttttt cctcttagag tggctatacc 1860



279

Phe Gln Gln Met Ile Glu Ser His Arg Leu Gln Lys Arg Val Gln Leu  
 260 265 270  
 Leu Gly Ser Val Pro His Glu Lys Val Arg Asp Val Leu Cys Gln Gly  
 275 280 285  
 Asp Ile Tyr Leu His Ala Ser Leu Thr Glu Ala Phe Gly Thr Ile Leu  
 290 295 300  
 Val Glu Ala Ala Ser Cys Asn Leu Leu Ile Val Thr Thr Gln Val Gly  
 305 310 315 320  
 Gly Ile Pro Glu Val Leu Pro Asn Glu Met Thr Val Tyr Ala Glu Gln  
 325 330 335  
 Thr Ser Val Ser Asp Leu Val Gln Ala Thr Asn Lys Ala Ile Asn Ile  
 340 345 350  
 Ile Arg Ser Lys Ala Leu Asp Thr Ser Ser Phe His Asp Ser Val Ser  
 355 360 365  
 Lys Met Tyr Asp Trp Met Asp Val Ala Lys Arg Thr Val Glu Ile Tyr  
 370 375 380  
 Thr Asn Ile Ser Ser Thr Ser Ser Ala Asp Asp Lys Asp Trp Met Lys  
 385 390 395 400  
 Met Val Ala Asn Leu Tyr Lys Arg Asp Gly Ile Trp Ala Lys His Leu  
 405 410 415  
 Tyr Leu Leu Cys Gly Ile Val Glu Tyr Met Leu Phe Phe Leu Leu Glu  
 420 425 430  
 Trp Leu Tyr Pro Arg Asp Glu Ile Asp Leu Ala Pro Lys Trp Pro Lys  
 435 440 445  
 Lys Thr Val Ser Asn Glu Thr Lys Glu Ala Arg Glu Thr  
 450 455 460

&lt;210&gt; 279

&lt;211&gt; 2900

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 279

ctcaatggga attgagtga gatcagtcctg atcgagagga atttgtacga ttcgtggaaa 60  
 accagcattt cgtagaaaaa gttgatacga tttacaacgg ttataatgaa agtctatcaa 120  
 tgatggacga cctgactaga gagttactac tatgggagaa aaaatattca aataacacta 180  
 atgccattca ataaacgcaa aacactgcaa tattattctc aaccaaagta taactgtaat 240  
 gaggcgaaca aacacatcta tacatatata tacatctata tggatataaa aacgactaat 300  
 tcaacgttgt ttttatcaac cgagcttact cttgtacggg taaccgcaag gatagctagt 360  
 tgcggatggt atagcgattt ggctggcacg atgattaagg aatccaaaca tctaattggac 420  
 tagcacattc tatcgattta cgggtcaggt aaacatagat attgggatat atcatatatc 480  
 cttactgagt aactataatt atggttcatc gaggaaggac tttgaagtca gacactgatg 540









<400> 282																
Met	Ala	Gly	Trp	Asp	Ile	Phe	Gly	Trp	Phe	Arg	Asp	Val	Leu	Ala	Ser	
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Leu	Gly	Leu	Trp	Asn	Lys	His	Gly	Lys	Leu	Leu	Phe	Leu	Gly	Leu	Asp	
			20					25					30			
Asn	Ala	Gly	Lys	Thr	Thr	Leu	Leu	His	Met	Leu	Lys	Asn	Asp	Arg	Leu	
		35					40					45				
Ala	Thr	Leu	Gln	Pro	Thr	Trp	His	Pro	Thr	Ser	Glu	Glu	Leu	Ala	Ile	
	50					55					60					
Gly	Asn	Ile	Lys	Phe	Thr	Thr	Phe	Asp	Leu	Gly	Gly	His	Ile	Gln	Ala	
65					70					75					80	
Arg	Arg	Leu	Trp	Lys	Asp	Tyr	Phe	Pro	Glu	Val	Asn	Gly	Ile	Val	Phe	
				85					90					95		
Leu	Val	Asp	Ala	Ala	Asp	Pro	Glu	Arg	Phe	Asp	Glu	Ala	Arg	Val	Glu	
			100					105					110			
Leu	Asp	Ala	Leu	Phe	Asn	Ile	Ala	Glu	Leu	Lys	Asp	Val	Pro	Phe	Val	
		115					120					125				
Ile	Leu	Gly	Asn	Lys	Ile	Asp	Ala	Pro	Asn	Ala	Val	Ser	Glu	Ala	Glu	
	130					135					140					
Leu	Arg	Ser	Ala	Leu	Gly	Leu	Leu	Asn	Thr	Thr	Gly	Ser	Gln	Arg	Ile	
145					150					155					160	
Glu	Gly	Gln	Arg	Pro	Val	Glu	Val	Phe	Met	Cys	Ser	Val	Val	Met	Arg	
				165					170					175		
Asn	Gly	Tyr	Leu	Glu	Ala	Phe	Gln	Trp	Leu	Ser	Gln	Tyr	Ile			
			180					185					190			

<400>	283						
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gctgttttcc	ctcatatcac	ataatacccg	gagaggctct	ttcctgcgac	agcgcaacat	120	
ccaaccatcc	taaaggtatg	ggtgtactga	cgatgcgatt	atttcattaa	gttctgtctt	180	
ttttgtataa	atgaaaaaag	aacggtgaaa	tccatagaaa	tacagagagc	gacgcaaaca	240	
gcgcgcagac	tctacgggta	atagactcac	atccacgtga	ccagtttcca	atcgaacttt	300	
ttcagtttgc	agggaatttat	tgttttacta	gcaaaggtag	cccacttacc	atcgaqctat	360	



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<210> 284
<211> 174
<212> PRT
<213> Candida albicans
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$\langle 210 \rangle$	285
$\langle 211 \rangle$	1229

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 285

```

agagaacgta ttgaagagga gaaaagggag aaaagaggtc aattggaaga acaacatcgt 60
tctgcatcaa atgcttctat ggcttcttta ttgtcagctg cttcaactac agcagcaact 120
aaaaatttga gtgtggctgg cacaaatcct tctcatacca ctgaaagaat gtttttaaat 180
ttacctttta acaattccct gttcaatgcc ccaccagtag aaattaattt taatgatctt 240
gaagttttgg aattgtacac tcaattagta ttataccgag atgatattac caaatctact 300
tttgaattag ctatatcacc agcaaatttg aatatttctc aacggaaaat catatcaatt 360
ttatgtaatt atttgaattt attagaattg tttgataatg gggtgataat aattagaaga 420
aaaccaggat acattgctca gtgtataact caacaatcta ttattcctaa ttctcaacag 480
gtgtctgggc caactcacc gcaacaacat caacagaatc aacttcaaca acagcaacag 540
caacaacatc aacatcaaca tccttcacat tcatcatcga tgatgaacct tcatcaattg 600
gggtggtacat tagctgttcc agcgcacctt gaattattaa gatcccaatc gcaatcagca 660
ttaccgttgc caagattgag acagcaaacc tctacaccaa ttcaacaaaa tcaacaagtt 720
cagcaccaaa atcaaccacc acaacaacaa cagcaacagc atgttcaacc acaatataat 780
tattacaatc agcaatctat tcaaagccaa ccacattctg cgagacctta ttctcaatca 840
tataatattt atcaacaaca acagcaacag cagcaacaac aagctcaaca acaagctcaa 900
caacaacaac aacaacaatt acaatatcaa cagggacacc agtcacaagt ttcaaacact 960
acattgaatt cttctagtgc tgctgcatta cttagatcaa gtagcagtag atcatttgtt 1020
gatgtgagat ccacacctcc cacaagtagt tttgctcaac agcaacaaca acaacaacaa 1080
caacagcaac agccgccact aacttcatca atccatgatt ctccaacacc acatcatcat 1140
ttaccacttc aacagcagcc accacaacca aatcattacc tatccaatta ccatcagggg 1200
gttgatctc aacaaaaaac tccattggc 1229

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&lt;210&gt; 286

&lt;211&gt; 409

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 286

```

Arg Glu Arg Ile Glu Glu Glu Lys Arg Glu Lys Arg Gly Gln Leu Glu
 1             5             10             15

Glu Gln His Arg Ser Ala Ser Asn Ala Ser Met Ala Ser Leu Leu Ser
          20             25             30

Ala Ala Ser Thr Thr Ala Ala Thr Lys Asn Leu Ser Val Ala Gly Thr
          35             40             45

Asn Pro Ser His Thr Thr Glu Arg Met Phe Leu Asn Leu Pro Phe Asn
          50             55             60

Asn Ser Ser Phe Asn Ala Pro Pro Val Glu Ile Asn Phe Asn Asp Leu
          65             70             75             80

Glu Val Leu Glu Leu Tyr Thr Gln Leu Val Leu Tyr Arg Asp Asp Ile
          85             90             95

Thr Lys Ser Thr Phe Glu Leu Ala Ile Ser Pro Ala Asn Leu Asn Ile
          100            105            110

Ser Gln Arg Lys Ile Ile Ser Ile Leu Cys Asn Tyr Leu Asn Leu Leu
          115            120            125

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<210> 287



Asn	Thr	Asn	Asn	Asn	Ser	Ser	Gly	Asn	Ser	Asn	Asn	Thr	His	Gly	
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Asn	Asn	Thr	Pro	Lys	Leu	Ser	Thr	Gln	Arg	Leu	Thr	Asn	Asn	Arg	Asn
65					70					75					80
Leu	Gln	Ser	Leu	Trp	Ile	Asn	Gln	Pro	Ser	Ile	Ala	Pro	Ser	Asn	Val
				85					90					95	
Val	Pro	Trp	Val	Glu	Gln	Gln	Gln	Gln	Gln	Thr	Leu	Asp	Ser	Leu	Glu
			100					105					110		
Asn	Asn	Thr	Lys	Thr	Asp	Ser	Ser	Asn	Asp	Ala	Ser	Ala	Thr	Asn	Asn
		115					120					125			
Asn	Asn	Val	Asn	Val	Asn	Val	Asn	Ala	Asn	Ala	Asn	Val	Asn	Ala	Asn
		130				135					140				
Ala	Asn	Ile	His	Ala	Gln	Thr	His	Val	Asn	Thr	Asn	Val	Asn	Ala	Asn
145					150					155					160
Thr	Thr	Ala	Thr	Ser	Ile	Asn	Ala	Ser	Thr	Ile	Leu	Asn	Thr	Thr	Pro
				165					170					175	
Ser	Ile	Asn	Asp	Thr	Asn	Asp	Asn	Ala	Lys	Lys	Ile	Asn	Val	Ser	Met
			180					185					190		
Ile	Ser	Asn	Asn	Asn	Asn	Asn	Asn	Ser	Asn	Asn	Asn	Asn	Asn	Asn	Thr
		195					200					205			
Asn	Asn	Ser	Ser	Thr	Gly	Ser	Ser	Asn	Ile	Ala	Asn	Met	Leu	Pro	Ser
		210				215					220				
Val	Ser	Asn	Ala	Thr	Thr	Met	Asn	Asn	Ser	Asn	Ser	Ile	Asn	Ser	Thr
225					230					235					240
Thr	Asn	Asn	Thr	Thr	Ile	Asn	Glu	Ala	Asp	Asp	Asp	Glu	Leu	Ile	Pro
				245					250					255	
Thr	Ala	Ile	Val	Ile	Lys	Asn	Ile	Pro	Phe	Ala	Ile	Lys	Lys	Glu	Gln
			260					265					270		
Leu	Leu	Asp	Val	Met	Thr	Lys	Leu	Asn	Leu	Pro	Leu	Pro	Tyr	Ala	Phe
		275					280				285				
Asn	Tyr	His	Phe	Asp	Asn	Gly	Val	Phe	Arg	Gly	Leu	Ala	Phe	Ala	Asn
		290				295					300				
Phe	Thr	Ser	Thr	Asp	Glu	Thr	Ser	Ala	Val	Val	Asn	Gln	Leu	Asn	Gly
305					310					315					320
Arg	Glu	Ile	Gly	Gly	Arg	Lys	Leu	Arg	Val	Glu	Tyr	Lys	Lys	Met	Leu
				325					330					335	
Pro	Ala	Gln	Glu	Arg	Glu	Arg	Ile	Glu	Arg	Glu	Lys	Arg	Glu	Lys	Arg
			340					345					350		

Gly Gln Leu Glu Glu Gln His Arg Ser Ala Ser Asn Ala Ser Leu Ala  
 355 360 365  
 Ser Leu Leu Ser Ala Ala Ser Thr Thr Ala Ala Thr Lys Asn Leu Ser  
 370 375 380  
 Val Ala Gly Thr Asn Pro Ser His Thr Thr Glu Arg Met Phe Leu Asn  
 385 390 395 400  
 Leu Pro Phe Asn Asn Ser Ser Phe Asn Ala Pro Pro Val Glu Ile Asn  
 405 410 415  
 Phe Asn Asp Leu Glu Val Leu Glu Leu Tyr Thr Gln Leu Val Leu Tyr  
 420 425 430  
 Arg Asp Asp Ile Thr Lys Ser Thr Phe Glu Leu Ala Ile Ser Pro Ser  
 435 440 445  
 Ile Phe Glu Tyr Phe Ser Thr Glu Asn His Ile Asn Leu Cys Asn Tyr  
 450 455 460  
 Leu Asn Leu Leu Glu Leu Phe Asp Asn Gly Leu Leu Leu Ile Arg Lys  
 465 470 475 480  
 Lys Pro Gly Ser Ile Ala Gln Cys Ile Thr Gln Lys Ser Ile Ile Pro  
 485 490 495  
 Asn Ser Gln Gln Val Ser Gly Pro Thr His Pro His His His Gln Lys  
 500 505 510  
 Asn Gln Leu His Gln Gln Gln Gln Gln His Thr Ser Thr Ser Thr Ser  
 515 520 525  
 Leu Thr Phe Ile Ile Asp Asp Glu Pro Ser Ser Ile Gly Trp Tyr Ile  
 530 535 540  
 Ser Cys Ser Ser Ala Pro  
 545 550

&lt;210&gt; 289

&lt;211&gt; 3254

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 289

ataaaaaaag aaatacaatt aaaaaaatTT tccttctgtg aaaaggcaat ttcgggtcta 60  
 gtagtaaaca aagcttaata atttctccca ttcaaattta caacggacga tgcagaaagt 120  
 agttttcaaa ttcagtttct tttcttttat atatttttct ttactttctc ttcctttctt 180  
 cctgacagta tattaataaa tattcttttt aacttatttt tcaatcaaga aggtactgaa 240  
 gatatcaatt aactctcagt taaatccata ttaccagttg tggaataatc agaagaaaaa 300  
 aaaaaaagag agaaaaatca cggaattac gttctcaaca gaaaataaca ataatttttt 360  
 tttattcatt ccaaggtata acaagaacgt taggaataat ataaaattat caccaaagct 420  
 gccatcaacg tgtgtcgaca accaatcgac tctccctta actagaacca tagaacctca 480  
 acatttgttt ctatagaaaa atgaagtttg aaaaaggtaa agtgagaatt ttgcctaaac 540

<400> 290  
Met Lys Phe Glu Lys Gly Lys Val Arg Ile Leu Pro Lys Pro Ser Pro  
1 5 10 15

Thr Pro Thr Asn Pro Gln Thr Pro Leu Pro Leu Leu Pro Ala Gln Thr  
 20 25 30  
 Lys Pro Val Asn Ser Lys Arg Lys Ser Ala Ala Ser Thr Pro Gly Asn  
 35 40 45  
 Glu Ser Lys Lys Ser Arg Lys Ser Asn Ser Thr Ala Ser Thr Pro Asn  
 50 55 60  
 Ser Ala Thr Pro Thr Ser Val Gly Thr Pro Pro Gln Lys Thr Ser Lys  
 65 70 75 80  
 Pro Thr Gly His Arg Pro Val Thr Ser Cys Thr Phe Cys Arg Gln His  
 85 90 95  
 Lys Ile Lys Cys Asn Ala Ser Asp Asn Tyr Pro Asn Pro Cys Glu Arg  
 100 105 110  
 Cys Lys Lys Met Gly Leu Lys Cys Glu Ile Asp Pro Glu Phe Arg Pro  
 115 120 125  
 Arg Lys Gly Ser Gln Ile Gln Ser Leu Lys Ser Asp Val Asp Glu Leu  
 130 135 140  
 Lys Ala Lys Ile Glu Met Leu Thr Lys Asn Glu Ser Leu Leu Thr Gln  
 145 150 155 160  
 Ala Leu Asn Gln His Asn Leu Asn His Ala Ser Gln Gln Gln Gln Ser  
 165 170 175  
 Ser Gly Ser Gln Ser Gln Gln Gln His Pro Pro Asn Pro Gln Arg Ala  
 180 185 190  
 Leu Ser Tyr Thr Ser Ala Asn Ser Ser Pro Gln Val Ala Phe Ser Asn  
 195 200 205  
 Ala Ser Pro Ile Pro Ser Val Thr Ser Ile Gln Gln Asn Ala Pro Leu  
 210 215 220  
 Thr His Glu Asn Ser Asp Asn Ser Pro Tyr Ala Leu Asn Thr Pro Glu  
 225 230 235 240  
 Asn Ile Glu Glu Leu Gln Pro Ile Ser Glu Phe Ile Leu Gly Asp Val  
 245 250 255  
 Thr Leu Pro Leu Asn Arg Ala Asn Glu Leu His Asp Lys Phe Met Thr  
 260 265 270  
 Thr His Leu Pro Phe Leu Pro Ile Ile Ile Ser Arg Ser Ala Thr Glu  
 275 280 285  
 Leu Tyr His Lys Ser Gln Leu Leu Phe Trp Ala Val Ile Leu Thr Ala  
 290 295 300  
 Ser Leu Ser Glu Pro Glu Pro Lys Leu Tyr Met Ser Leu Ala Ser Leu  
 305 310 315 320



Ile Lys Gln Leu Ala Ile Glu Thr Cys Trp Ile Lys Thr Pro Arg Ser  
 325 330 335  
 Thr His Val Ile Gln Ala Leu Ile Ile Leu Ser Ile Trp Pro Leu Pro  
 340 345 350  
 Asn Glu Lys Val Leu Asp Asp Cys Ser Tyr Arg Phe Val Gly Leu Ala  
 355 360 365  
 Lys Asn Leu Ser Leu Gln Leu Gly Leu His Arg Gly Gly Glu Phe Ile  
 370 375 380  
 Gln Glu Phe Ser Arg Asn Gln Val Ser Leu Gly Pro Asp Ala Glu Arg  
 385 390 395 400  
 Trp Arg Thr Arg Ser Trp Leu Ala Val Phe Phe Cys Glu Gln Phe Trp  
 405 410 415  
 Ser Ser Leu Leu Gly Leu Pro Pro Ser Ile Asn Thr Thr Asp Tyr Leu  
 420 425 430  
 Leu Glu Asn Ala Arg Val Asp Lys Ser Leu Pro Lys Asn Phe Arg Cys  
 435 440 445  
 Leu Ile Ser Leu Ser Ile Phe Gln Cys Lys Leu Val Asn Ile Met Gly  
 450 455 460  
 Ile Ser Val Thr Arg Pro Asp Gly Leu Leu Glu Pro Ser Asn Arg Ala  
 465 470 475 480  
 Gly Ser Leu Ser Leu Leu Asp Arg Glu Leu Glu Arg Leu Arg Phe Lys  
 485 490 495  
 Leu Gln Phe Glu Glu Gly Gly Pro Ile Glu Val Tyr Tyr Leu Tyr Ile  
 500 505 510  
 Lys Leu Met Ile Cys Cys Phe Ala Phe Leu Pro Gly Thr Pro Ile Glu  
 515 520 525  
 Asp Gln Val Lys Tyr Val Ser Phe Ala Tyr Leu Ser Ala Thr Arg Ile  
 530 535 540  
 Val Thr Ile Val Ser Lys Met Val Asn Asp Ile Ser Leu Ile Glu Leu  
 545 550 555 560  
 Pro Ile Tyr Ile Arg Gln Ala Val Thr Tyr Ser Val Phe Met Leu Phe  
 565 570 575  
 Lys Leu His Leu Ser Arg Tyr Leu Ile Asp Lys Tyr Val Asp Ser Ala  
 580 585 590  
 Arg Gln Ser Ile Val Thr Val His Arg Leu Phe Arg Asn Thr Leu Ser  
 595 600 605  
 Ser Trp Lys Asp Leu Gln Asn Asp Ile Ser Arg Thr Ala Lys Val Leu  
 610 615 620

Glu	Asn	Leu	Asn	Met	Val	Leu	Tyr	Asn	Tyr	Pro	Glu	Ile	Phe	Leu	Asn	625	630	635	640
Asp	Ser	Glu	Asn	Glu	Asp	Ser	Ser	Ile	Ile	Thr	Arg	Met	Arg	Ser	His	645	650	655	
Leu	Thr	Ala	Ser	Leu	Phe	Tyr	Asp	Leu	Val	Trp	Cys	Val	His	Glu	Ala	660	665	670	
Arg	Arg	Arg	Ser	Val	Leu	Asp	Lys	Gly	Lys	Arg	Gln	Ala	Gln	Pro	Asn	675	680	685	
Lys	Lys	Ile	Leu	Pro	Leu	Pro	Phe	Tyr	Asn	Gln	Ile	Thr	Lys	Asp	Asp	690	695	700	
Phe	Lys	Thr	Ile	Thr	Thr	Thr	Ser	Pro	Asn	Gly	Thr	Thr	Ile	Thr	Thr	705	710	715	720
Leu	Val	Pro	Thr	Asp	Gln	Ala	Met	Asn	Gln	Ala	Lys	Ser	Lys	Ser	Phe	725	730	735	
Asp	Ser	Ser	Lys	Pro	Leu	Glu	Ile	Asn	Gly	Ile	Pro	Leu	Pro	Met	Leu	740	745	750	
Glu	Ala	Thr	Gly	Ser	Thr	Arg	Glu	Val	Leu	Asp	Ser	Leu	Pro	Ser	Gln	755	760	765	
Ser	Leu	Pro	Ser	Gln	Ala	Pro	Thr	Leu	Gln	Gln	Tyr	Pro	Met	Gln	Gln	770	775	780	
Asp	Gln	Gln	Gln	Gln	Glu	Pro	Ser	Gln	Gln	Gln	Gln	Gln	Lys	His	Ser	785	790	795	800
Gln	Gln	Ser	Gln	Gln	Tyr	Gln	Gln	Gln	Gln	Gln	Ser	Asn	Gln	Gln	Gln	805	810	815	
Pro	His	Leu	Gln	His	Gln	Arg	Gln	Phe	Gln	Gln	Ser	Pro	Pro	Pro	Gln	820	825	830	
Phe	Ser	Met	Ile	Ser	Ser	Thr	Pro	Pro	Leu	Gln	Gln	Pro	Pro	Phe	Ile	835	840	845	
Leu	Ala	Asn	Ser	Pro	Leu	Pro	Gln	Thr	Tyr	Leu	Pro	Lys	Ile	Asp	Glu	850	855	860	
Met	Asn	Met	Ser	Pro	Glu	Val	Lys	Gln	Glu	Asn	Ser	Val	Ala	Pro	Phe	865	870	875	880
Ala	Ser	Gln	Ile	Thr	Asn	Phe	Phe	Asp	Gln	Gln	Thr	Ser	Gly	Trp	Phe	885	890	895	
Asn	Asn	Asp	Asn	Gln	Asp	Asp	Asp	Phe	Leu	Gly	Trp	Phe	Asp	Val	Asn	900	905	910	
Met	Met	Gln	Glu	Lys												915			

<210> 291  
 <211> 908  
 <212> DNA  
 <213> Candida albicans

<400> 291  
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 taactactaa accttttttt ttattttatt attttgtatt ttgttatatt aatcaaacta 180  
 ttatcattca tctatatata catccccatc gattcatctg acataatagt atgtatgatc 240  
 atacagaggg aaaatcaccc tttttattat taccaagggtc tcaatgatta gtgtggctag 300  
 cgtctgttac tacttacccc gtgtttgtag ataattgcc aacaatcttt aattgaccat 360  
 cgaccacaaa aataatatgg aaataatact aacagaactt agaaacatca ctcataatga 420  
 gatcacaatt caaagacgag catccttttg gtatgtatta catgattttt agtcctctga 480  
 atcttcttcc gatcatcata tactaacatt ttcgtgggtg ttattcttta atagaaaaga 540  
 gacaagccga ggcagccaga attgctcaga ggttcaagga tagagtacca gtcactctgtg 600  
 aaaagggttg gaattccgat atccccgaaa ttgataaacg taaatattta gtgccagtgg 660  
 atttgactgt tgggtcaattt gtttacgtta ttagaaaaag aatcaagtta ccaagcgaaa 720  
 aagccatttt catctttgtc aatgacatat tacccecaac cgctgcatta atcagtacaa 780  
 tctacgaaga acacaaggac gaagatggtt tcttatacgt tttatactct ggagagaata 840  
 cttttggcga gaaactagca attgacattt catcattaga tttcagtgat atccctgatt 900  
 atgttttaa 908

<210> 292  
 <211> 135  
 <212> PRT  
 <213> Candida albicans

<400> 292  
 Met Arg Ser Gln Phe Lys Asp Glu His Pro Phe Glu Lys Arg Gln Ala  
 1 5 10 15  
 Glu Ala Ala Arg Ile Ala Gln Arg Phe Lys Asp Arg Val Pro Val Ile  
 20 25 30  
 Cys Glu Lys Val Glu Asn Ser Asp Ile Pro Glu Ile Asp Lys Arg Lys  
 35 40 45  
 Tyr Leu Val Pro Val Asp Leu Thr Val Gly Gln Phe Val Tyr Val Ile  
 50 55 60  
 Arg Lys Arg Ile Lys Leu Pro Ser Glu Lys Ala Ile Phe Ile Phe Val  
 65 70 75 80  
 Asn Asp Ile Leu Pro Pro Thr Ala Ala Leu Ile Ser Thr Ile Tyr Glu  
 85 90 95  
 Glu His Lys Asp Glu Asp Gly Phe Leu Tyr Val Leu Tyr Ser Gly Glu  
 100 105 110  
 Asn Thr Phe Gly Glu Lys Leu Ala Ile Asp Ile Ser Ser Leu Asp Phe  
 115 120 125  
 Ser Asp Ile Pro Asp Tyr Val

130

135

<210> 293  
 <211> 2891  
 <212> DNA  
 <213> *Candida albicans*

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 agcagcaaag ttcgcccta aatatgagtc aagtcaca gaaacccaaa tcgtttggta 180  
 gattgtatac catgtactac tttcattttc catttggtat gcttacgaca actgaaacca 240  
 tgctacttca tacgttttga ttgatgtttg ccttattggg tgccatggg atctacgctt 300  
 atttgccttc aagtatcatg tttgcaatct ccagagcata ctattatggt tttggcatgg 360  
 atattagtac catcaacggg tatggcaaac agcgtgtct acttagtttt atagtttaaa 420  
 aatttggttaa tataaaccca aagtttctaa caggctctgt ttgctcgact aaaaaagaat 480  
 tttgtcaaac gcgtatcaga atgtttaccc tttttttttt taccacagat caaatgaatg 540  
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297

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<210> 294

<211> 796

<212> PRT

<213> Candida albicans

<400> 294

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			20					25					30		
Val	Gln	Lys	Val	Val	Lys	Arg	Lys	Leu	Pro	Thr	Thr	Thr	Asn	Pro	Lys
		35					40					45			
Pro	Ala	Lys	Ile	Leu	Thr	Thr	Asp	Pro	Gly	Ser	Thr	Lys	Tyr	Val	Ile
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Gln	Trp	Arg	Lys	Lys	Thr	Ser	Lys	Lys	Asn	Lys	Thr	Trp	Asp	Gly	Asp
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Gly	Tyr	Ala	Val	Ile	Lys	Gln	Leu	Glu	Asn	Gly	Ala	Cys	Glu	Ile	Ser
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Ile	Lys	Asn	Ser	Asp	Gly	Lys	Pro	Met	Gly	Lys	Arg	Val	Phe	Thr	Ala
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Thr	Pro	Asn	Leu	Asp	Asp	Val	Ile	Ser	Val	Gly	Pro	Tyr	Glu	Leu	Glu
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Leu	Asp	Glu	Lys	Val	Gly	Ser	Asn	Ser	Thr	Pro	Gln	Thr	Val	Thr	Arg
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Val	Thr	His	Gln	Phe	Lys	Lys	Val	Ala	Pro	Pro	Thr	Ala	Ser	Ser	Arg
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Lys	Pro	Leu	Tyr	Asp	Asp	Cys	Ala	Asp	Ala	Ile	Ala	Leu	Pro	Pro	Pro
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Pro	Lys	Ala	Lys	Asp	Tyr	Val	Lys	Val	Asn	Ile	Asp	Pro	His	Leu	Ala
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Lys	Val	Leu	Arg	Pro	His	Gln	Val	Glu	Gly	Val	Lys	Phe	Met	Tyr	Glu
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Cys	Leu	Met	Gly	Tyr	Arg	Gly	Phe	Gly	Gly	His	Gly	Cys	Leu	Leu	Ala
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Asp	Glu	Met	Gly	Leu	Gly	Lys	Thr	Leu	Met	Thr	Ile	Thr	Thr	Ile	Trp
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 Lys Asn Lys Leu Ser Ser Lys Phe Leu Asp Asn Asp Ala Thr Ser Lys  
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 Ser Asp Val Phe Asp Asn Asp Asp Leu Lys Asn Ile Phe Glu Ile Asp  
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 Thr Ser Thr Ile Ser Asn Thr His Asp Leu Leu Glu Cys Val Cys Glu  
                   690                                  695                                  700  
 Gly Asp Gly Ser Met Leu Ser Gln Pro Thr Ile Glu Glu Ser Glu Pro  
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 Pro Pro Lys Gln Ala Trp Val Thr Ala Leu Glu Leu Lys Lys Lys Ile  
                   725                                  730                                  735  
 Asp Asp Gly Glu Ala Leu Lys Arg Thr Ala Val Lys Phe Ala Leu Asn  
                   740                                  745                                  750  
 Asp Tyr Arg His Tyr Asn Pro Glu Val Asn Arg Asn Leu Asp Phe Asp  
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 Ser Ala Leu His Arg Ile Ala Asn Asn Ser Ser Tyr Glu Asn Lys Gln  
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&lt;210&gt; 295

&lt;211&gt; 2643

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 295

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&lt;210&gt; 296

&lt;211&gt; 714

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 296

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Asn Tyr Pro Thr Thr Asp Asn Gly Ser Pro Thr Pro Gln Ala Glu Lys
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Ser Leu Lys Thr Leu Ile Asp Leu Leu Tyr Asp Lys Gly Phe Ala Ala

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			595					600					605		
Met	Phe	Val	Ser	Glu	His	Gly	Phe	Leu	Ile	Leu	Ser	Tyr	Leu	Leu	Phe
			610					615					620		
Glu	Phe	Ser	Ser	Leu	Phe	Lys	Ser	Gln	Val	Glu	Trp	Glu	Asn	Asp	Phe
			625					630					635		640
Val	Asp	Asn	Asp	Ile	Lys	Leu	Arg	His	Asp	Tyr	Tyr	Ser	Gly	Lys	Val

303

	645		650		655
Lys Pro Thr Tyr Lys Val His Ser Asp Glu Leu Trp Glu Lys Phe Thr					
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Pro Gln Ser Thr Leu Asn Phe Thr Gly Pro Lys Pro Thr Ala Glu Thr					
	675		680		685
Asp Asp Lys Val Glu Lys Ile Ala Ser Thr Glu Asp Ala Tyr Ser Thr					
	690		695		700
Ser Ala Glu Lys Ser Thr Thr Thr Ala Thr					
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&lt;210&gt; 297

&lt;211&gt; 1784

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 297

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&lt;210&gt; 298

&lt;211&gt; 461

&lt;212&gt; PRT















310

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Ile Pro Lys Cys Ala Thr Gly Pro Gly Phe Ser Cys Lys Leu Asp Asp  
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Gln Cys Gly Val Asn Ser Thr Tyr Pro Ser Glu Leu Thr Phe Tyr Trp  
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Asp Tyr Lys Asn Val Thr Tyr Asn Ala Pro Leu Gly Asp Phe  
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&lt;210&gt; 303

&lt;211&gt; 1886

&lt;212&gt; DNA

<213> *Candida albicans*

&lt;400&gt; 303

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agttctggag agatttttca aaacttctat tataaataga accctataag tccataataa 420
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acaatatact caatthttctt ggcggttagtg ccccttatat tcaaagaaac ggatatggga 660
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tctttaaaga actaa 1635

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<210> 306

<211> 236

<212> PRT

<213> Candida albicans

<400> 306

Met Lys Leu Asn Ile Ser Tyr Pro Ala Asn Gly Thr Gln Lys Ser Met  
1 5 10 15

Asp Ile Asp Asp Asp Thr Lys Leu Arg Val Ser Thr Glu Lys Arg Met  
20 25 30

Gly Gln Glu Val Glu Gly Asp Ser Val Gly Asp Glu Phe Lys Gly Tyr  
35 40 45

Ile Phe Lys Ile Thr Gly Gly Asn Asp Lys Gln Gly Val Pro Met Lys  
50 55 60

Gln Gly Val Met His Pro Thr Arg Val Arg Leu Leu Leu Ser Lys Gly  
65 70 75 80

His Ser Cys Tyr Arg Pro Arg Arg Thr Gly Glu Arg Lys Arg Lys Ser  
85 90 95

Val Arg Gly Cys Ile Val Ala Gln Asp Leu Ser Val Leu Ala Leu Ser  
100 105 110

Ile Val Lys Gln Gly Asp Asn Glu Ile Glu Gly Leu Thr Asp Thr Thr  
115 120 125

Val Pro Lys Arg Leu Gly Pro Lys Arg Ala Asn His Ile Arg Lys Phe  
130 135 140

Phe Gly Leu Thr Lys Glu Asp Asp Val Arg Asp Phe Val Val Arg Arg  
145 150 155 160

Glu Val Thr Lys Gly Asp Lys Thr Tyr Thr Lys Ala Pro Lys Ile Gln

314

	165		170		175
Arg Leu Val Thr Pro Gln Thr Leu Gln Arg Lys Arg Ala Leu Lys Ala	180	185	190		
Lys Lys Val Lys Asn Ala Gln Gln Gln Arg Asp Ala Ala Ala Glu Tyr	195	200	205		
Ala Gln Leu Leu Ala Lys Arg Leu His Glu Arg Lys Glu Glu Arg Ala	210	215	220		
Glu Ile Lys Lys Lys Arg Ala Glu Ser Leu Lys Asn	225	230	235		

<210> 307  
 <211> 1520  
 <212> DNA  
 <213> Candida albicans

<400> 307

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ggggttggtg	gttctatatt	aattgggttg	ttggccgttt	tattttactt	gagaaagaga	180
aacaaccgtg	attatgaagg	tggatggact	ttctggagaa	agaatgagaa	attgggaagt	240
gatgagttct	tcaatggtga	attgggtgtc	agagacagaa	atattaatca	aggatcaa	300
ttttaacaa	ggcttatttt	ggatgagggt	ggtttttttt	ataagtattt	tgtagttgaa	360
tttaaaattt	tgtaccttaa	agtcttttaa	tttaatttta	ataaaaagtg	gtgatttggc	420
aaacttcaag	agtatatatt	gtgaaaaaaa	aaaaaaaaatt	tggaaactgaa	cgcgtctaac	480
atcttatacc	tctaagcaaa	atgtcagagt	actctgtgta	tcaacagttg	aatgaagata	540
caaacgcaac	taaataatac	tataaattac	tacagctacc	atcaaagata	ctaaatcaac	600
ttgaatccaa	gtcaactaac	ttgtatataa	aatctgatat	caattcccta	gcattatgca	660
ctgattcaga	aactttcaag	ttacgacaaa	tgaaccattc	caatacagtc	ttgctattga	720
acaaagaacc	tgacaacaag	ttaattgggt	ttcagaaaac	cagttatgaa	tatgagttga	780
cagaaatcaa	aggttcgatc	gatacgtccg	atatccctat	tttcaacgga	caaacagcac	840
agcaacctat	tgattttgata	gcatttgaag	ataattcgat	ttgttcacat	caagagtttt	900
tatcgaattg	gtatgagttg	ggagggttgt	aaattgataa	tggagcatat	ataatgagtg	960
cagatattat	tactgaacta	ttatatctat	taatacacc	attgatgagt	ttacaagtgc	1020
acgagttttc	tcoggaagat	gtttcatcca	tcatacgcgc	cccttataat	gactcaatgg	1080
taacatcaat	catacacaaa	ttttgcacta	tagaaagtga	gaaatatcaa	ttgaatgatt	1140
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atatttcaga	gttcttattg	aattggaaaa	ctagtttgcc	gtcattctat	aacctccat	1260
tggacatcag	tcaattggca	ggctattact	gtcccccaat	cgaaaacaaa	atattgtatg	1320
tcgaccaga	atctttatca	gaaaatttga	gtcaacgatt	caaagaattg	tttgaattgg	1380
ataaaagtgt	gaactatgat	gagtttattc	cattcattaa	aaagtttggt	cctgccggta	1440
aaaaggtcga	ctcaattatt	ttaaagtatg	gcaagaagaa	gaaagttggt	agagatagat	1500
ttatagtctg	tcctagataa					1520

<210> 308  
 <211> 339  
 <212> PRT  
 <213> Candida albicans

<400> 308

Met Ser Glu Tyr Ser Val Tyr Gln Gln Leu Asn Glu Asp Thr Asn Ala
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1	5	10	15
Thr Lys Tyr Thr Tyr Lys Leu Leu Gln Leu Pro Ser Lys Ile Leu Asn	20	25	30
Gln Leu Glu Ser Lys Ser Thr Asn Leu Tyr Ile Lys Ser Asp Ile Asn	35	40	45
Ser Leu Ala Leu Cys Thr Asp Ser Glu Thr Phe Lys Leu Arg Gln Met	50	55	60
Asn His Ser Asn Thr Val Leu Leu Leu Asn Lys Glu Pro Asp Asn Lys	65	70	75
Leu Ile Gly Phe Gln Lys Thr Ser Tyr Glu Tyr Glu Leu Thr Glu Ile	85	90	95
Lys Gly Ser Ile Asp Thr Ser Asp Ile Pro Ile Phe Asn Gly Gln Thr	100	105	110
Ala Gln Gln Pro Ile Asp Leu Ile Ala Leu Glu Asp Asn Ser Ile Cys	115	120	125
Ser His Gln Glu Phe Leu Ser Asn Trp Tyr Glu Leu Gly Gly Cys Glu	130	135	140
Ile Asp Asn Gly Ala Tyr Ile Met Ser Ala Asp Ile Ile Thr Glu Leu	145	150	155
Leu Tyr Leu Leu Ile Thr Lys Leu Met Ser Leu Gln Val His Glu Phe	165	170	175
Ser Pro Glu Asp Val Ser Ser Ile Ile Thr Pro Pro Tyr Asn Asp Ser	180	185	190
Met Val Thr Ser Ile Ile His Lys Phe Cys Thr Ile Glu Ser Glu Lys	195	200	205
Tyr Gln Leu Asn Asp Leu Lys Ile Thr Gln Trp Phe Gly Ile Val Glu	210	215	220
Met Ser Lys Ile Asn His Lys Met Thr Asp Ile Ser Glu Phe Leu Leu	225	230	235
Asn Trp Lys Thr Ser Leu Pro Ser Phe Tyr Asn Pro Pro Leu Asp Ile	245	250	255
Ser Gln Leu Ala Gly Tyr Tyr Cys Ser Pro Ile Glu Asn Lys Ile Leu	260	265	270
Tyr Val Asp Pro Glu Ser Leu Ser Glu Asn Leu Ser Gln Arg Phe Lys	275	280	285
Glu Leu Phe Glu Leu Asp Lys Ser Trp Asn Tyr Asp Glu Phe Ile Pro	290	295	300
Phe Ile Lys Lys Phe Val Pro Ala Gly Lys Lys Val Asp Ser Ile Ile			









319

agaaaatttt cgcttcttac gataagacct tgtagttgc cgactcaaga agaattggaac 1200  
 caaagaaatt cgggtggcgt ggtgccagag caagattcca aaaatcttac cgtaa 1256

<210> 314  
 <211> 142  
 <212> PRT  
 <213> Candida albicans

<400> 314  
 Met Ser Thr Gln Ser Val Gln Thr Phe Gly Lys Lys Lys Thr Ala Thr  
 1 5 10 15  
 Ala Val Ala His Val Lys Ala Gly Lys Gly Leu Ile Lys Ile Asn Gly  
 20 25 30  
 Ser Pro Ile Thr Leu Val Gln Pro Glu Ile Leu Arg Phe Lys Val Tyr  
 35 40 45  
 Glu Pro Leu Thr Leu Val Gly Leu Asp Lys Phe Gln Gly Ile Asp Ile  
 50 55 60  
 Arg Val Lys Val Thr Gly Gly Gly His Val Ser Gln Val Tyr Ala Ile  
 65 70 75 80  
 Arg Gln Ala Ile Ala Lys Gly Leu Val Ala Tyr His Gln Lys Tyr Val  
 85 90 95  
 Asp Glu Ala Ser Lys Asn Glu Leu Lys Lys Ile Phe Ala Ser Tyr Asp  
 100 105 110  
 Lys Thr Leu Leu Val Ala Asp Ser Arg Arg Met Glu Pro Lys Lys Phe  
 115 120 125  
 Gly Gly Arg Gly Ala Arg Ala Arg Phe Gln Lys Ser Tyr Arg  
 130 135 140

<210> 315  
 <211> 959  
 <212> DNA  
 <213> Candida albicans

<400> 315  
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 ggacatcttg aataacttaaa attctgaact tgatcaccag atccttttct tttacataat 120  
 tagatatgat ggatagggtta gaatcgtctt taaagagaag gtataatatc taactgattt 180  
 ggcgagggtg tggaaaagtc actccactgt atatatctc ggagtttaac gtactacagt 240  
 tcagtggggt gaatacctaa ataggggggt agaatacgaa ctcctacaaa ttttaaggag 300  
 actatgaccc gaaaagagaa gaaaaattta ttactctaag aactttatat acctccacaa 360  
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 ttttaacttat tagcttggtga aaatctcact tcaattcaag ttctctttca attgacatta 480  
 tagtattttcc caattcaatt atggcttctc atgcttctctg tatattctgt aaaattatca 540  
 aagggtgaaat tccttctttc aagttaattg aaactgcaaa gacttattcc ttcttgga 600  
 ttcaaccaat tgctgaagcc cacgttttaa ttatccctaa acaccatggg gcaaagttgc 660  
 acaacattcc agacgactac cttagtgaac ttttaccagt tgtcaaaaaa ttgacaaaag 720

tcttgaaatt ggacgaaaat aatactccag aaggtgaagg ttataacgtt ttacagaaca 780  
 acggaagaat tgctcatcaa gttgttgatc acgttcactt ccatttgatt cctaaaaagg 840  
 atgaggctac aggttttaggt gttggttggc ctgctgaagc cactgatttt gataaattag 900  
 gaaaattgca tgagaaatta aaggaagaat tggctaaggt agataatgaa aaattataa 959

<210> 316  
 <211> 152  
 <212> PRT  
 <213> Candida albicans

<400> 316  
 Met Ala Ser His Ala Ser Cys Ile Phe Cys Lys Ile Ile Lys Gly Glu  
 1 5 10 15  
 Ile Pro Ser Phe Lys Leu Ile Glu Thr Ala Lys Thr Tyr Ser Phe Leu  
 20 25 30  
 Asp Ile Gln Pro Ile Ala Glu Ala His Val Leu Ile Ile Pro Lys His  
 35 40 45  
 His Gly Ala Lys Leu His Asn Ile Pro Asp Asp Tyr Leu Ser Asp Ile  
 50 55 60  
 Leu Pro Val Val Lys Lys Leu Thr Lys Val Leu Lys Leu Asp Glu Asn  
 65 70 75 80  
 Asn Thr Pro Glu Gly Glu Gly Tyr Asn Val Leu Gln Asn Asn Gly Arg  
 85 90 95  
 Ile Ala His Gln Val Val Asp His Val His Phe His Leu Ile Pro Lys  
 100 105 110  
 Lys Asp Glu Ala Thr Gly Leu Gly Val Gly Trp Pro Ala Glu Ala Thr  
 115 120 125  
 Asp Phe Asp Lys Leu Gly Lys Leu His Glu Lys Leu Lys Glu Glu Leu  
 130 135 140  
 Ala Lys Val Asp Asn Glu Lys Leu  
 145 150

<210> 317  
 <211> 297  
 <212> DNA  
 <213> Candida albicans

<400> 317  
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 gtgtgtgaga gccagagaaa ccaaactgac tgagtgatcg tctctcaaca atttatttct 120  
 cctcgtctta ttttttttct ttcttttctt ttctcttctt tcttcttctt cttctttttc 180  
 ttcttctttt cttcttttacc aaaacactag tattttcaaca tgagagataa gtggagaaaa 240  
 aagagagtta gaagattaaa gagaaagaga cggaagggtta gagctagatc caagtaa 297

321

<210> 318  
 <211> 25  
 <212> PRT  
 <213> Candida albicans

<400> 318  
 Met Arg Asp Lys Trp Arg Lys Lys Arg Val Arg Arg Leu Lys Arg Lys  
           1                  5                  10                  15

Arg Arg Lys Val Arg Ala Arg Ser Lys  
                   20                  25

<210> 319  
 <211> 1303  
 <212> DNA  
 <213> Candida albicans

<400> 319  
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 tgttgtgtgg aataaattta aaatccttct tattggtgtc tagactttgc tttttgtggt 180  
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 taaaacatat tttttttccg tattaacaaa tatgtgtgaa gttttgtcct ggtggtttct 300  
 cactgttttt cttttttttt ctggtagtat caattaacgc ttagatccaa tacagttttg 360  
 gtaacttgta cacgaacaaa atctcaaatt tgttactgtg tgaaccaaca aggaagagaa 420  
 aaaaaaaccc atacaaaaat ttttcagtat caaggaatta gaagagacgt tttaatcaac 480  
 aaagttcaaa tctatcaaca atggtatggt taatatcgat attatccata gatgtacatg 540  
 tatecctaag ggtttcatta tttggaaagt tatgtttatg ggagttctat ttattaagat 600  
 atgggataag aattaaagta ttggatgagt agtacaagac caacaaagag aaatagcccc 660  
 ctttccctcc actattcaat atactcaaca acattatcaa gttaaaagtt cagaagatac 720  
 acgtaaatga aaagtttaata ccaagaagaa tacaaattac cagtccatac cgtgtttggg 780  
 tttagattac tatattttac aagaaacata ttatatgaaa tgatacccaa tccacagcga 840  
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 aaatgaaaca ttaataactaa ctaacttttt ttttatttat taggccggtg ttaaaaacttt 960  
 cgaattaaga actaaatcta aggaacaatt agaattctcaa ttggttgaat tgaaacaaga 1020  
 attggccact ttaaaagttc aaaaattaca aagaccaagt ttaccaagaa ttcacactgt 1080  
 tcgtaaaaac attgctagag tattgactgt tattaacttg aatcaaagag aaaatgttgc 1140  
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 ttaagaaga aaattgacta aatttgaagc ttctcaagaa actgaaaaag ctagaaaaca 1260  
 aagaattgct tttccacaaa gaaaatttgc tattaaagct taa 1303

<210> 320  
 <211> 120  
 <212> PRT  
 <213> Candida albicans

<400> 320  
 Met Ala Gly Val Lys Thr Phe Glu Leu Arg Thr Lys Ser Lys Glu Gln  
           1                  5                  10                  15

Leu Glu Ser Gln Leu Val Glu Leu Lys Gln Glu Leu Ala Thr Leu Lys  
                   20                  25                  30

Val Gln Lys Leu Gln Arg Pro Ser Leu Pro Arg Ile His Thr Val Arg



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acaatagtgt tccatttaga gcagggtgact ggaaatgtga aaattgcatg tatcacaatt 2160
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&lt;210&gt; 322

&lt;211&gt; 729

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 322

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Met Ser Asp Ile Tyr Ile Ile Ile His Ile Ser Thr Thr Cys Asp Asp
  1             5             10             15

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```

Ser Pro Thr Phe Val Thr Lys Asp Ser Ser Glu Leu Ile Glu Phe Ala
      20             25             30

```

```

Trp Glu Thr Val Asp Ser Val Thr Leu Glu Thr Leu Tyr Lys Gly Ser
    35             40             45

```

```

Asn Leu Val Arg Pro Thr Asn Thr Pro Ile Thr Pro Tyr Cys Ser Lys
    50             55             60

```

```

Ile His Arg Ile Thr Trp Asp Asn Val Lys Asn Ala Gly Ser Phe Lys
    65             70             75             80

```

```

Asp Ala Ile Thr Asn Phe Asp Gln Tyr Val Gln Glu His Ile Ile Ser
      85             90             95

```

```

Lys Lys Lys Glu Phe Ser Ile Val Met Phe Asp Ile Ser Lys Leu Arg
    100            105            110

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```

Val Gln Leu Val Arg Glu Ala Arg Asp Lys Ser Val Val Leu Pro Ser
    115            120            125

```

```

Tyr Leu Gln His Pro Arg Ile Phe Asp Leu Pro Arg Glu Tyr Leu Asn
    130            135            140

```

```

Trp Gln Ser Ser His Pro Glu Thr Leu Ser Tyr Pro Pro Thr Ser Leu
    145            150            155            160

```

```

Thr Asn Ile Ile Thr Ala Leu Glu Val Glu Val Glu Asn Ile Ser Glu
    165            170            175

```

```

Tyr Val Asp Leu Pro Asn Phe Ser Ser Thr Pro Ser Pro Ser Lys Ala
    180            185            190

```









Met 1	Ser	Asp	Ser	Gly 5	Tyr	Thr	Leu	Ile	Tyr 10	Glu	Pro	Asn	Thr	Ala 15	Thr
Lys	Val	Ser	Val 20	Asn	Glu	Phe	Lys	Asn 25	Leu	Leu	Glu	Lys	Gly 30	Lys	Asp
Asp	Val	Lys 35	Val	Asp	Thr	Met	Lys 40	Lys	Ile	Leu	Ile	Thr 45	Ile	Leu	Asn
Gly	Asp 50	Pro	Leu	Pro	Asp	Leu 55	Leu	Met	His	Ile	Ile 60	Arg	Phe	Val	Met
Pro 65	Ser	Arg	Asn	Lys	Glu 70	Leu	Lys	Lys	Leu	Leu 75	Tyr	His	Tyr	Trp	Glu 80
Val	Cys	Pro	Lys	Met 85	Asp	Glu	Ser	Gly	Lys 90	Met	Arg	His	Glu	Met 95	Ile
Leu	Val	Cys	Asn 100	Ala	Ile	Gln	Arg	Asp 105	Leu	Gln	His	Pro	Asn 110	Glu	Tyr
Ile	Arg	Gly 115	Asn	Thr	Leu	Arg	Tyr 120	Leu	Thr	Lys	Leu 125	Lys	Glu	Pro	Glu
Leu	Leu 130	Glu	Thr	Leu	Val	Pro 135	Asn	Val	Arg	Gln	Cys 140	Leu	Glu	His	Arg
His 145	Ala	Tyr	Val	Arg	Lys 150	Asn	Ala	Val	Phe	Ala 155	Leu	Trp	Ser	Ile	His 160
Lys	Val	Ser	Asp	His 165	Leu	Ala	Pro	Asp 170	Ala	Asp	Glu	Leu	Ile	Tyr 175	Arg
Phe	Leu	Tyr	Glu 180	Glu	Asn	Asp	Ser	Val 185	Cys	Lys	Arg	Asn	Ala 190	Phe	Val
Cys	Leu 195	Gly	Asp	Leu	Asn	Arg	Glu 200	Ala	Ala	Leu	Gln 205	Tyr	Ile	Gln	Asp
Asn	Ile 210	Ser	Val	Ile	Glu	Thr 215	Leu	Asp	Pro	Leu	Ile 220	Gln	Leu	Ala	Phe
Ile 225	Glu	Phe	Ile	Lys	Lys 230	Asp	Ser	Ile	Gln	Asn 235	Pro	Ala	Leu	Lys	Gln 240
Gln	Tyr	Ala	Gln	Leu 245	Met	Thr	Glu	Ile	Ile 250	Glu	Ser	Ser	Ser	Asn 255	Val
Val	Met	Tyr	Glu 260	Ala	Ala	Asn	Thr	Leu 265	Thr	Val	Leu	Thr	Ser 270	Asn	Pro
Gln	Ser	Ile	Leu	Leu	Ala	Gly	Asn 280	Lys	Phe	Val	Glu	Leu 285	Ala	Thr	Arg



Val Ser Ile Leu Arg Val Gly Glu Ser Ser Leu Val Ser Lys Lys Ile  
 595 600 605  
 Asp Glu Asp Ser Ala Asp Arg Ile Leu Ser Tyr Ile Lys Ile Leu Asn  
 610 615 620  
 Asp Glu Glu Asp Leu Gln Glu Ile Lys Thr Ser Phe Leu Glu Asp Thr  
 625 630 635 640  
 Lys Asp Ala Phe Lys Ala Gln Ile Asn Asn Ala Glu Leu Lys Lys Ala  
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 660 665 670  
 Ala Ile Val Phe Arg Gln Leu Asp Lys Asp Asn Lys Lys Ser Lys Ala  
 675 680 685  
 Ser Val Asp Asp Val Ala Ala Ala Ser Gly Ser Asn Glu Leu Lys Lys  
 690 695 700  
 Glu Asn Leu Ser Ser Arg Leu Asn Lys Ile Ile Gln Leu Thr Gly Phe  
 705 710 715 720  
 Ser Asp Pro Ile Tyr Ala Glu Ala Phe Val Lys Val His Gln Tyr Asp  
 725 730 735  
 Val Val Leu Asp Val Leu Leu Val Asn Gln Thr Thr Thr Thr Leu Arg  
 740 745 750  
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 755 760 765  
 Lys Pro Thr Thr Ala Asn Ile Gly Pro His Gly Phe Tyr Lys Val Gln  
 770 775 780  
 Thr Thr Ile Lys Val Thr Ser Ala Asp Thr Gly Val Ile Phe Gly Asn  
 785 790 795 800  
 Ile Val Tyr Asp Gly Gln His Ser Asp Asp Ser Arg Ile Val Ile Leu  
 805 810 815  
 Asn Asp Val His Val Asp Ile Met Asp Tyr Ile Lys Pro Ala Thr Cys  
 820 825 830  
 Ser Glu Ser Gln Phe Arg Lys Met Trp Asn Glu Phe Glu Trp Glu Asn  
 835 840 845  
 Lys Ile Thr Ile Lys Ser Pro Ile Glu Thr Leu Lys Glu Tyr Leu Asp  
 850 855 860  
 Glu Leu Met Lys Gly Thr Asn Met Gln Cys Leu Thr Pro Gly Ala Val  
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```

&lt;210&gt; 328

&lt;211&gt; 1034

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 328

```

Met Leu Lys Thr Arg Leu Lys Gln Ser Arg Ala Ile Ser Arg Val Val
  1                      5                      10                      15

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```

Arg Arg Tyr Ala Cys Ser His Pro Ile Ser Pro Asn Leu Asp Lys Tyr
      20                      25                      30

```

```

Pro Val Gly Leu Lys Leu His Gly Tyr Glu Val Thr Gln Thr Ser Pro
      35                      40                      45

```

```

Ile Pro Glu Phe Ser Leu Thr Ala Val Ser Leu Lys His Thr Glu Ser
      50                      55                      60

```

```

Gly Ala Thr His Leu His Leu Asp Ser Pro Asn Asp Ser Asn Asn Val
      65                      70                      75                      80

```

```

Phe Ser Ile Ala Phe Lys Thr Asn Pro Pro Asp Asn Thr Gly Val Pro
      85                      90                      95

```

```

His Ile Leu Glu His Thr Thr Leu Cys Gly Ser Lys Lys Phe Pro Val
      100                      105                      110

```

```

Arg Asp Pro Phe Phe Lys Met Thr Asn Arg Ser Leu Ser Asn Phe Met
      115                      120                      125

```

```

Asn Ala Met Thr Gly His Asp Tyr Thr Phe Tyr Pro Phe Ala Thr Thr
      130                      135                      140

```

```

Asn Ser Lys Asp Phe Glu Asn Leu Met Asp Val Tyr Leu Ser Ser Val
      145                      150                      155                      160

```

```

Phe Glu Pro Gln Leu Asn His Thr Asp Phe Leu Gln Glu Gly Trp Arg

```





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Gln	Glu	Ile	Ile	Val	Glu	Asn	Glu	Lys	Leu	Ile	Glu	Lys	Phe	Asp	Lys
				805					810					815	
Asp	Ile	Ser	Ser	Asn	Arg	Pro	Thr	Leu	Ser	Leu	Thr	Val	Thr	Asp	Gly
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Leu	Ser	Ala	Leu	Leu	Asn	Ser	Phe	Asn	Tyr	Asn	His	Thr	Ser	Glu	Asn
		835					840					845			
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Ser	Gln	Leu	Tyr	Ser	Phe	Lys	Asn	Leu	His	Ser	Lys	Ile	Arg	Glu	Ser
			885					890						895	
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Thr	Phe	Arg	Asp	Ser	Leu	Ser	Tyr	Gly	Leu	Asp	Ala	Asn	Trp	Asn	Asp
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Lys	Asp	Leu	Gln	Glu	Ala	Lys	Leu	Arg	Val	Phe	Gln	Ser	Val	Asp	Ala
945				950						955					960
Pro	Ile	Asn	Ile	Ser	Ser	Gln	Gly	Ala	Ser	Ala	Phe	Phe	Glu	Asn	Ile
			965					970						975	
Asp	Asp	Tyr	Leu	Arg	Gln	Glu	Arg	Arg	Glu	Asn	Phe	Leu	Gly	Thr	Thr
			980				985						990		
Leu	Lys	Asp	Leu	Arg	Asp	Val	Thr	Glu	Lys	Tyr	Leu	Val	Asp	Asn	Gln
		995					1000					1005			
Asn	Asn	Leu	Val	Thr	Val	Ile	Gly	Asp	Asn	Glu	Ile	Leu	Asn	Val	Asp
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<210> 329

<211> 1366

<212> DNA

<213> Candida albicans

<400> 329

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```

<210> 330

<211> 145

<212> PRT

<213> Candida albicans

<400> 330

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Met Pro Leu Val Val Gln Glu Gln Gly Ser Phe Gln His Ile Leu Arg
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Leu Leu Asn Thr Asn Ile Asp Gly Arg Ile Lys Ile Met Tyr Ala Leu
      20             25             30

Thr Lys Ile Arg Gly Val Gly Arg Tyr Ala Asn Leu Val Cys Lys
 35             40             45

Lys Ala Asp Val Glu Leu Thr Lys Arg Ala Gly Glu Leu Thr Gln Glu
 50             55             60

Glu Leu Glu Arg Ile Val Thr Ile Met Gln Asn Pro Thr Asn Tyr Lys
 65             70             75             80

Ile Pro Ala Trp Phe Leu Asn Arg Gln Lys Asp Gln Val Asp Gly Lys
      85             90             95

Asp Tyr His Val Leu Ala Asn Asn Leu Glu Ser Lys Leu Arg Asp Asp
 100             105             110

Leu Glu Arg Leu Lys Lys Ile Arg Ser His Arg Gly Ile Arg His Phe
 115             120             125

Trp Gly Leu Lys Val Arg Gly Gln His Thr Lys Thr Thr Ser Arg Gly

```

130

135

140

Arg

145

&lt;210&gt; 331

&lt;211&gt; 1327

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 331

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&lt;210&gt; 332

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 332

```

Met Ala Lys Phe Ile Lys Ser Gly Lys Val Ala Ile Val Val Arg Gly
 1           5           10           15
Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly
          20           25           30
Thr Lys Ser His Pro Phe Pro His Ala Ile Val Ala Gly Ile Glu Arg
          35           40           45
Ala Pro Leu Lys Val Thr Lys Lys Met Asp Ala Lys Lys Val Thr Lys
          50           55           60
Arg Thr Lys Val Lys Pro Phe Val Lys Leu Val Asn Tyr Asn His Leu

```

340

65		70		75		80									
Met	Pro	Thr	Arg	Tyr	Ser	Leu	Asp	Val	Glu	Ser	Phe	Lys	Ser	Ala	Val
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Thr	Ser	Glu	Ala	Leu	Glu	Glu	Pro	Ser	Gln	Arg	Glu	Glu	Ala	Lys	Lys
			100					105					110		
Val	Val	Lys	Lys	Ala	Phe	Glu	Glu	Lys	His	Gln	Ala	Gly	Lys	Asn	Lys
		115					120					125			
Trp	Phe	Phe	Gln	Lys	Leu	His	Phe								
	130					135									

<210> 333  
 <211> 1157  
 <212> DNA  
 <213> Candida albicans

<400> 333

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<210> 334  
 <211> 218  
 <212> PRT  
 <213> Candida albicans

<400> 334

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Asn	Asp	Ala	Ile	Lys	Gly	Ile	Asp	Glu	Arg	Val	Gly	Ser	Leu	Asp	Val
		20						25					30		
Lys	Leu	Ser	Lys	Ile	Asn	Ser	Glu	Leu	Ser	Thr	Tyr	Gln	Gln	Lys	Ile





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taagggcaa	gccaaagaat	atttacaatg	agattgttga	tgacaaaagc	aacttttctc	2040
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<210> 339
<211> 819
<212> DNA
<213> Candida albicans
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<400>	339						
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agcattcgtc	caaattgaga	ccctcaatta	cattttgtca	aaaaaattgg	tccttagtgt	180	
tgctatcgat	aacgaagggtg	aaggcagttt	agcttggaga	catttagata	acttagttac	240	
atctcatctt	ccgtttcag	aaatcgttga	tttaccgtgc	agcgcttata	tgtattgcta	300	
cttgttccca	gcaccacagc	aatatagcaa	tcataaataa	attgccccgc	ggttgacagt	360	
gtatatcttc	gaggaatggc	aacctttgcc	ccccctctga	aaaacaatat	aaatagagtc	420	
aattttctcta	gtagaggtaa	attctttgaa	tcttgttttt	tttcgacata	caccataaat	480	
cccatagaaa	actgcaaaat	gtctgacgcc	ggaagaaaaa	acatttctac	taaaatcaac	540	
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<210> 340
<211> 106
<212> PRT
<213> Candida albicans
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```

<400> 340 .
Met Ser Asp Ala Gly Arg Lys Asn Ile Ser Thr Lys Ile Asn Glu Ala
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Ile Thr Pro Glu Ser Glu Lys Ser Thr Leu Glu Lys Gly Lys Glu Gln
          20          25          30

Val Thr Ser Thr Leu Asp Lys Ala Val Gly Ser Asn Val Pro Asp Asn
          35          40          45

Gln Lys Ser Phe Thr Gln Thr Val Ala Asp Ser Val Gln Gln Gly Ser
          50          55          60

Asp Asn Ala Lys Ala Asp Leu Lys Lys Gln Ser Glu Gln Ala Glu Gly
  65          70          75          80

Glu Gln Arg Pro Leu Ser Lys Gln Leu Lys Asn Met Ser Arg Leu Pro
          85          90          95

Lys Ser Lys Leu Glu Arg Ser Ser Asn Thr
          100          105

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```
<210> 341
<211> 884
<212> DNA
<213> Candida albicans
```

```

<400> 341
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gtagcattcg tccaaattga gacctcaat tacattttgt caaaaaaatt ggtccctagt 180
gttgctatcg ataacgaagg tgaaggcagt ttagcttgga ggcatttaga gaacttagtt 240
acatctcatc ttccgtttcg agaaatcggt gatttaccgt gcagcgctta tattgattgc 300
tacttgttcc cagcaccaca gcaatatagc aatcataaat aaattgcccc gcggttgaca 360
gtgtatatct tcgaggaatg gcaacctttg cccccccttc gaaaaacaat ataaatagag 420
tcaattttctc tagtagaggt aaattccttg aatcttgttt tttttcgaca aacaccataa 480
atcccataga aaactgcaaa atgtctgacg ccggaagaaa aaacatttct actaaaatca 540
acgaagctat aacccccgaa tccgaaaagt ctaccttgga aaagggcaag gaacaagtca 600
ccagtaccct tgacaaagct gttggctcaa atgttccaga taacaaaaaa tctttcactc 660
aaactgttgc agacaacgtg caacaagggt ccgataatgc taaagctgat ttgaagaaac 720
aatccgaaca agcagagggc gaagcaaaga cccttgctga aacagctcaa gaatatgtcg 780
agggtgccaa aactgaaatt ggaaaggctg ctgaatacgt gagtggagtt gtcaccgggtg 840
ctaccgaagg tgccaaaacc ggcgctgata gtactaaaaa atag 884

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<210> 342
<211> 127
<212> PRT
<213> Candida albicans

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```

<400> 342
Met Ser Asp Ala Gly Arg Lys Asn Ile Ser Thr Lys Ile Asn Glu Ala
  1             5             10             15

Ile Thr Pro Glu Ser Glu Lys Ser Thr Leu Glu Lys Gly Lys Glu Gln
          20             25             30

Val Thr Ser Thr Leu Asp Lys Ala Val Gly Ser Asn Val Pro Asp Asn
          35             40             45

Gln Lys Ser Phe Thr Gln Thr Val Ala Asp Asn Val Gln Gln Gly Ser
          50             55             60

Asp Asn Ala Lys Ala Asp Leu Lys Lys Gln Ser Glu Gln Ala Glu Gly
          65             70             75             80

Glu Ala Lys Thr Leu Ala Glu Thr Ala Gln Glu Tyr Val Glu Val Ala
          85             90             95

Lys Thr Glu Ile Gly Lys Ala Ala Glu Tyr Val Ser Gly Val Val Thr
          100            105            110

Gly Ala Thr Glu Gly Ala Lys Thr Gly Ala Asp Ser Thr Lys Lys
          115            120            125

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<210> 343
<211> 1244
<212> DNA
<213> Candida albicans

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```

<400> 343

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352

145	150	155	160
Phe Thr Gly Val Lys Ala Val Ala Thr Gly Pro Lys Gln Gln Glu Ala			
	165	170	175
Thr Thr Tyr Leu Glu Lys Lys Phe Lys Lys Thr Asp Ala Val Lys Gly			
	180	185	190
Asp Trp Gln Lys Thr Val Glu Phe Ala Ile Ile Ala Leu Ser Ser Val			
	195	200	205
Ile Gly Thr Glu Phe Arg Lys Asn Asp Ile Glu Ile Gly Val Ala Thr			
	210	215	220
Glu Gly Glu Phe Arg Ile Leu Thr Pro Glu Glu Ile Asp Glu Arg Leu			
	225	230	235
Ile Ser Ile Ala Glu Gln Asp			
	245		

<210> 345  
 <211> 968  
 <212> DNA  
 <213> Candida albicans

<400> 345  
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 aattaatatg tatgtgacat accatataaa taaagctaca aatgggggata actatgtatt 180  
 taatgataaa tgaatggaag accagaatgt ataatgttat aagatagtga tttatattga 240  
 aaacaccctt aaaaaaatca accaccctac taaccgtcga attggaaatg tcaatttagt 300  
 tagcatcgaa aatcaacaaa gacatgggga atcattttaca tataaaaataa tgagagagaa 360  
 ttacaaaactg ctacgttatg ttttgttcat tatgtcttgt tcattatgtc ttgttcatta 420  
 tgtcaaaaaa tctatagtta cctacctcta catcaattta tgggtctgaaa tactaacatt 480  
 ttttttattt atagtgaata atgaagattg aagttgactc cttttcaggt tctaaaatct 540  
 acccaggtag aggtacttta tttgtcagag gtgactctaa aatttttaga ttccaatcct 600  
 caaaatctgc ttctttattc caacaaagaa agaaccctaa aagaatttct tggactgttt 660  
 tgtacagaag acaccacaaa aaaggtattt ctgaagaagc tgctaaaaag agaaccagaa 720  
 agaccgtcaa gcaccaaaga gctattgtcg gtgcttcttt ggaattgatc aaagaaagaa 780  
 gaagtcaaaa accatctgac agaaaagctg ctagagactc taaattagct aaagacaaag 840  
 aagctaaaaa agctgctaaa gctgccagaa aagctgaaaa ggctaaggct gttgcttctg 900  
 gtgcttctgt tgtttctaaa caacaagcta aaggttcttt ccaaaaagtt aaagctacct 960  
 cccgttaa 968

<210> 346  
 <211> 155  
 <212> PRT  
 <213> Candida albicans

<400> 346  
 Met Lys Ile Glu Val Asp Ser Phe Ser Gly Ser Lys Ile Tyr Pro Gly  
 1 5 10 15  
 Arg Gly Thr Leu Phe Val Arg Gly Asp Ser Lys Ile Phe Arg Phe Gln

	20		25		30	
Ser Ser Lys Ser Ala Ser Leu Phe Gln Gln Arg Lys Asn Pro Arg Arg	35	40	45			
Ile Ser Trp Thr Val Leu Tyr Arg Arg His His Lys Lys Gly Ile Ser	50	55	60			
Glu Glu Ala Ala Lys Lys Arg Thr Arg Lys Thr Val Lys His Gln Arg	65	70	75	80		
Ala Ile Val Gly Ala Ser Leu Glu Leu Ile Lys Glu Arg Arg Ser Gln	85	90	95			
Lys Pro Ser Asp Arg Lys Ala Ala Arg Asp Ser Lys Leu Ala Lys Asp	100	105	110			
Lys Glu Ala Lys Lys Ala Ala Lys Ala Ala Arg Lys Ala Glu Lys Ala	115	120	125			
Lys Ala Val Ala Ser Gly Ala Ser Val Val Ser Lys Gln Gln Ala Lys	130	135	140			
Gly Ser Phe Gln Lys Val Lys Ala Thr Ser Arg	145	150	155			

&lt;210&gt; 347

&lt;211&gt; 1418

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 347

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taatcaaatg gaaatttacc tattgaaaca caagtgtttt tactatccat atttagtttg 240
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tcccctttgt ctttaactaa tgtatttggg tacactacct gaacctacca gttcagttca 420
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gtcacgacag tgccgaaatc aacggtttag ttaaaaaaat gatcagaaat tggagagatg 720
ccgtgcaagc cgaaaagaac aacaaaaaga agttagcaat agcagctgga acaggaacag 780
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gtgctactga aaagagagca gtgaccgata gattcacttg tggcaagtgt aagcacaaga 1320
aggtcagtta ttatcaaatg caaacagat cagcggatga gcctttaact acattttgta 1380

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354

cttgtgaaaa ttgtggcaat agatggaagt tttcataa

1418

&lt;210&gt; 348

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 348

Met Asp Thr Lys Glu Ile Arg Ser Thr Val Ser Asn Leu Glu Lys Ala  
 1 5 10 15

Val Asp Asp Thr Thr Ile Leu Lys Leu Leu Asn Ile Leu Asn Asp Gly  
 20 25 30

Val Lys Pro Ser Glu Lys Leu Leu Arg Glu Thr Lys Val Gly Val Ala  
 35 40 45

Val Asn Lys Phe Arg Ser His Asp Ser Ala Glu Ile Asn Gly Leu Val  
 50 55 60

Lys Lys Met Ile Arg Asn Trp Arg Asp Ala Val Gln Ala Glu Lys Asn  
 65 70 75 80

Asn Lys Lys Lys Leu Ala Ile Ala Ala Gly Thr Gly Thr Gly Thr Pro  
 85 90 95

Ser Ser Ser Ala Ile Ser Pro Ser Ser Ser Gly Ser Gly Ser Thr Thr  
 100 105 110

Pro Lys Pro Ser Glu Ser Thr Thr Pro Ser Ala Ala Arg Lys Gly Pro  
 115 120 125

Arg Asn Pro Lys Thr Asp Gly Val Asn Thr Gln Leu Tyr Glu Asn Asp  
 130 135 140

Thr Arg Asn Ala Ser Val Ser Ala Leu Tyr Thr Ser Leu Ala Val Asp  
 145 150 155 160

Arg Asp Asp Ser Pro Lys His Ile Leu Arg Ile Ala Ile Glu Ile Glu  
 165 170 175

Ala Glu Val Tyr Lys Ser Glu Tyr Ser Lys Val Ser Asp Ser Tyr Arg  
 180 185 190

Asn Arg Leu Arg Ser Phe Thr Met Asn Leu Arg Asn Lys Lys Asn Pro  
 195 200 205

Glu Leu Arg Glu Arg Ile Leu Ser Lys Gln Ile Leu Pro Ala Ala Phe  
 210 215 220

Ile Lys Met Thr Pro Asn Glu Met Ala Pro Glu Ala Leu Lys Lys Glu  
 225 230 235 240

Ile Glu Lys Leu His Lys Gln Asn Leu Phe Asp Ala Gln Gly Ala Thr  
 245 250 255

355

Glu Lys Arg Ala Val Thr Asp Arg Phe Thr Cys Gly Lys Cys Lys His  
 260 265 270

Lys Lys Val Ser Tyr Tyr Gln Met Gln Thr Arg Ser Ala Asp Glu Pro  
 275 280 285

Leu Thr Thr Phe Cys Thr Cys Glu Asn Cys Gly Asn Arg Trp Lys Phe  
 290 295 300

Ser  
 305

<210> 349  
 <211> 1301  
 <212> DNA  
 <213> Candida albicans

<400> 349  
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 acaaagggta agcattcgta ccaggaagtc tggaattaaa cggtagttac ttccagtata 180  
 tatggtgttc attgtgtttt gtgtctaaag ttgcgttagg gctaaagccc taatcaatag 240  
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 gaatgaaaaat gaaaaaaaaa agaataattt tgtagatcgc atagtgtgag cgcgcacaca 360  
 cacacaaaact ttgtagtgtt acagttttct tctttcccat acactctcgc agtcgcacgc 420  
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 tcaactagta ataaccaaca atgcoacta gattaactaa aaccagaaaa cacagaggta 540  
 atgtttcttg tatgtacaat ttcactaaag ttttaacgga tgaaagagta ttgaatgttc 600  
 aaggacatat ggagatttag agaaaacatg gaaaactaat cgaaaatgaa taatgaatgg 660  
 aaaatttttt aaactgaata tcagaataga cacaacacaa cagatccaga gtcattatca 720  
 cattgatcat acaaccaaaag caatgaatat gagtagtttg ggaaaccaca acatacgagt 780  
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 gattaccaga agttccagtc attgtcaaag ccagatttgt ttctaaatta gctgaagaaa 1260  
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<210> 350  
 <211> 149  
 <212> PRT  
 <213> Candida albicans

<400> 350  
 Met Pro Thr Arg Leu Thr Lys Thr Arg Lys His Arg Gly Asn Val Ser  
 1 5 10 15

Ala Gly Lys Gly Arg Ile Gly Lys His Arg Lys His Pro Gly Gly Arg  
 20 25 30

Gly Lys Ala Gly Gly Gln His His His Arg Thr Asn Leu Asp Lys Tyr







<212> PRT

<213> Candida albicans

<400> 354

Met	Gly	Lys	Gln	Tyr	Ile	Ser	Thr	Val	Ser	Ala	Ser	Gln	Ala	His	Lys	1	5	10	15
Ser	Asp	Ile	Leu	Gly	Val	Ala	Ile	Thr	Asn	Lys	Phe	Thr	Val	Ser	Val	20	25	30	
Ser	Ser	Asp	Gly	Tyr	Ala	Lys	Phe	Trp	Asp	Asn	Lys	Gln	Asp	Glu	Val	35	40	45	
His	Ser	Pro	Lys	Glu	Phe	Val	Gln	Ser	Val	Phe	Ile	Asp	Lys	Ser	Gly	50	55	60	
Ile	His	Ala	Val	Ala	Ala	Tyr	Glu	Asn	Val	Leu	Pro	Ser	Ser	Thr	Leu	65	70	75	80
Lys	Val	Thr	Leu	Leu	Ala	Phe	Ala	Cys	Phe	Asn	Gly	Ser	Ile	Ile	Phe	85	90	95	
Arg	Tyr	Tyr	Ile	Asn	Asp	Asp	Phe	Ser	Thr	Ile	Glu	Ser	Leu	Thr	Asp	100	105	110	
Asp	Ile	Lys	Ser	Phe	Glu	Ser	Asn	Cys	Trp	Thr	Pro	Gly	Phe	Tyr	Arg	115	120	125	
Asp	Pro	Glu	Ser	Lys	Gln	Asp	Tyr	Phe	Ile	Thr	Thr	Lys	Thr	Asn	Gly	130	135	140	
Thr	Thr	Glu	Val	His	Leu	Leu	Asn	Ile	Val	Asp	Glu	Asn	Glu	Lys	Ala	145	150	155	160
Val	Ile	Thr	Phe	Glu	Lys	Phe	Gly	Gln	Leu	Lys	Gly	Asn	Ser	Ser	Ser	165	170	175	
Phe	Pro	Asn	Ser	Leu	Ala	Ile	Cys	Pro	Thr	Glu	Asn	Lys	Lys	Cys	Ala	180	185	190	
Val	Gly	Tyr	Ile	Asn	Gly	Asp	Val	Leu	Leu	Tyr	Asp	Phe	Val	Ser	Leu	195	200	205	
Lys	Leu	Ile	Tyr	Thr	Phe	Arg	Ser	Ser	Asp	Leu	Val	Thr	Ser	Arg	Asn	210	215	220	
Ser	Gln	Ser	Thr	Ser	Ile	Pro	Arg	Val	Leu	Ala	Phe	Ser	Pro	Gly	Gly	225	230	235	240
Thr	Leu	Leu	Ala	Val	Ala	Arg	Asp	Asn	Gln	Ala	Ala	Gly	Ser	Ile	Thr	245	250	255	
Leu	Tyr	Asp	Val	Glu	His	Gly	Glu	Asn	Val	Gly	Ser	Leu	Ala	Thr	Pro	260	265	270	
Ser	His	Ser	Ala	Lys	Ser	Val	Val	Gly	Gly	Phe	Ala	His	Gln	Gly	Trp	275	280	285	

<210> 356

360

<211> 174  
<212> PRT  
<213> Candida albicans

<400> 356  
Met Ser Asp Lys Ser Gln Asn Val Met Arg Glu Leu Arg Ile Glu Lys  
1 5 10 15  
Leu Val Leu Asn Ile Cys Val Gly Glu Ser Gly Asp Arg Leu Thr Arg  
20 25 30  
Ala Ala Lys Val Leu Glu Gln Leu Ser Gly Gln Thr Pro Val Gln Ser  
35 40 45  
Lys Ala Arg Tyr Thr Val Arg Thr Phe Gly Ile Arg Arg Asn Glu Lys  
50 55 60  
Ile Ala Val His Val Thr Val Arg Gly Pro Lys Ala Glu Glu Ile Leu  
65 70 75 80  
Glu Arg Gly Leu Lys Val Lys Glu Tyr Gln Leu Arg Ser Lys Asn Phe  
85 90 95  
Ser Ala Thr Gly Asn Phe Gly Phe Gly Ile Asp Glu His Ile Asp Leu  
100 105 110  
Gly Ile Lys Tyr Asp Pro Ser Ile Gly Ile Tyr Gly Met Asp Phe Tyr  
115 120 125  
Val Val Met Gly Arg Ala Gly Ala Arg Val Thr Arg Arg Lys Arg Ala  
130 135 140  
Arg Ser Thr Ile Gly Asn Ser His Lys Thr Asn Lys Glu Asp Thr Ile  
145 150 155 160  
Gln Trp Phe Lys Thr Arg Tyr Asp Ala Glu Val Leu Asp Lys  
165 170

<210> 357  
<211> 919  
<212> DNA  
<213> Candida albicans

<400> 357  
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tcattattgac atgataagga tttatcaata ctgttaggtc tatagcccta actttaatca 180  
tttacacgtg atacaaaaaa gttgtttgat cccgcacgac tatgagtacg cactcactaa 240  
ttatagcctg aaaaaaaaaa tttccacata gtaaggggat tttgtatggt ggtgcgctcg 300  
cctaagacgt ctgcatacat tttctaaagt cacactgata tagggatggt gtggtagtga 360  
ttgtgtgttc ccaccaaata actttgcgga cactctcata tactcaattt ttttcttaca 420  
aaaatttttt ttctttctact tttttcaaga attcttcttt tacaattcaa caacatcaat 480  
catgggtaaa ggtaaaccac gagggcttaa ctctgctaga aaattaagag ttcacagaag 540  
aaacaacaga tgggctgac aagcttataa agctagatta ttaggtaccg ctttcaaatc 600  
ttctccattt ggtgggttcac ctacacgcaa aggtatcggt ttggaaaaaa ttggtattga 660

361

```

atctaaacaa ccaaactctg ctatcagaaa atgtgtcaga gtccaattaa tcaaaaacgg 720
taagaaagtc actgctttcg ttccaaacga tggttgtttg aactttgttg acgaaaatga 780
cgaagtcttg ttggctgggt tcggtagaag aggtaaagct aagggggata ttccaggggt 840
tagattcaag gttgttaaag tttccggtgt ctctttatta gctttatgga aagaaaagaa 900
agaaaagcca agatcatag                                     919

```

&lt;210&gt; 358

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 358

```

Met Gly Lys Gly Lys Pro Arg Gly Leu Asn Ser Ala Arg Lys Leu Arg
  1          5          10          15

```

```

Val His Arg Arg Asn Asn Arg Trp Ala Asp Gln Ala Tyr Lys Ala Arg
          20          25          30

```

```

Leu Leu Gly Thr Ala Phe Lys Ser Ser Pro Phe Gly Gly Ser Ser His
  35          40          45

```

```

Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ser Lys Gln Pro
  50          55          60

```

```

Asn Ser Ala Ile Arg Lys Cys Val Arg Val Gln Leu Ile Lys Asn Gly
  65          70          75          80

```

```

Lys Lys Val Thr Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Val
          85          90          95

```

```

Asp Glu Asn Asp Glu Val Leu Leu Ala Gly Phe Gly Arg Arg Gly Lys
  100          105          110

```

```

Ala Lys Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser
  115          120          125

```

```

Gly Val Ser Leu Leu Ala Leu Trp Lys Glu Lys Lys Glu Lys Pro Arg
  130          135          140

```

Ser

145

&lt;210&gt; 359

&lt;211&gt; 1164

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 359

```

aattcatttg atctctaaga agatgaacag gccttgaatg ggaggggttg gttcgacttc 60
cacgaaatgt gggttgaaaa acttgagtcc tcaaaaaggt tctctcgtaa aaggccagag 120
aaagaaaaaa ccaccaaaccc cccaccacca acctaacctt ttccttccat ccattcctct 180
ttccttactt tgcaaagtgt gaatccagtt atattcatta aagatcctat aaaatacgat 240
tattcacaat ttattatatc ttactcccgc aaattcatta attgtaatcg tattgattta 300
gttatacttt gtcaaatacac cgaatcaaata caattgaatg aaattttatg tttttattat 360

```

Gly His Lys Ile Leu Leu Ser Met Ala Ile Phe Leu Thr Ser Asn Lys  
180 185 190

Leu Ile Ile Gly Ile Thr Gly Ser Asn Leu Leu Ile Asn Lys Lys Phe  
 195 200 205  
 Lys Ser Gln Leu Gln Thr Phe Asn Gln Arg Gln Asn Leu Val Ile Gln  
 210 215 220  
 Phe Ile Asn Leu Leu Leu Leu Ser Glu Thr Ser Val Ile Phe Phe Glu  
 225 230 235 240  
 Ile Tyr Glu Ile Asn Asp Val Cys Gly Pro Thr Gly Tyr Ile Asn Asp  
 245 250 255  
 Ile Asp Asn Leu Ile Ile Ser Gln Glu Thr Lys Ser Gly Gly Glu Phe  
 260 265 270  
 Val Asn Lys Phe Arg Lys Asp His Gly Phe Lys Leu Leu Asp Ile Thr  
 275 280 285  
 Ile Ile Lys Val Ile Gly Gly Asn Ile Glu Glu Asn Ser Trp Lys Gly  
 290 295 300  
 Lys Leu Ser Ser Thr Asp Ile Arg Glu Gln Glu Tyr Asn Arg Leu Leu  
 305 310 315 320  
 Asn Gln

&lt;210&gt; 361

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 361

caagagtaaa atctaaatcg ttccaatgat tttggacagc tcatagggtta agagggtctac 60  
 atgtgttggg ggcagtagta ttggtattaa gtgggtgggt catggtatta gagagtgggt 120  
 gttataaaaag aaggttgtga tttttttttt ccactggtgg tgggtgtgct gattgtactg 180  
 ctgttcactt tattgtttcg tttcgttttt ctttgtttt gttgacgttg acattttttt 240  
 tgctgttgtt gttgtatggg aatttttgta ttagttgttc ttttttgttt ttttttactt 300  
 gttcaaagtt tcatataata ataataattct tgttttcata tttttttttt cagaacaaga 360  
 acaaatacaa cttatataat ttgatcttac tcttatcccc aggtttttct atttgttttt 420  
 gggtttgcca ttcatatata tatatctatt attcaaataca atttgaggag tatcattaat 480  
 tttaaattata tcagttaaca atgtcgtatc gtgggtcctaa tcaatttggt aatcaacctc 540  
 cacatcatgg aataccttct caacctcaac cacatattgg tccaatatct tccagcaaaa 600  
 gtcctttaga acaatttgaa gatgttgcta aaaaagttga agattggatc gatgattatt 660  
 ttaaagtctt gaaaccatac gtcccagcaa ttggttagagc atttttggtg gccactttct 720  
 atgaggatac ttaagaatac ttcactcaat ggaatgaaca agtttattac ttgcacaact 780  
 atagactacta ttggcggttg ttgaccgttt tattcttgat caataatatg gtgggttatga 840  
 cagttgcac cacttttagta attgccagaa aaaagaataa cattgctact attgcattga 900  
 tcgttggtgt tattatacaa ggtattgggt atggtttatt gtttgatgct caatttggtt 960  
 tgagaaactt gtccgttggt ggagggttag tattagcatt ttccgatagt attgttagag 1020  
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 ctgattgggc attgggtaga gttttcatta ttataatcgg gttaacttct tgtgcttcaa 1200  
 ttgttgttgg ttacaagaca aagttttcag ctgctatcat gcttattgtt ttattcttat 1260

364

acaatgtgtt cactaaccaa ttctgggctt atgcattctca agatgctaga cgtgactttt 1320  
 tgagatatga attcttccaa gttttgtcaa ttgtgggagg attattgtta gtggttaatg 1380  
 caggtgctgg tgaattctcc atcgatgaaa agaaaaagat ttattaa 1427

&lt;210&gt; 362

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 362

Met Ser Tyr Arg Gly Pro Asn Gln Phe Gly Asn Gln Pro Pro His His  
 1 5 10 15

Gly Ile Pro Ser Gln Pro Gln Pro His Ile Gly Pro Ile Ser Ser Ser  
 20 25 30

Lys Ser Pro Leu Glu Gln Phe Glu Asp Val Ala Lys Lys Val Glu Asp  
 35 40 45

Trp Ile Asp Asp Tyr Phe Lys Val Leu Lys Pro Tyr Val Pro Ala Ile  
 50 55 60

Gly Arg Ala Phe Leu Val Ala Thr Phe Tyr Glu Asp Thr Leu Arg Ile  
 65 70 75 80

Phe Thr Gln Trp Asn Glu Gln Val Tyr Tyr Leu His Asn Tyr Arg His  
 85 90 95

Tyr Trp Arg Trp Leu Thr Val Leu Phe Leu Ile Asn Asn Met Val Val  
 100 105 110

Met Thr Val Ala Ser Thr Leu Val Ile Ala Arg Lys Lys Asn Asn Ile  
 115 120 125

Ala Thr Ile Ala Leu Ile Val Val Val Ile Ile Gln Gly Ile Gly Tyr  
 130 135 140

Gly Leu Leu Phe Asp Ala Gln Phe Val Leu Arg Asn Leu Ser Val Val  
 145 150 155 160

Gly Gly Leu Val Leu Ala Phe Ser Asp Ser Ile Val Arg Asp Lys Arg  
 165 170 175

Ser Leu Asn Met Pro Gly Leu Pro Met Leu Asn Asn Gln Asp Asn Lys  
 180 185 190

Lys Tyr Phe Leu Leu Ala Gly Arg Ile Leu Leu Val Leu Leu Phe Leu  
 195 200 205

Gly Phe Val Phe Ser Ser Asp Trp Ser Leu Gly Arg Val Phe Ile Ile  
 210 215 220

Ile Ile Gly Leu Thr Ser Cys Ala Ser Ile Val Val Gly Tyr Lys Thr  
 225 230 235 240

Lys Phe Ser Ala Ala Ile Met Leu Ile Val Leu Phe Leu Tyr Asn Val







275	280	285
Glu Lys Ala Ala Lys Lys Trp Glu Lys Glu Ser Gly Ser Arg Lys Ala		
290	295	300
Ala Glu Glu Ala Ala Ala Lys Lys Ala Ala Glu Glu Ala Ala Ala Lys		
305	310	315
Lys Ala Ala Glu Glu Ala Ala Ala Leu Lys Ala Asn Ser Lys Lys Ala		
	325	330
Lys Glu Ala Ala Lys Ala Ala Lys Lys Lys Asn Lys Arg Asn Ile Arg		
	340	345
Ala Ala Val Lys Asp Asn Asn Tyr Phe Gly Asp Ser Ala Lys Ser Ala		
355	360	365
Asp Ile Asp Ala Asp Val Asp Leu Leu Ile Glu Lys Phe Asp Asp Val		
370	375	380
Lys Leu Gly Glu Val Ala Asp Lys Val Lys Asp Ala Asp Ala Ala Ser		
385	390	395
Val Lys Ser Thr Phe Val Glu Val Ala Lys Glu Leu Val Gly Ala Gly		
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Ser Leu Asp Ala Ser Tyr Leu Lys Tyr Phe Asn		
420	425	

<210> 365  
 <211> 1178  
 <212> DNA  
 <213> Candida albicans

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 caaacaacaaa aaaactaact tcttccccca atatgctgcg tatagtgaga aatcttcttc 360  
 tctcttgcca tactatcgca tttttttttt tggtaactca cgaaacctaa ttggaaagaa 420  
 gaaaagagaa aaaaaaaaaa ttttcagttt tcaatagatt tcagtttttg aattatacat 480  
 attagagaaa caagttaaca atggatgtt cattagattt accatgagtt atggagggat 540  
 attcctggat gatcagaata tcataatata ggagtatact attttactgg aatcaagata 600  
 taattgaatt gaaataaaaa ttgaataaga ggaagcatag aatacggaaat gatgattaac 660  
 aaatcagaaa acattgtact accgaataat gaattaggat caacatatta atatcaacta 720  
 ctactttaa aagaacaggaa aatgagaaga gaatcagcat gaaagttacc acctcagaaa 780  
 acgtcaaaga aatatacttt tgggtgtggat ccatgtgtta ttactgaaat catcgaaacg 840  
 aatataaccc tcctttttccc acattgacat aagtcagaca caatctttca aataaaacat 900  
 gtaataactaa ctattatttt tttttcgtat aggttttagt tcaagattta ttacatccat 960  
 ctccagccac tgaagctaaa caacacaaat tgaaaacttt agttcaacaa ccaagatctt 1020  
 tctttatgga cgttaaatgt caaggatgtc ttaatatcac cactgttttc agtcacgctc 1080  
 aaactgctgt cacttgtgac tcttggttcta ctgttttgtg taccaccaact ggtggttaaag 1140  
 ctaaattgac tgaagggtgt tcattcagaa gaaagtaa 1178

368

<210> 366  
 <211> 82  
 <212> PRT  
 <213> *Candida albicans*

<400> 366  
 Met Val Leu Val Gln Asp Leu Leu His Pro Ser Pro Ala Thr Glu Ala  
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 Lys Gln His Lys Leu Lys Thr Leu Val Gln Gln Pro Arg Ser Phe Phe  
                   20                  25                  30  
 Met Asp Val Lys Cys Gln Gly Cys Leu Asn Ile Thr Thr Val Phe Ser  
           35                  40                  45  
 His Ala Gln Thr Ala Val Thr Cys Asp Ser Cys Ser Thr Val Leu Cys  
           50                  55                  60  
 Thr Pro Thr Gly Gly Lys Ala Lys Leu Thr Glu Gly Cys Ser Phe Arg  
           65                  70                  75                  80  
 Arg Lys

<210> 367  
 <211> 1179  
 <212> DNA  
 <213> *Candida albicans*

<400> 367  
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 cggatcatat aaatttggaa ggagctacca aagcagaaat gatagcaaaa aaaaacagga 180  
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 aacaacaacg agggaagaaa aaaaacttaa ttaggtgaac aaaaattaat gtgtgagcgt 360  
 gtacatgcac aattttcaat tggttattct cagcactaa caaactcaac ctccattgtg 420  
 agaaaagaga tttttctttg aaaaaaaatt tacatacata tcttagttca ctagtaactt 480  
 tcgaagacaa catagacaag atgggtatgt tccagtatag caatattcaa caatgagata 540  
 caagatattc ctccaatata aagagattaa tgggtgtttt gatagagtgt aaagccatgt 600  
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 tgaaacgaat tttctgggat agcgttcaaa caatcaaacc tatccagggt tcttatgaca 720  
 attaagaaaa caagtcaata ttatcaaaga tggagtttta taaggagaga tattgaaaca 780  
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 aaagaatgcc gtaaacatac ccaacacaaa gttacccaat acaaagctgg taaagcttct 960  
 ttgttcgctc aaggtaaaaa agatatgac agaaaacaat ccggttatgg tgggtcaaacc 1020  
 aaacaaattt tccacaagaa agccaagact accaaaaaag ttgttttgag attggaatgt 1080  
 gttgtctgta aaaccaaggc tcaattacca ttgaaaagat gtaaacattt cgaattgggt 1140  
 ggtgacaaaa aacaaaaaag tcaagcttta caattttta 1179

<210> 368

<211> 106  
<212> PRT  
<213> Candida albicans

<400> 368

Met Val Asn Val Pro Lys Thr Arg Lys Thr Tyr Cys Lys Gly Lys Glu  
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Cys Arg Lys His Thr Gln His Lys Val Thr Gln Tyr Lys Ala Gly Lys  
20 25 30  
Ala Ser Leu Phe Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser  
35 40 45  
Gly Tyr Gly Gly Gln Thr Lys Gln Ile Phe His Lys Lys Ala Lys Thr  
50 55 60  
Thr Lys Lys Val Val Leu Arg Leu Glu Cys Val Val Cys Lys Thr Lys  
65 70 75 80  
Ala Gln Leu Pro Leu Lys Arg Cys Lys His Phe Glu Leu Gly Gly Asp  
85 90 95  
Lys Lys Gln Lys Gly Gln Ala Leu Gln Phe  
100 105

<210> 369  
<211> 3583  
<212> DNA  
<213> Candida albicans

<400> 369

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taatgtggac gtgtcaacga aaccggaaaa tataaatagc agagataaca aaactgagaa 360  
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gaaaccaaca attaccaaga aaacttcatt cactgattac ttaaaatctg ccaaaactaa 480  
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tgaaactgtt atagcagatg accttccacg tctcgatgaa ggaaagaaac ttttacgtga 960  
acaaacagca gatgtaaaga gacataaatt gaagaaaaca aaattgaata ctatttttag 1020  
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actaccagaa gatgaccaac atcctgattt tcaaaattca aaagcaacaa cagaaatcag 1140  
taacgataaa acagaagtaa ataagccaga agtgaaagag gttggcgaga aagagagaaa 1200  
tcaccaacta gaagatagat taccaattaa aaaagagaaa atgcgggtcg agaattgcaa 1260  
gacatctgaa aacggtgtca gttcaaaatc agaattctaag atttcaaagt cgaagaaact 1320  
accttacaaa gttaaactgt attcaagtgg tcgatcatta ttacaacgag cttgcaagaa 1380



Gln Gln Ser Glu Gln Leu Leu Thr Asp Lys Lys Asp Asn Lys Ser Glu  
 65 70 75 80  
 Pro Asn Ser Glu Val Asn Leu Lys Asp Asn Asn Asp Asp Ser Lys Ala  
 85 90 95  
 Thr Ala Gly Cys Ala Leu Gly Pro Asp Lys Asn Thr Gly Lys Asn Asp  
 100 105 110  
 Ser Asp Lys Ser Glu Thr Thr Gln Pro Lys Leu Ala Arg Ser Glu Ser  
 115 120 125  
 Phe Ala Asp Thr Ser Leu Leu Ser Pro Val Asn Glu Ser Asp Thr Asp  
 130 135 140  
 Phe Asn Phe Asn Glu Leu Ala Glu Ile Pro Glu Ala Lys Asp Gly Ser  
 145 150 155 160  
 Val Val Ala Ala Asn Val Ser Glu Asn Ile Asp Glu Asn Glu Asn Ile  
 165 170 175  
 Ser Glu Ala Glu Thr Val Ile Ala Asp Asp Leu Pro Arg Leu Asp Glu  
 180 185 190  
 Gly Lys Lys Leu Leu Arg Glu Gln Thr Ala Asp Val Lys Arg His Lys  
 195 200 205  
 Leu Lys Lys Thr Lys Leu Asn Thr Ile Phe Ser Ser Asp Glu Glu Glu  
 210 215 220  
 Glu Glu Ile Gln Glu Pro Asp Phe Lys Leu Gln Glu Pro Glu Lys Leu  
 225 230 235 240  
 Pro Glu Asp Asp Gln His Pro Asp Phe Gln Asn Ser Lys Ala Thr Thr  
 245 250 255  
 Glu Ile Ser Asn Asp Lys Thr Glu Val Asn Lys Pro Glu Val Lys Glu  
 260 265 270  
 Val Gly Glu Lys Glu Arg Asn His Gln Leu Glu Asp Arg Leu Pro Ile  
 275 280 285  
 Lys Lys Glu Lys Met Arg Ser Glu Asn Ala Lys Thr Ser Glu Asn Gly  
 290 295 300  
 Val Ser Ser Lys Ser Glu Ser Lys Ile Ser Lys Ser Lys Lys Leu Pro  
 305 310 315 320  
 Tyr Lys Val Lys Arg Asp Ser Ser Gly Arg Ser Leu Leu Gln Arg Ala  
 325 330 335  
 Cys Lys Lys Gly Asn Phe Ala Asp Val Gln Asp Tyr Ile Glu Arg Gly  
 340 345 350  
 Ala Ser Ala Asn Glu Lys Asp Phe Cys Gly Phe Thr Cys Leu His Glu  
 355 360 365





Glu	Lys	Lys	Ser	Glu	Asp	Lys	Ile	Thr	Lys	Thr	Val	Asn	Glu	His	Val	675	680	685	
Ser	Asn	Arg	Lys	Pro	His	Glu	Ser	Thr	Gly	Arg	Lys	Leu	Glu	Lys	Thr	690	695	700	
His	Ser	Asn	Glu	Glu	Arg	Lys	Arg	Lys	Arg	Glu	Trp	Ser	Asp	Asp	Glu	705	710	715	720
Pro	Lys	Glu	Pro	His	Leu	Leu	Lys	Lys	Ser	Lys	Ser	Asp	Leu	Lys	Leu	725	730	735	
Lys	Ser	Leu	His	Arg	Glu	Phe	Thr	Ser	Asp	Asp	His	His	Thr	Ser	Glu	740	745	750	
Ser	His	Ser	Asp	Ser	Phe	Ala	Glu	Lys	Arg	Lys	His	Leu	Ser	Ala	Thr	755	760	765	
Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ser	Gln	Ala	Val	770	775	780	
Ile	Lys	Ala	Gln	Glu	Glu	Gln	Lys	Ile	Lys	Asp	Ala	Glu	Glu	Ala	Arg	785	790	795	800
Leu	Trp	Gln	Glu	Lys	Val	Glu	Ala	Lys	Lys	Arg	Ala	Arg	Arg	Glu	Met	805	810	815	
Phe	Leu	Lys	Ser	Glu	Lys	Glu	Lys	Glu	Gln	Lys	Arg	Lys	Glu	Glu	Glu	820	825	830	
Glu	Leu	Arg	Ala	Gln	Glu	Glu	Lys	Arg	Ile	Ala	Lys	Ala	Lys	Gln	Glu	835	840	845	
Glu	Gln	Glu	Arg	Leu	Ala	Arg	Glu	Ala	Glu	Glu	Lys	Ser	Lys	Glu	Leu	850	855	860	
Glu	Glu	Lys	Lys	Val	Gly	Leu	Arg	Gln	Gln	Leu	Thr	Leu	Asp	His	Tyr	865	870	875	880
Pro	Val	Gly	Leu	Arg	Tyr	Cys	Lys	Phe	Asp	Gly	Asn	Pro	Asn	Ile	Ser	885	890	895	
Ala	Val	Asp	Lys	Phe	Leu	Pro	Phe	Tyr	Val	Phe	Val	Ile	Asp	Asp	Lys	900	905	910	
Lys	Tyr	Ala	Val	Asp	Leu	Gln	Val	Ser	Leu	Ile	Thr	Ser	Thr	Val	Val	915	920	925	
Ser	Lys	Val	Ile	Asn	Thr	Val	Gln	Pro	His	Gln	Lys	Arg	Glu	Ile	Asn	930	935	940	
Ala	Thr	Glu	Lys	Ser	Lys	Leu	Trp	Lys	Leu	Phe	Phe	Lys	Phe	Ile	Gly	945	950	955	960
Ile	Asp	Pro	Arg	Asn	Pro	Asn	Cys	Asp	Gln	Arg	Ser	Ser	Ile	Thr	Asn	965	970	975	

Gly Gln Lys Gln Phe Gln Asn Leu Leu Leu His Phe Val Glu Val Asp  
 980 985 990

Leu Ala Glu Glu Phe Leu Lys Glu Phe Pro Glu Val His Ser Lys Ala  
 995 1000 1005

Lys Asp Asn Gln Ile Asp Val Ser Leu Glu Ser Leu Ser Gly Phe Ser  
 1010 1015 1020

Asp Cys Val Lys Asp Asp Ile Ile Val Asp Gly Asn Leu Glu Ile Asp  
 1025 1030 1035 1040

Ile Asp Ser Lys Lys Ile Glu Lys Phe Ile Pro Pro His Leu Asn Thr  
 1045 1050 1055

Arg Lys Asp Ile Ile Arg Thr Val Ser Thr Leu Ala His Pro Leu Trp  
 1060 1065 1070

<210> 371  
 <211> 659  
 <212> DNA  
 <213> Candida albicans

<400> 371  
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 atttggtttt gttcgtgtct cggtcattga gggtgggtaa attggttttc ttttgagaat 180  
 tgtgagcatg caatgtcgca tgcaaatatg atgtcgctca attgcgacat actacttagg 240  
 gctatagacc tattgcacgt gcgttagttt taaacctaaa aaaacaattt tgtgcagtcg 300  
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 aaggcgaaaa aaaaaaaaaa taaacttgaa tattttggaa tccccctttt gattactaca 480  
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<210> 372  
 <211> 52  
 <212> PRT  
 <213> Candida albicans

<400> 372  
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Lys Ser Ile Cys Arg Lys Cys Tyr Ala Arg Leu Pro Pro Arg Ala Thr  
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Asn Cys Arg Lys Arg Lys Cys Gly His Thr Asn Gln Leu Arg Pro Lys  
 35 40 45

Lys Lys Leu Lys  
50

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<211> 2297  
<212> DNA  
<213> *Candida albicans*

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<210> 374  
<211> 598  
<212> PRT  
<213> *Candida albicans*

376

&lt;400&gt; 374

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Glu Asp Ser Ser Asp Glu Leu Lys Asp Leu Val Gln Glu Phe Glu Leu
      20              25              30

Lys Tyr Ala Glu Leu Lys Lys Asn Lys Ala Leu Lys Lys Arg Arg Ser
      35              40              45

Gln Ser Pro Ser Glu Asp Met Ser Asn Lys Gln Lys Pro His Gln Pro
      50              55              60

Glu Val Pro Arg Thr Pro Glu Lys Ala Lys Val His Leu Asp Lys Val
      65              70              75              80

Val Glu Glu Pro Lys Gln Arg Ile Phe Thr Lys Lys Glu Pro Arg Asp
      85              90              95

Ser Lys Ile Lys Glu Ser Asn Phe Leu Asn Lys Leu Tyr Glu Thr Ser
      100             105             110

Asn Lys His Asp Lys Glu Asp Ala His Lys Ile Asp Phe Ser Lys Arg
      115             120             125

Arg Phe Glu Phe Gln Leu Asp Lys Tyr Thr Phe Thr Pro Lys Asp Val
      130             135             140

Val Asp Asp Leu Glu Pro Ile Ser Lys Leu Tyr Leu Arg Arg Arg Tyr
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Leu Ala Gln Ser Gln Ile Ala Asp Ile Ile Ala Glu Thr Asp Ser Asn
      165             170             175

Met Lys Phe Leu Lys Ile Asp Lys Phe Leu Ala Lys Thr His Lys Ser
      180             185             190

Asn Asn Tyr Ala Glu Pro Lys Tyr Cys Asn Trp Cys Leu Val Ala Phe
      195             200             205

Val Val Arg Lys Asp Pro Val Gln Val Ala Ala Asn Asn Ser Lys Tyr
      210             215             220

Ile Lys Leu Lys Val Gly Asn Phe Met Asn Ser Val Asp Leu Met Leu
      225             230             235             240

Phe Asp Lys Ala Phe Gln Lys Asn Gly Lys Ile Gln Pro Gly Asp Leu
      245             250             255

Leu Phe Ile Leu Asn Pro Leu Ile Asn Lys Tyr Glu Ile Gln Val Gly
      260             265             270

Lys Gly Gln Phe Gln Ser Gly Phe Asn Leu Lys Val Glu Asn Thr Asn
      275             280             285

Val Ser Ser Ile Leu Glu Ile Gly Ser Leu Arg Asp Phe Gly Phe Cys
      290             295             300

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Lys Phe Thr Arg Lys Leu Asp Asn Ser Arg Cys Lys Arg Ala Ile Asn  
 305 310 315 320  
 Thr Arg Thr Gln Glu Phe Cys Asp Ile His Leu Asp Met Lys Phe Lys  
 325 330 335  
 Ser Ser Thr Arg Met Glu Leu Asn Gly Ser Val Ser Ile Arg Ser Pro  
 340 345 350  
 Gln Lys Asn Lys Lys Lys Met Tyr Met Asn Lys Asn Gly Ser Gly Phe  
 355 360 365  
 Ile Lys Gln Tyr Asn Glu Glu Ser Thr Val Ile Gly Thr Ser Tyr Gly  
 370 375 380  
 Ser Pro Leu Asp Pro Lys Arg Tyr Gln Asp Pro Lys Val Leu Gln Asn  
 385 390 395 400  
 Gln Ile Lys Arg Arg Lys Leu Ile Asp Asp Lys Ala Lys Glu Met Leu  
 405 410 415  
 Glu Gln Lys Leu Ser Lys Leu Gly Ser Ala Ser Leu Leu Asn Asn Leu  
 420 425 430  
 Gln Leu Ser Lys Lys Glu Ala Thr Asp Lys Leu Ala Ser Asp Arg Ser  
 435 440 445  
 Lys Ser Lys Gly Phe Thr Asn Thr Met Ile Ser His Ile Gly Phe Asp  
 450 455 460  
 Pro Thr Gly Thr Ser Leu Asn Gln Asn Ser Thr Ser Leu Gly Ser Lys  
 465 470 475 480  
 Ser Met Glu Lys Ser Arg Ala Arg Glu Leu His Asp Leu Ser Val Glu  
 485 490 495  
 Thr Ser Gly His Lys Ser Leu Ser Ser Ser Lys Gln Asp Arg Gln Ser  
 500 505 510  
 Lys Val Ala Lys Trp Asn Thr Asn Ile Arg Thr Leu Gln Asn Tyr Asp  
 515 520 525  
 Arg Arg Val Ala Ser His Ser Leu Ser Thr Ser Arg Arg Leu Gln Asn  
 530 535 540  
 Leu Val Gly Lys Gln Thr His Ala Thr Leu Val Asp Lys Arg Lys Arg  
 545 550 555 560  
 Val Val Val Ser Asp Asp Glu Gln Pro Gly Met Glu Glu Asp Glu Glu  
 565 570 575  
 Asp Ile Glu Ile Gln Phe Asp Asp Glu Lys Ser Lys Met Ser Tyr Met  
 580 585 590  
 Lys Met Thr Gly Ala Arg  
 595

<210> 375  
 <211> 1499  
 <212> DNA  
 <213> *Candida albicans*

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 caaaattgag aaaaccattt atgcaagtcg tgtactgggt atattcttgg tcaattgcta 240  
 cacttttgta atgaatactg taatgtagcc gacgtgggtt gaanaatata tatttaagta 300  
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<210> 376  
 <211> 332  
 <212> PRT  
 <213> *Candida albicans*

<400> 376  
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 Leu Pro Thr Lys Pro Pro Cys Arg Val Phe Phe Lys Asn Glu Tyr Glu  
 20 25 30  
 Gln Pro Ser Gly Ser Val Lys Leu Arg Gly Met Gly His Leu Val Gly  
 35 40 45  
 Gln Ser Ile Asp Val Ala Arg Lys Leu Gly Lys Ser Asn Val Ala Val  
 50 55 60  
 Phe Ser Ser Ser Gly Gly Asn Ala Gly Leu Ala Ala Tyr Ala Ser  
 65 70 75 80

Gln Phe Phe Gly Val Ser Cys Thr Val Val Leu Pro Glu Ser Ser Lys  
85 90 95

Pro Thr Val Ile Glu Lys Leu Lys Ser Leu Gly Ala Asp Val Ile Ile  
100 105 110

His Gly Lys His Trp Gly Glu Ala Asp Asn Tyr Leu Thr Asp Phe Val  
115 120 125

Ile Lys Asn Leu Asp Lys Thr Val Tyr Pro Val Tyr Cys His Pro Phe  
130 135 140

Asp Asp Pro Leu Leu Trp Glu Gly His Ser Lys Ile Ile Thr Glu Ile  
145 150 155 160

Ile Asp Gln Lys Gln Leu Pro Asn Phe Asp Lys Val Lys Gly Val Ile  
165 170 175

Cys Ser Val Gly Gly Gly Gly Leu Tyr Asn Gly Ile Val Glu Gly Leu  
180 185 190

Glu Asn His Lys Glu Ile Pro Val Leu Ala Ile Glu Thr Lys Gln Ala  
195 200 205

Ala Thr Phe His Glu Ala Val Lys Glu Gly Lys Val Val His Leu Gln  
210 215 220

Lys Val Gln Thr Leu Ala Thr Ser Leu Ala Ser Pro Tyr Leu Ser Ser  
225 230 235 240

Lys Ala Leu Ala Asn Tyr Ile Glu Arg Pro Thr Val Leu Ala Glu Ile  
245 250 255

Asp Asp Leu Asp Ala Val Lys Gly Val Val Asp Val Tyr Asp His Phe  
260 265 270

Gly Tyr Met Val Glu Pro Ala Cys Gly Ala Ser Val Ala Ser Val Met  
275 280 285

His Arg Gln Asp Leu Leu Asn Lys Phe Gly Thr Leu Ser Pro Asp Asp  
290 295 300

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Ile Asp Glu Tyr Arg Ser Leu Leu Glu Lys Asp Ser  
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<210> 377

<211> 2564

<212> DNA

<213> Candida albicans

<400> 377

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&lt;210&gt; 378

&lt;211&gt; 687

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 378

Met Arg Ser Ser Gln Ser Ser Trp Leu Pro Arg Ile Gly Leu Leu Tyr  
1 5 10 15

Val Ala Leu Val Ile Leu Ile Pro Phe Leu Val Ser Pro Lys His Ala  
20 25 30

Phe Ala Val Ala Ala Val Ser Asp Asp Glu Ser Ser Thr Asp Asn Tyr







645

650

655

Tyr Gly Gly Ala Ala Gly Glu Gly Ala Gly Gly Ala Gly Asp Ala Lys  
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Phe Gly Asp Asp Asp Ser Asp Asp Glu Phe Asp His Asp Glu Leu  
 675 680 685

<210> 379  
 <211> 1346  
 <212> DNA  
 <213> Candida albicans

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<210> 380  
 <211> 281  
 <212> PRT  
 <213> Candida albicans

<400> 380  
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Ile Val Val Asp Ser Lys Ser Asp Lys Ile Ile Ser Ile Gly Tyr Asn  
 35 40 45

Tyr Thr Asn His Ser Leu Asn Gly Thr Gln His Ala Glu Phe Ile Ala

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<211> 1062

<212> PRT

<213> Candida albicans

<400> 384

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Val Met Thr Pro	Glu Lys Pro Lys Met	Val Ser Lys Ile	Phe Gly Lys			
	355	360	365			
Ser Ala Lys Ile	Arg Arg Ala Tyr Thr	Pro Thr His Thr	Ser Thr Pro			
	370	375	380			
Met Ala Val Ser	Ser Leu Asn Pro Pro	Ser Ser Ser Thr	Ser Asn Ser			
385	390	395	400			
Thr Thr Ala Ala	Ile Thr Ser Thr Ser	Pro Ala Ala Asp	Glu His Tyr			
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Asp Ile Asp Asn	Asp Cys Asp Ser Pro	Ser Lys Asn Arg	Lys Ser Ser			
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Asn Ile Ser Ala	Ser Ser Ile Ile Ile	Tyr Gln Asp Glu	Asn His Ile			
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Lys Ser Asn His	Ala Arg Lys Ser Ser	Asn Pro Ile Pro	Tyr Pro Pro			
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Gln Thr Ala Phe	Asn Ser Ser Gly Leu	Val Lys Lys Asn	Ser Ile Ser			
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Gly Ser Ser Asp	Arg Lys Leu Pro Pro	Glu Thr Pro Ile	Lys Arg Asn			
	530	535	540			
Pro Leu Met Ile	Leu Asn Thr Asn Lys	Val Val Pro Pro	Tyr Ser Ser			
545	550	555	560			
Gly Phe Ala Glu	Gly Lys Asp Val Met	Gly Asp Gln His	Asp Ile Tyr			
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Ser His Ile Pro	Cys Gln Asn Gln Arg	Phe Pro Gly Ser	Val Asn Pro			
	580	585	590			
Asn Thr Thr Thr	Asn Asn Asn Asn Thr	Gln Gln His His	Asp Ser Asp			
	595	600	605			
Leu Ser Ile Glu	Val Gly Arg Asn Asn	Ser Tyr Asp Ala	Ser Ser Ser			

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     945                      950                      955                      960  
 Phe Asp Leu Glu Gly Asp Arg Asn Tyr Ile Ala Pro Glu Leu Ile Asn  
                     965                      970                      975  
 Asp Lys Ile Tyr Thr Pro Phe Ala Asp Ile Phe Ser Leu Gly Leu Ile  
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 <211> 887  
 <212> DNA  
 <213> Candida albicans

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 <211> 51  
 <212> PRT

392

<213> *Candida albicans*

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Leu Gly Ile  
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&lt;210&gt; 387

&lt;211&gt; 893

&lt;212&gt; DNA

<213> *Candida albicans*

&lt;400&gt; 387

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&lt;210&gt; 388

&lt;211&gt; 130

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 388

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Glu Phe Glu Tyr Ile Asp Asp His Arg Ser Gly Lys Ile Val Val Gln  
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&lt;210&gt; 390

&lt;211&gt; 1372

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 390

Met Pro Asp Asn Ile Glu Asp Arg Ser Glu Ile Pro Ser Asp Ala Lys  
1 5 10 15

Glu Ile Val Thr Thr Asn Glu Ile Glu Ala Thr Asp Ser Glu His Thr  
20 25 30







Gly Ile Pro Leu Phe Val Val Met Asn Lys Glu Val Asp Val Asn Ser  
 645 650 655  
 Phe Gly Phe Ile Arg Lys Lys Leu Leu Glu Thr Val Ser Leu Leu Ser  
 660 665 670  
 Lys Ile Asp Leu Val Asp Glu Tyr Glu Lys Ile Lys Arg Ser Asn Glu  
 675 680 685  
 Asp Tyr Val Glu Lys Val Phe Tyr Lys Lys Ser Asp Phe Pro Ala Leu  
 690 695 700  
 Ser Gln Pro Leu Glu Thr Ser Asp Cys Glu Lys Asn Asn Asn Asn Thr  
 705 710 715 720  
 Ser Asp Asn Asp Asp Asp Glu Asp Ala Asp Asn Asp Glu Gly Tyr Asp  
 725 730 735  
 Ser Glu Val Ser Leu Ala Asn Pro Tyr Leu Gly Ala Asn Phe Gly Phe  
 740 745 750  
 Lys Ile Met Tyr Val His Asp Tyr Ser Pro Lys Leu Asn Ser Asn Leu  
 755 760 765  
 Arg Ser Arg Tyr Asn His Asp Gln Thr Thr Lys Phe Lys Gln Thr Glu  
 770 775 780  
 Arg Val Ile Asn Val Pro Thr His Lys Pro Thr Phe Ser Asp Phe Lys  
 785 790 795 800  
 Pro Leu Ser Asp Gln Leu Ser Glu Ser Lys Arg Asn Tyr Tyr Phe Tyr  
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 Pro Asp Tyr Lys Lys Met Asp Asp Glu Met Asp Gln Leu Val Glu Glu  
 820 825 830  
 Val Asn Gln Asn Leu Ala Glu Gln Xaa Glu Ala Arg Ser Ser Gly Ser  
 835 840 845  
 Glu Asn Ser Ser Arg Ala Ser Glu Glu Gln Asp Gly Phe Val Leu Ile  
 850 855 860  
 Asn Lys Glu Asp Thr Leu Lys Gln Gln Ser Thr Val Pro Ala Ala Ala  
 865 870 875 880  
 Glu Thr Val Pro Pro Pro Leu Pro Val Arg Asn Asn Thr Gly Val His  
 885 890 895  
 Ile Pro Ser Ser Asp Glu Glu Thr Glu Ser Glu Ala Asn Leu Gly Ser  
 900 905 910  
 Leu Phe Asp Ser Thr Ser Asn Leu Pro Leu Pro Pro Pro Ser Thr Tyr  
 915 920 925  
 Ser Glu Ser Thr Lys Pro Ser Asn Val Asn Ser Pro Met Glu Ser Asn  
 930 935 940

Phe Glu Ser Ser Ser Ala Asp Leu Asn Ser Gly Thr Thr Leu Ile Ser  
 945 950 955 960  
 Lys Asp Thr Val Leu Leu Cys Asp Trp Asp Lys Glu Ile Tyr Gln Lys  
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 Cys Phe Gly Asp Lys Glu Leu Gln Ala Trp Glu Asn Ile Ser Asn Leu  
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 Pro Asn Pro Glu Leu Glu Lys Asn Arg Ala His Phe Glu Arg Gln Arg  
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 Lys Ala Lys Ile Thr Leu Ser Asp Cys Leu Lys Ser Phe Ser Thr Pro  
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 Glu Ile Leu Gly Glu His Asp Leu Trp Tyr Cys Pro Arg Cys Thr Glu  
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 His Lys Arg Ala Thr Lys Thr Ile Gln Leu Trp Ser Thr Gly Asp Ile  
 1045 1050 1055  
 Leu Thr Ile His Leu Lys Arg Phe His Ser Ala Arg Ala Phe Ser Asp  
 1060 1065 1070  
 Lys Ile Asp Val Leu Val Asp Phe Pro Ile Glu Gly Leu Asp Ile Ser  
 1075 1080 1085  
 Ser Tyr Val Ala Asn Thr Asp Leu Thr Pro Glu Asp Cys Leu Tyr Asp  
 1090 1095 1100  
 Leu Ile Ala Val Asp Asn His Tyr Gly Gly Leu Gly Gly Gly His Tyr  
 1105 1110 1115 1120  
 Thr Ala Ser Val Lys Asn Phe Arg Asp Asp Lys Trp Tyr Tyr Phe Asn  
 1125 1130 1135  
 Asp Ser Arg Val Thr Glu Ile Asn Asn Pro Gln Glu Val Val Ala Asn  
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 Ser Ala Tyr Leu Leu Phe Tyr Arg Arg Arg Ser Ser Lys Gly Ala Gly  
 1155 1160 1165  
 Ile Leu Gly Gly Glu Asn Phe Ile Asp Leu Leu Gln Lys Gly Arg Glu  
 1170 1175 1180  
 Glu Tyr Ser Glu Ser Leu Gln Lys Lys Arg Leu Val Leu Gln Asn Val  
 1185 1190 1195 1200  
 Gly Gln Ile Val Asn Thr Tyr Ala Lys Ile Glu Gln Asp Ile Ile Asp  
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 Glu Gln Glu Gln Glu Gln Glu Gln Glu Glu Pro Val Gln Glu Pro  
 1235 1240 1245

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400

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&lt;210&gt; 392

&lt;211&gt; 896

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 392

```

His Phe Leu Asn Ser Asn Glu Leu Ser Ser Pro Met Pro Pro Ser Phe
  1              5              10              15

Ser Ile Asn Tyr Gly Ser Glu Trp Asp Leu Glu Ile Ile Gln Thr Ser
      20              25              30

Leu Asp Asn Glu Lys Glu Ser Glu Thr Lys Ser Phe Thr Gly Glu Leu
      35              40              45

Glu Tyr Thr Ser Thr Ser Ser Asn Gly Glu His Asp Thr Thr Thr Thr
      50              55              60

Ala Thr Lys His Glu Leu Ile Leu Gln Gln Ile Leu Asn Ser Asn Asp
      65              70              75              80

Glu Ser Tyr Ile Asn Pro Lys Ser Leu Thr Phe Asp Pro Leu Lys Ile
      85              90              95

Phe Thr Lys Gln Leu Ile Gly Glu Leu Ile Lys Ile Asn Gln Phe Tyr
      100              105              110

Asn Ser Lys Glu Ser Glu Ile Phe Lys Ile Tyr Asn Asn Leu Ile His
      115              120              125

Asp Leu Gln Asn Gln Asn Ile Asn Ile Asp Asp Val Phe Lys Phe Thr
      130              135              140

Gln Ala Tyr Asn Tyr Ser Asp Pro Asn Ile Ile Asn Thr Asp Asp His

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145		150		155		160
His Gln Tyr	His Leu Lys Ser Thr	Leu Ser Arg Thr Val	Thr Asn Ala			
	165	170	175			
Ser Val Phe	Asp Thr Ile Asn His	Ile Asp Asn Asp Tyr	Asp Asn Asn			
	180	185	190			
Asn Asn Asn	Gln Lys Asn Asn Tyr	Asp Leu Glu Lys Gln	Asn Asn Thr			
	195	200	205			
Thr Val Ala	Ile His Asp Asp Asp	Ser Glu Asp Asp	Glu Glu Glu			
	210	215	220			
Glu Glu Glu	Glu Thr His Ser His	Asp Ser Val Leu Leu	Asn His Thr			
	225	230	235	240		
His Phe Asn	Val Lys Gln Gln Leu	Lys Ile Thr Leu Lys	Arg Lys Ala			
	245	250	255			
Ile Thr Leu	Phe Ile Asn Leu Ser	Glu Leu Lys Ser	Phe Ile Glu Leu			
	260	265	270			
Asn Arg Ile	Gly Phe Thr Lys Ile	Cys Lys Lys Phe	Asp Lys Thr Cys			
	275	280	285			
Gly Tyr Ser	Ile Lys Gln Asp Phe	Ile Asn Glu Phe	Leu Pro Gln Tyr			
	290	295	300			
Ser Arg Val	Phe Glu Asn Asp Thr	Ile Glu Glu Leu	Asp Tyr Lys Leu			
	305	310	315	320		
Asn Gln Ile	Ile Lys Ile Tyr Ala	Phe Leu Ser Asn	Lys Leu Thr Thr			
	325	330	335			
Gln Ser Thr	Thr Lys Glu Asp Leu	Asp Asn Ile Lys	Phe Glu Leu Arg			
	340	345	350			
Ser Tyr Leu	Arg Asp His Ile Val	Phe Glu Arg Asn	Thr Val Trp Lys			
	355	360	365			
Asp Leu Leu	Ser Leu Glu Lys Lys	Ser Tyr Asn Ile	Asp Leu Asp Asn			
	370	375	380			
Ser Val Val	Gln Asn Asn Lys Met	Gly Asp Glu Gly	His Ile Ile Asn			
	385	390	395	400		
Ser Met Met	Asn Leu Ser Met Lys	Arg Ile Asn Leu	Pro Gln Cys Leu			
	405	410	415			
Lys Lys Leu	Ile Lys Tyr Asp His	Ile Asp Ile Pro	Gln Phe Leu Leu			
	420	425	430			
Thr Thr Gln	Met Leu Lys Ile Ile	Ile Ile Val Ile	Val Phe Ile Ile			
	435	440	445			
Leu Leu Ala	Val Lys Thr Phe Asn	Asp Pro Val Gln	Gly Arg Cys Leu			



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gcattagtag	ttcaccaaaa	gattttcttca	ccagagagcc	accacggatc	catagtaaat	960	
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tatctactga	tgaattgcgt	tcagttaaat	cacatactga	attagctgaa	actgctaagt	1080	
gagtgagaat	gttagccaaa	aattttatccc	gagcaaccat	tcaatttagac	gttagagcta	1140	
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Ser Ala Asn Asn Arg Ala Ala Lys Glu Val Leu Ser Arg Leu Ser Thr



165										170					175						
Asp	Glu	Leu	Arg	Ser	Val	Lys	Ser	His	Thr	Glu	Leu	Ala	Glu	Thr	Ala						
			180					185					190								
Asn	Gly	Val	Arg	Met	Leu	Ala	Lys	Asn	Leu	Ser	Arg	Ala	Thr	Ile	Gln						
		195					200					205									
Leu	Asp	Val	Arg	Ala	Ile	Met	Ile	Ile	Thr	Lys	Ala	Arg	Asp	Asn	Gly						
	210					215					220										
Leu	Ile	Tyr	Leu	Thr	Lys	Glu	Val	Val	Glu	Trp	Ile	Leu	Asp	Gln	His						
225					230					235					240						
Pro	His	Ile	Thr	Ile	Tyr	Ala	Asp	Glu	Lys	Leu	Ala	Lys	Ser	Lys	Arg						
				245					250					255							
Phe	Asn	Pro	Glu	Ser	Ile	Ile	Ala	Asn	Tyr	Pro	Asn	Gly	Cys	Lys	Lys						
			260					265					270								
Leu	Lys	Tyr	Trp	Asn	Lys	Lys	Leu	Thr	Thr	Lys	Asn	Pro	Glu	Ile	Phe						
		275					280					285									
Asp	Leu	Val	Leu	Thr	Leu	Gly	Gly	Asp	Gly	Thr	Val	Leu	Phe	Ala	Ser						
	290					295					300										
Asn	Leu	Phe	Gln	Lys	Ile	Val	Pro	Pro	Ile	Leu	Ser	Phe	Ser	Leu	Gly						
305					310					315					320						
Ser	Leu	Gly	Phe	Leu	Thr	Asn	Phe	Glu	Phe	Ser	Ala	Phe	Arg	Thr	Val						
				325					330					335							
Leu	Ser	Lys	Cys	Phe	Asp	Ser	Gly	Val	Lys	Ala	Asn	Leu	Arg	Met	Arg						
			340					345					350								
Phe	Thr	Cys	Arg	Val	His	Thr	Asp	Glu	Gly	Lys	Leu	Ile	Cys	Glu	Gln						
		355					360					365									
Gln	Val	Leu	Asn	Glu	Leu	Val	Val	Asp	Arg	Gly	Pro	Ser	Pro	Tyr	Val						
	370					375					380										
Thr	His	Leu	Glu	Leu	Tyr	Gly	Asp	Gly	Ser	Leu	Leu	Thr	Val	Ala	Gln						
385					390					395					400						
Ala	Asp	Gly	Leu	Ile	Ile	Ala	Thr	Pro	Thr	Gly	Ser	Thr	Ala	Tyr	Ser						
				405					410					415							
Leu	Ser	Ala	Gly	Gly	Ser	Leu	Val	His	Pro	Gly	Val	Ser	Ala	Ile	Ser						
			420					425					430								
Val	Thr	Pro	Ile	Cys	Pro	His	Thr	Leu	Ser	Phe	Arg	Pro	Ile	Leu	Leu						
		435																			

406

465		470		475		480
Gly Tyr Tyr Val Thr Ile Gln Ala Ser Pro Phe Pro Leu Pro Thr Val						
	485			490		495
Met Ser Ser Lys Thr Glu Tyr Ile Asp Ser Val Ser Arg Asn Leu His						
	500			505		510
Trp Asn Ile Arg Glu Gln Gln Lys Pro Phe Ser Ser Tyr Leu Lys Pro						
	515			520		525
Glu Thr Arg Gln Ser Ile Ala Glu Ser Glu Arg Leu Asp Asn Leu His						
	530			535		540
Ile Ser Ser Glu Gln Asp Glu Ser Asn His Glu Glu Pro Glu Ile Thr						
	545			550		555
Glu Asp Phe Asp Ile Asn Tyr Thr Asp Asn Glu Arg Asp Ser Ser Ser						
	565			570		575
Ser Thr Pro Ser Glu Glu Ser Asn Glu Glu Cys Ala Asn Thr Thr Thr						
	580			585		590

&lt;210&gt; 395

&lt;211&gt; 1042

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 395

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&lt;210&gt; 396

&lt;211&gt; 253

&lt;212&gt; PRT

<213> Candida albicans

<400> 396

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Met Ser Leu Pro Ala Ser Phe Asp Leu Thr Pro Glu Asp Ala Lys Leu
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Leu Leu Ala Ala Asn Val His Leu Gly Ala Lys Asn Val Gln Val His
          20          25          30

Asn Lys Pro Tyr Val Tyr Lys Thr Arg Pro Asp Gly Met Asn Ile Ile
          35          40          45

Asn Ile Gly Lys Thr Trp Glu Lys Ile Val Leu Ala Ala Arg Ile Ile
          50          55          60

Ala Ala Val Pro Asn Ala Ser Asp Val Ala Val Cys Ser Ser Arg Thr
          65          70          75          80

Phe Gly Gln Arg Ala Val Leu Lys Phe Ala Ala His Thr Gly Ala Thr
          85          90          95

Ala Ile Ala Gly Arg Phe Thr Pro Gly Asn Phe Thr Asn Tyr Ile Thr
          100          105          110

Arg Ser Phe Lys Glu Pro Arg Leu Val Val Val Thr Asp Pro Arg Thr
          115          120          125

Asp Ala Gln Ala Ile Lys Glu Ser Ser Tyr Val Asn Ile Pro Val Ile
          130          135          140

Ala Leu Thr Asp Met Gln Ser Pro Ser Glu Tyr Val Asp Val Ala Ile
          145          150          155          160

Pro Cys Asn Asn Lys Gly Lys His Cys Ile Gly Leu Ile Trp Trp Leu
          165          170          175

Leu Ala Arg Glu Val Leu Arg Leu Arg Gly Ile Ile Pro Asp Arg Thr
          180          185          190

Thr Glu Trp Ser Val Met Pro Asp Leu Tyr Phe Tyr Arg Asp Pro Glu
          195          200          205

Glu Ile Glu Gln Asn Ala Val Glu Glu Ala Lys Thr Glu Gly Val Glu
          210          215          220

Gly Ala Pro Val Ala Glu Ala Glu Thr Glu Trp Thr Gly Glu Thr Glu
          225          230          235          240

Asp Val Asp Trp Ala Asp Ser Gly Ala Thr Pro Ser Cys
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<210> 397

<211> 1335

<212> DNA

<213> Candida albicans

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<210> 398
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<212> PRT
<213> Candida albicans
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			20					25					30				
Ala	Leu	Val	Val	Pro	Trp	Thr	Asn	Ser	Asp	Asn	Glu	Tyr	Asn	Glu	Gly		
		35					40					45					
Ala	Met	Ser	Leu	Ala	Val	Ala	Leu	Ala	Arg	Tyr	Phe	Thr	Lys	Met	Ser		
	50					55					60						
Ile	Trp	Ser	Lys	Asn	Ile	Ile	Phe	Val	Phe	Pro	Glu	Thr	Gly	His	Arg		
65					70					75					80		
Pro	Leu	Arg	Ser	Trp	Val	Glu	Ala	Tyr	His	Thr	Val	Leu	Asp	Asp	Thr		
				85					90					95			
Ala	Gly	Ser	Ile	Glu	Ala	Ala	Ile	Ile	Met	Glu	Tyr	Gly	Lys	Asn	Gly		
			100					105					110				
Asp	Tyr	Phe	Glu	Tyr	Tyr	Asp	Met	Phe	Tyr	Glu	Gly	Leu	Asn	Gly	Gln		
		115					120					125					



Tyr Cys Gly Tyr Lys Pro Val Lys Glu Lys Ser Glu  
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<210> 399  
 <211> 1190  
 <212> DNA  
 <213> *Candida albicans*

<400> 399  
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 gattgatttt tgctggtaaa caattagaag atggcagaac cttgtctgac tacaacatcc 1140  
 aaaaagaatc taccttgcac ttggtcttga gattgagagg tggtttctaa 1190

<210> 400  
 <211> 229  
 <212> PRT  
 <213> *Candida albicans*

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 Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp  
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 Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
 35 40 45  
 Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
 50 55 60  
 Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe  
 65 70 75 80  
 Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser  
 85 90 95

Asp Thr Ile Asp Asn Val Lys Ser Lys Ile Gln Asp Lys Glu Gly Ile  
 100 105 110  
 Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp  
 115 120 125  
 Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His  
 130 135 140  
 Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu  
 145 150 155 160  
 Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp  
 165 170 175  
 Asn Val Lys Ser Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln  
 180 185 190  
 Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu  
 195 200 205  
 Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg  
 210 215 220  
 Leu Arg Gly Gly Phe  
 225

&lt;210&gt; 401

&lt;211&gt; 2390

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 401

```

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```

```

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```

&lt;210&gt; 402

&lt;211&gt; 629

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 402

```

Met Arg Ile Leu Cys Val Ala Glu Lys Pro Ser Ile Ser Lys Glu Val
  1             5             10             15

```

```

Ala Asn Ile Leu Gly Gly Gly Arg Lys Lys Val Arg Asn Ser Arg Glu
          20             25             30

```

```

Lys Phe Ile Lys Asn Tyr Asp Phe Thr Phe Thr Phe Asn Ser Glu Asp
          35             40             45

```

```

Gly Pro Cys Gln Val Thr Met Thr Ser Val Ala Gly His Ile Thr Gly
          50             55             60

```

```

Leu Asp Phe Gly Ser Ala Phe Ser Trp Gly Asn Cys Val Pro Gly Arg
          65             70             75             80

```

```

Leu Phe Glu Ala Asp Ile Lys Thr Ile Ile Thr Lys Lys Ser Ile Tyr
          85             90             95

```

```

Glu Asn Ile Ala Glu Glu Ala Arg Asn Ala Asp Lys Leu Met Ile Trp
          100             105             110

```

```

Thr Asp Cys Asp Arg Glu Gly Glu Tyr Ile Gly Phe Glu Ile Met Asn
          115             120             125

```

```

Ala Ala Arg Lys Tyr Asn Arg Asn Leu Gly Leu Asn Asn Ile Trp Arg
          130             135             140

```

```

Ala Arg Phe Ser His Leu Glu Arg Asn His Ile Ile Arg Ala Ala Lys
          145             150             155             160

```

```

Asn Pro Val Asn Leu Asp Met Ser Ala Val Ser Ala Val Ser Cys Arg

```





414

465                      470                      475                      480  
 Lys Asp Gly Lys Thr Ser Pro Pro Asn His Met Thr Glu Pro Glu Leu  
                                  485                      490                      495  
 Ile Ala Leu Met Asp Ala Asn Gly Ile Gly Thr Asp Ala Thr Ile Ala  
                                  500                      505                      510  
 Glu His Ile Asn Lys Ile Glu Thr Arg His Tyr Ile Asn Lys Leu Lys  
                                  515                      520                      525  
 Lys Gly Lys Asn Glu Tyr Ile Leu Pro Thr Pro Leu Gly Met Gly Leu  
                                  530                      535                      540  
 Ile Glu Gly Leu Glu Lys Met Glu Phe Glu Asp Val Ser Leu Ser Lys  
 545                                   550                      555                      560  
 Pro Phe Leu Arg Lys Ser Leu Glu Arg Ser Leu Glu Asp Ile Ala Thr  
                                  565                      570                      575  
 Gly Ser Arg Pro Lys Val Asp Val Leu Asn Thr Thr Ile Gly Val Tyr  
                                  580                      585                      590  
 Val Asp Ala Tyr Ser Val Cys Ser His Gln Ile Leu Val Leu Cys Asn  
                                  595                      600                      605  
 Glu Cys Arg Arg Ile Ile Leu Gly Asn Ser Ser Asn Asn Asn Asn Asn  
                                  610                      615                      620  
 Asn Asn Asn Asn Thr  
 625

&lt;210&gt; 403

&lt;211&gt; 3098

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 403

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```

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tgattgcatt ggatggtgaa gatgtattga tagttaatcg agatggtaca actgtacgga 3060
aaccacctca atatttcagt tcagaatggg actattaa 3098

```

&lt;210&gt; 404

&lt;211&gt; 865

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 404

```

Met Ile Asp Asn Ile Ile Asn Asn Leu Gln Ile Ile Leu Gln Gln Asn
  1                      5                      10                      15

```

```

Asp Asp Asn Phe Thr Ser Pro His Asp Asp Val Ile Tyr Arg Pro His
      20                      25                      30

```

```

Ser Ala Arg Val Ala Arg Tyr Gln Val Ile Ile Ala Ser Thr Leu Gly
      35                      40                      45

```

```

Leu Thr Ala Leu Leu Leu Phe Ser Ile Leu Arg Leu Lys Tyr Pro Lys
      50                      55                      60

```

```

Ile Tyr Val Ala Asn Phe Asn His Leu Asn Phe Ser Leu His Ser Thr
      65                      70                      75                      80

```



Ser Leu Arg Lys Gly Trp Phe Gly Leu Phe Gly Pro Lys Val Asp Ser  
 385 390 395 400  
 Ile Asn Tyr Tyr Thr Asp Lys Leu Glu Val Ile Asp Lys Glu Ile Thr  
 405 410 415  
 Arg Ala Arg Thr Arg Glu Tyr Pro Ala Thr Ser Thr Ala Phe Leu Thr  
 420 425 430  
 Met Lys Thr Val Ala Glu Ala Gln Met Leu Ala Gln Ala Val Leu Asp  
 435 440 445  
 Pro Lys Val Asn His Leu Ile Thr Asn Leu Ala Pro Ala Pro His Asp  
 450 455 460  
 Ile Arg Trp Asp Asn Leu Ser Leu Thr Arg Gln Asp Arg Asn Thr Lys  
 465 470 475 480  
 Ile Leu Ala Val Thr Ile Phe Ile Gly Ile Met Ser Leu Leu Leu Val  
 485 490 495  
 Tyr Pro Val Arg Phe Met Ala Ser Phe Leu Asn Thr Lys Ser Ile Ser  
 500 505 510  
 Lys Ile Trp Pro Ser Leu Gly Lys Ala Ile Glu Ser His Lys Trp Ala  
 515 520 525  
 Glu Thr Leu Ile Thr Gly Leu Leu Pro Thr Tyr Leu Phe Thr Ile Leu  
 530 535 540  
 Asn Ile Val Ile Pro Phe Phe Tyr Val Trp Ile Ser Glu Lys Gln Gly  
 545 550 555 560  
 Tyr Leu Ser His Ser Asp Glu Glu Leu Ser Ser Val Ser Lys Asn Phe  
 565 570 575  
 Phe Tyr Ile Phe Val Asn Leu Phe Leu Val Phe Thr Thr Phe Gly Thr  
 580 585 590  
 Ala Ser Phe Val Asp Thr Thr Lys Ile Ala Phe Asp Leu Ala Arg Ser  
 595 600 605  
 Leu Arg Asp Leu Ser Met Phe Tyr Val Asp Leu Ile Ile Leu Gln Gly  
 610 615 620  
 Leu Gly Ile Phe Pro Phe Lys Leu Leu Leu Val Gly Asn Leu Leu Arg  
 625 630 635 640  
 Phe Leu Val Asn Ser Leu Phe Arg Cys Lys Thr Pro Arg Asp Tyr Leu  
 645 650 655  
 Asn Leu Tyr Lys Pro Pro Val Phe Asn Phe Gly Leu Gln Leu Pro Gln  
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 675 680 685

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Ser Tyr Ala Ser Asn Leu Gln Leu Pro Asn Lys Gly Pro Tyr Asn Val  
180 185 190

Thr Ile Asp Leu Ser Val Asn Leu Asn Lys Gln Leu Tyr Gln Asp Arg  
 195 200 205  
 Phe Glu Trp Asp Met Asn Gln Asn Glu Val Thr Pro Glu Ile Phe Ala  
 210 215 220  
 Glu Ile Val Val Ala Asp Leu Gly Leu Ser Leu Glu Phe Lys Asn Ala  
 225 230 235 240  
 Ile Ser His Ala Leu His Glu Ile Ile Ile Arg Val Lys Lys Glu Val  
 245 250 255  
 Ile Asp Gly Thr Phe Asp Asn Glu Met His Asn Leu His Leu Val Lys  
 260 265 270  
 Gly Ile Met Phe Glu Gln Gly Ile Arg Ile Phe Thr Glu Asn Ser Val  
 275 280 285  
 Gln Asn Gly Asn Asp Arg Trp Glu Pro Leu Val Glu Val Leu Thr Ser  
 290 295 300  
 Ser Glu Ile Glu Arg Arg Glu Asn Glu Arg Val Arg Asn Leu Arg Arg  
 305 310 315 320  
 Leu Lys Arg Glu Asn Met Arg Arg Asp Tyr Asp Asp His Ser Arg Arg  
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 Arg Gln Ala Gly Lys Arg Arg Tyr Asp Glu Leu Glu Gly Ala Trp Val  
 340 345 350

&lt;210&gt; 407

&lt;211&gt; 737

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 407

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```
<210> 408
<211> 78
<212> PRT
<213> Candida albicans
```

```

<400> 408
Met Ala Arg Glu Ile Lys Asp Ile Lys Glu Phe Val Glu Leu Ala Arg
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Arg Ser Asp Ile Lys Ser Ala Ile Val Lys Val Asn Ala Lys Val Asn
                20                      25                      30

Ala Asn Gly Lys Lys Phe Lys Gln Thr Lys Phe Lys Val Arg Gly Ser
          35                      40                      45

Arg Tyr Gln Tyr Thr Leu Val Val Asn Asp Ala Ser Lys Ala Lys Lys
  50                      55                      60

Leu Gln Gln Ser Leu Pro Pro Thr Leu Lys Ile Thr Asn Leu
  65                      70                      75

```

```
<210> 409
<211> 1348
<212> DNA
<213> Candida albicans
```

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aagacaacaa	tacaatgtca	aatctttggc	aattagacaa	aatgatgaag	ttttagtgtg	1140	
tagaggttct	aaaaaaggtt	ctgaaggtaa	agttaattct	gtttatagat	tgaaatttgc	1200	
tattcgaagt	gataaattac	ataagagaaa	atcaaatggc	gcttctgttc	caatcaacat	1260	
tcaccatct	aaagttgtca	ttactaaatt	acatttggag	aaagatagaa	aagctttgat	1320	
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<210> 410
<211> 127
<212> PRT
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&lt;213&gt; Candida albicans

&lt;400&gt; 410

Met Ala Lys Ile Ser Ile Asp Val Ser Ser Ser Arg Ser Lys Ala Arg  
 1 5 10 15

Lys Ala Tyr Phe Thr Ala Ser Ser Val Glu Arg Arg Val Leu Leu Ser  
 20 25 30

Ala Pro Leu Ser Lys Glu Leu Arg Gln Gln Tyr Asn Val Lys Ser Leu  
 35 40 45

Pro Ile Arg Gln Asn Asp Glu Val Leu Val Val Arg Gly Ser Lys Lys  
 50 55 60

Gly Ser Glu Gly Lys Val Asn Ser Val Tyr Arg Leu Lys Phe Ala Ile  
 65 70 75 80

Gln Val Asp Lys Leu Gln Lys Glu Lys Ser Asn Gly Ala Ser Val Pro  
 85 90 95

Ile Asn Ile His Pro Ser Lys Val Val Ile Thr Lys Leu His Leu Asp  
 100 105 110

Lys Asp Arg Lys Ala Leu Ile Gln Arg Lys Gly Gly Lys Ala Glu  
 115 120 125

&lt;210&gt; 411

&lt;211&gt; 1631

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 411

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 aggttgaaaa caaagattac tattcccagg attatgatac ctttgtggag gaatatcccc 1320

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atgcaactcc tgaggatttg aaattgatgt ggaagggttg gaaaggggtg caaagagaaa 1620
tgaccaagta a                                     1631

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&lt;210&gt; 412

&lt;211&gt; 376

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 412

```

Met Phe Val Tyr Trp Ile Asn Asn Leu Cys Glu Ile Ile Gln Cys Ile
  1             5             10             15

Cys Trp Arg Arg Arg Arg Gln Gly Arg Thr Phe Phe Pro Ser Tyr Phe
      20             25             30

Phe Phe Ser Leu Ser Leu Phe Phe Gln Ser His Cys Ser Ser Val Lys
      35             40             45

Gly Trp Leu Phe Cys Ala Glu Pro Cys Gly Ser Val Asn Ala Arg His
      50             55             60

Arg Val Ile Phe Gly Glu Thr Lys Arg Ile Leu Lys Asn Arg Gly Leu
      65             70             75             80

Asn Ser Thr Thr Asp Trp Leu Asp Asp Lys Met Gln Ser Val Phe Ile
      85             90             95

Arg Thr Phe Ala Thr Ser Arg Ile Glu Phe Gln Arg Tyr Gln Pro Arg
      100            105            110

Phe Val Asn Thr Ile Lys Glu Thr Val Lys Ser Ala Gln Glu Lys Ser
      115            120            125

Tyr Ser Ile Thr Arg Pro Leu Gly Leu Ser Lys Pro Val Leu Leu Asn
      130            135            140

His Lys Leu Ser Asp Thr Tyr Ser Leu Ser Asn Ile Tyr Glu Glu Leu
      145            150            155            160

Phe Gly Gln Lys Ser Lys Glu Arg Arg Gln Lys Gln Leu Asp Tyr Asp
      165            170            175

Leu Lys His Ser Pro Ile Tyr Glu Val Lys Ser Phe Glu Asn Thr Lys
      180            185            190

Gly Lys Ile Phe Thr Pro Pro Val Ser Tyr Phe Arg Gln Asp Lys Ser
      195            200            205

Leu Tyr Phe Pro Asp Phe Ile Ala Lys Thr Leu Ala Gly Asn Gln Arg
      210            215            220

Ser Leu Tyr Asp Ser Leu Asp Asn Arg Leu Ser Ile Val Lys Leu Phe

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<400>	413					
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agaattgctg	gtgcgcacaaa	agattatatgt	tattttatgt	gcgttgttat	cctgcacact	240
aaaattgagc	agtgtacaca	cacacatat	gggtgtgatt	tttattcttg	ttttttcgtc	300
gtctctcac	gtttaagctc	taagtgaatt	tgtgtgtgct	gtaaatagtgt	gtgtgttcca	360
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ggcgtgaaat	tgaaaaatcc	acccaaccca	ttttcccat	acaaaatgtc	cacatcagaa	1140
aagtcaaat	gttgaacaaa	ccaaaattcg	acttgggttc	attattgggt	ttgcacgggt	1200

425

aaggttcaac cgaagaaaaa ggtaagaaag tttcttctgg tttcaaagat gttgttttag 1260  
aatctgttta a 1271

&lt;210&gt; 414

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 414

Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Leu  
1 5 10 15  
Lys Lys Lys Val Val Asp Pro Phe Thr Arg Lys Asp Trp Phe Asp Ile  
20 25 30  
Lys Ala Pro Thr Thr Phe Glu Asn Arg Asn Val Gly Lys Thr Leu Ile  
35 40 45  
Asn Arg Ser Thr Gly Leu Lys Asn Ala Ala Asp Gly Leu Lys Gly Arg  
50 55 60  
Val Phe Glu Val Cys Leu Ala Asp Leu Gln Gly Ser Glu Asp His Ser  
65 70 75 80  
Tyr Arg Lys Ile Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Leu  
85 90 95  
Leu Thr Asn Phe His Gly Leu Asp Phe Thr Ser Asp Lys Leu Arg Ser  
100 105 110  
Leu Val Arg Lys Trp Gln Ser Leu Val Glu Ala Asn Val Thr Val Lys  
115 120 125  
Thr Ser Asp Asp Tyr Val Leu Arg Val Phe Ala Ile Ala Phe Thr Lys  
130 135 140  
Arg Gln Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Gln Ser Ser Lys  
145 150 155 160  
Leu Arg Glu Val Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Val  
165 170 175  
Ser Asn Cys Thr Leu Ala Gln Leu Thr Ser Lys Leu Ile Pro Glu Val  
180 185 190  
Ile Gly Arg Glu Ile Glu Lys Ser Thr Gln Thr Ile Phe Pro Leu Gln  
195 200 205  
Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Gln Pro Lys Phe Asp  
210 215 220  
Leu Gly Ser Leu Leu Ala Leu His Gly Glu Gly Ser Thr Glu Glu Lys  
225 230 235 240  
Gly Lys Lys Val Ser Ser Gly Phe Lys Asp Val Val Leu Glu Ser Val  
245 250 255

<210> 415  
 <211> 1517  
 <212> DNA  
 <213> *Candida albicans*

<400> 415  
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 agttgtggat cctattttta ataaaacaat aatagtaata aaaaaaaaaa ccttctttgc 180  
 ttttcgagaa tttgtaacac attgtttctt tcttcccaca gcaaccaaatt tttattttat 240  
 tttttctttt gggacttacc cacagttgct caattatgta taacaagggg agaaactctg 300  
 tgggattccc tccttaaaaa tatagcaatc ctttttcttc acaacgattg ctatatgacc 360  
 cccccctaa gcattcattg cttttatata tatttaataa tgtatttctc ttgttcagga 420  
 taattatcac tatttgtgac gtttaatttt tacatttctt cttcttcttc ttcctatttc 480  
 aacattaaag aacattta atgtatttcc caatcattgt atgggtatat gtatctatca 540  
 cttttgtggt tgccaattat gggtttgatc aatggacaaa tgatgattta aaacaatttt 600  
 taaaagaacg taaagttgca ttcaatgatg ccttgagaaa tccaaaatta attagtttgg 660  
 ctaatgaaga agctaagaaa ttagaaaaag gttacaagaa agttactgaa gaattaaata 720  
 acaatttgaa tcctccagat gattcattaa atgattattt gaattttgat tacttatttg 780  
 ggaaaagaaa agaaaattat tcaattaaag aatggatttt tgaaagttgg ccagtaacca 840  
 gtttgcaaac ttttttaact caaaaataata tccaatatag tgcaaaggat accaaagatg 900  
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 taaaagaatt tagttatcaa gccactcatt caattagaga ttccaaagaa tctttatttg 1140  
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 agtctcaacc ttggatcaca aaggagagaac aaaagtctca gaaaaagaag ggtagtaatt 1440  
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 tgggcaatct tgactaa 1517

<210> 416  
 <211> 338  
 <212> PRT  
 <213> *Candida albicans*

<400> 416  
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 20 25 30  
 Phe Leu Lys Glu Arg Lys Val Ala Phe Asn Asp Ala Leu Glu Asn Pro  
 35 40 45  
 Lys Leu Ile Ser Leu Ala Asn Glu Glu Ala Lys Lys Leu Glu Lys Gly  
 50 55 60



<210> 417  
 <211> 2243  
 <212> DNA  
 <213> *Candida albicans*

<400> 417  
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 attaaagtga aaaaacaattt ccgaaaaaag aagaaaatcg aacacattag aaaaagaaac 180  
 gaacaaaaga aaaaaaattt caaattgtag ttgcatgtat ataaaaataat ataaaagata 240  
 tatcaccagc acaactgatt actttttatt tatatcacct gtcaacaaca aatttccaaa 300  
 taaatacaac tcagaaaaaa cacttactat cttttcttag tttggtttct ataattctat 360  
 taaacattct tgcccttcat ccttgattat catattagat cttatcttta atttgtttga 420  
 aaaaaataata ccaataatct tcccattaga acttacaaca caacaacaaa aaaaccatt 480  
 ctaaactact attctccatt atgaaaattt tcagattatt ttcactacta atcgtacaat 540  
 ttatcataaa taccactggt gcagtatcac ctgtgtcagc agttttacca aaactgagtt 600  
 tcagtccatt tgattcacca gaattttgtt cacagatcat aactcccact tgtaatacaa 660  
 ctttcaccta cattgatgaa ttgaataaag atattcgctc ctacttgctg gaatttagca 720  
 agaccctgta tttccgttat tttaaagtca atttagataa acaatgtcgt ttttggaatg 780  
 ctcaacattt ttgtgctagt gaaaactgtg ctgttgaaat attggaagat ttcaattgga 840  
 gtcaagtcac caatgaaagt ttgaaacctt caggattagg taagatttca ttacctgaca 900  
 aatcatcaat tgataattcc attgaaaccg aagaagttca aacttggtgaa gatttagatt 960  
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 attgtttccc taataactaat ccaatgtcag tgacaaatga tgccgacaat ggtgggtaac 1140  
 aatgtatcga aaagaacttg ttttatcgtg ttggtagtgg tatgcatgct tcaattgcag 1200  
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 ccttagtgtc ccaagctata gttaaattga gtgaaatttt accattgaga gagttcattc 1380  
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 tcgaatcagt cgaagtttat gatcgtttgt tgtttagatga cattattcct agtttggaag 1500  
 caaatgttgt gtttaatact tccaacttgt ttgataatag caatttgagg gatgaattta 1560  
 gatcaagatt tagaaacatt tctgccatta tggatttgtt tggttgtgat agatgcagaa 1620  
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 acaactatga taatcacaat ttgaaattta gaagaattga aattggtgcc ttgattaata 1740  
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 acaacaaacc aggtaacgga tttgccttcc catttgttag tccattacct cagaaaaaac 1920  
 ctgaccaaac caacaccccc aaaaatcaac aacaaaaaca acctcaagaa actgacaaaa 1980  
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 aatacagtca agtccttgga taa 2243

<210> 418  
 <211> 580  
 <212> PRT  
 <213> *Candida albicans*

<400> 418  
 Met Lys Ile Phe Arg Leu Phe Ser Leu Leu Ile Val Gln Phe Ile Ile  
 1 5 10 15  
 Asn Thr Thr Val Ala Val Ser Pro Val Ser Ala Val Leu Pro Lys Ser  
 20 25 30







[illegible]

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<210> 421
<211> 1031
<212> DNA
<213> Candida albicans
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<400> 424
Met Leu Ile Pro Lys Glu Asp Arg Lys Lys Ile His Gln Tyr Leu Phe
  1             5             10             15

Gln Glu Gly Val Val Val Ala Lys Lys Asp Phe Asn Gln Pro Lys His
      20             25             30

Asp Glu Ile Asp Thr Arg Asn Leu Phe Val Ile Lys Ala Leu Gln Ser

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35					40					45						
Leu	Thr	Ser	Lys	Gly	Tyr	Val	Lys	Thr	Gln	Phe	Ser	Trp	Gln	Tyr	Tyr	
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Tyr	Tyr	Thr	Leu	Thr	Asp	Glu	Gly	Val	Glu	Phe	Leu	Arg	Thr	Glu	Leu	
65					70					75					80	
Asn	Ile	Pro	Glu	Gly	Ile	Leu	Pro	Leu	Thr	Arg	Leu	Lys	Asn	Ala	Pro	
85					90					95						
Ala	Glu	Arg	Pro	Arg	Pro	Ser	Arg	Gly	Gly	Pro	Arg	Arg	Gly	Gly	Tyr	
100					105					110						
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115																

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<210> 425
<211> 2840
<212> DNA
<213> Candida albicans
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aggctccgtc	aattttccaac	tccatcagca	gttcaaataa	tatagattca	atactaaaac	1020
gacctgtaca	tctacgtgag	gcatacaacgt	attcagtgaa	tgataatgac	caccgaaatc	1080
tttgtctacc	aaactcaact	gaaaggttta	ctgcttcacc	ttcgaacaat	attggtaatg	1140
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<400> 426																
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			20					25					30			
Ile	Ser	Lys	Gln	Asn	Ser	Thr	Lys	Thr	Asp	Phe	Phe	Ala	Ala	Arg	Leu	
		35		8			40					45				
Ala	Ser	Ala	Val	Asp	Asp	Ile	Glu	Ser	Ser	Asp	Ser	Asp	Glu	Thr	Phe	
	50					55					60					
Ile	Tyr	Glu	Asn	Asn	Asp	Thr	Glu	Leu	Asp	Asp	Asn	Ala	Ser	Asn	Ile	
65					70					75					80	
Asn	Asn	Asn	Asn	Asn	Asn	Ser	Thr	Asn	Asn	Ile	Ile	Asn	Leu	Asp	Asn	
				85					90					95		
Ala	Ser	Val	Asn	Gly	Ser	Met	Ile	Ala	Ser	Ser	Asn	Ala	Met	Val	Thr	
			100					105					110			
Gly	Pro	Pro	Gly	Thr	Ser	Ile	Ala	Leu	Gly	Ser	Gly	Leu	Arg	Ser	Pro	
		115					120					125				
Ser	Ile	Leu	Glu	Gly	Glu	Gln	Leu	Gln	Tyr	Phe	His	Asp	Pro	Val	Arg	
	130					135					140					
Gln	Gln	Gln	Phe	Lys	Leu	Pro	Ser	Thr	Lys	Ala	Pro	Ser	Ile	Ser	Asn	
145					150					155					160	
Ser	Ile	Ser	Ser	Ser	Asn	Asn	Ile	Asp	Ser	Ile	Leu	Lys	Arg	Pro	Val	
				165					170					175		





Gln	His	His	Tyr	Tyr	Tyr	Asp	Tyr	Asp	Asp	Phe	Asp	Gln	Glu	Ser	Gln	
				485					490					495		
Ile	Asn	Gly	Pro	Asn	Phe	Asp	Leu	Pro	Asp	Leu	Pro	Ile	Asn	Arg	Ser	
				500					505					510		
Ala	Ser	Arg	Asn	Phe	Asn	Asn	Asn	Asn	Asn	Pro	Lys	Arg	Phe	Gly	Asp	
				515					520					525		
Ser	His	Phe	Phe	Leu	Pro	Arg	Lys	Thr	Asp	Gln	Tyr	Ser	Gln	Arg	Thr	
				530					535					540		
Ser	Phe	Leu	Lys	Ser	Cys	Ile	Tyr	Thr	Phe	Val	Cys	Ile	Leu	Ile	Val	
				545					550					555		
Leu	Thr	Ile	Gly	Phe	Val	Leu	Gly	Phe	Val	Leu	Ala	Thr	Thr	Lys	Asp	
				565					570					575		
Leu	Thr	Asp	Val	Gly	Ile	Thr	Ser	Ile	Glu	Asn	Pro	Ile	Val	Ser	Lys	
				580					585					590		
Asp	Glu	Leu	Val	Phe	Asn	Val	Val	Ile	Glu	Ala	Phe	Asn	Pro	Gly	Trp	
				595					600					605		
Phe	Ser	Val	Asp	Ile	Asn	Glu	Val	Glu	Leu	Asp	Leu	Phe	Ala	Arg	Ser	
				610					615					620		
Gly	Tyr	Leu	Pro	Asp	Thr	Asp	Asn	Ser	Lys	Ile	Ser	Asn	Met	Gly	Gly	
				625					630					635		
Ser	Gln	Lys	Val	Glu	Thr	Val	Lys	Leu	Gly	Thr	Ile	Leu	Asn	Phe	Glu	
				645					650					655		
Ser	Val	Leu	Asn	Phe	Lys	Gly	Gly	Phe	Leu	Ser	Arg	Glu	Pro	Thr	Ile	
				660					665					670		
Gln	Lys	Gly	Gly	Ile	Arg	Leu	Leu	Tyr	Pro	Gly	Lys	Asn	Val	Thr	Ala	
				675					680					685		
Glu	Ala	Lys	Leu	Val	Val	Asn	Met	Ala	Asp	Ile	Lys	Ile	Ala	Ala	Ser	
				690					695					700		
Asn	Ser	Ile	Ala	Lys	Glu	Ser	Thr	Thr	Ser	Asn	Asp	Thr	Asn	Asp	Asn	
				705					710					715		
Asp	Asn	Ser	Lys	Lys	Trp	Glu	Ile	Ile	Ser	Ser	Asn	Pro	Phe	Asp	Leu	
				725					730					735		
Ile	Ile	Thr	Gly	Val	Leu	Lys	Tyr	Asp	Leu	Pro	Phe	Ser	Arg	Thr	Ser	
				740					745					750		
Arg	Ser	Val	Val	Val	Arg	Lys	Thr	Gly	Tyr	Ile	Asp	Pro	Thr	Leu	Phe	
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Val	Ile	Pro	Gln	Gly	Glu	Asn	Asn	Ile	Ser	Ile						
				770					775							

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<400> 428
Met Ile Arg Lys Gln Ala Arg Glu Arg Arg Glu Tyr Leu Tyr Arg Lys
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Ala Leu Gln Leu Gln Glu Ser Ser Leu Thr Glu Lys Arg Gln Gln Leu
          20             25             30
Lys Ala Ala Leu Ala Ser Gly Lys Ser Leu Ser Lys Glu Leu Ala Glu
      35             40             45
Asp Glu Lys Leu Gln Arg Asp Phe Ile Tyr Asp Glu Ser Glu Gln Ile
    50             55             60
Glu Ile Asp Asp Glu Tyr Ser Arg Leu Ser Gly Ile Ser Asp Pro Lys
  65             70             75             80
Val Val Ile Thr Thr Ser Arg Asp Pro Ser Val Lys Leu Leu Gln Phe
          85             90             95

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ctaggaacag	gaaaaataaa	aacgaataaa	caaaaacccc	ccaatcggca	tgcatacgga	180	
ttcttttcagc	ccaattactt	tattttttgcc	cactttctttt	ggattagggc	aatagcccta	240	
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gttggtaaac	tttttttttt	ttcgcagggt	ttgaaaaaaaa	aatcattttt	acagtttaca	360	
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<400> 431

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<210> 432

<211> 251

<212> PRT

<213> Candida albicans

<400> 432

Met Val Asn Ala Ile Leu Ser Lys Lys Lys Lys Leu Val Ala Asp Gly  
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Val Phe Tyr Ala Glu Leu Asn Glu Phe Phe Thr Arg Glu Leu Ala Glu  
20 25 30

Gln Gly Tyr Ala Gly Val Glu Val Arg Lys Thr Pro Ser Lys Leu Glu  
35 40 45

Val Ile Val Lys Ala Ser Asn Thr Gln Gly Val Leu Gly Glu Gln Gly  
50 55 60

Arg Arg Ile His Glu Leu Thr Ser Leu Ile Val Lys Arg Phe Lys Leu  
65 70 75 80

Ser Pro Glu Gly Ile Ala Ile Tyr Ala Glu Arg Val Glu Glu Arg Gly  
85 90 95

Leu Ser Ala Ala Val Gln Ala Glu Ala Leu Lys Ala Lys Leu Leu Ser  
100 105 110

Gly Leu Pro Ile Arg Arg Ala Ala Tyr Gly Val Leu Arg Phe Ala Met  
115 120 125

Gly Ala Gly Ala Lys Gly Val Glu Val Val Ile Ser Gly Lys Leu Arg  
130 135 140

Ala Ala Arg Ala Lys Ser Gln Lys Tyr Ala Asp Gly Phe Met Ile His

<400>	433					
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agtaagtaat	attagttgtg	ctcctcggtt	tcccaattca	tatgctattt	gagctccatt	180
accactggct	ccaccagtaa	tcataaacac	tttcccctgc	atgtctcgct	cccacgtatt	240
ggtggcacca	tggaaataat	acttggtcc	agcaagagtt	aatagaatgg	gaagaacggt	300
aggtccatat	tctttaattt	ggtcccaata	tggaatcacc	tctggcccat	caaacacaac	360
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ggaggttgga	atttgttcac	aaattgggtg	cctttttatt	cttcttgtcc	ttttttttt	480
cagtgtctaac	ataattttggg	atgtatgtat	tgaaaaaaaaa	aaattttgta	caatttcttg	540
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Met 1	Tyr	Val	Leu	Lys 5	Lys	Lys	Asn	Phe	Val 10	Gln	Phe	Leu	Val	Leu 15	Val
Leu	Pro	Leu	Ile 20	Ser	Ser	Leu	Ser	Tyr 25	Lys	Phe	Thr	Asn	Met 30	Asp	Glu
Val	Val	Phe 35	Tyr	Ile	Ala	Gln	Gly 40	Asp	Pro	Ala	Asp	Lys 45	His	Ser	Gln
Glu	Ser 50	Tyr	Gly	Tyr	Val	Thr 55	Ser	Ile	His	Ser	Ser 60	Lys	Gln	Tyr	Ala
Ser 65	Tyr	Arg	Gln	Ala	Asp 70	Ser	His	Ile	Asn	Gly 75	Thr	Ala	Ile	Thr	Gly 80
Ile	Gly	Pro	Gly	Glu 85	Arg	Ile	Phe	Thr	Ala 90	Val	Pro	Asn	Lys	Ala	Leu
Ile	Asn	Val 100	Tyr	Ser	Trp	Gly	Lys	Glu 105	Ser	Val	Asp	Gln 110	Arg	Ile	Pro
Ile	Pro 115	Glu	Ala	Leu	Thr	Cys	Ile	Thr 120	Leu	Ile	Asn	His 125	Pro	Asn	Gly
Ser 130	Asn	Asn	Asn	Ser	Asp	Asn 135	Asp	Asp	Asn	Gln	Leu 140	Tyr	Lys	Leu	Pro
Asn 145	Tyr	Arg	Val	Pro	Trp 150	Leu	Leu	Ala	Gly	Gly 155	Ser	Lys	Ser	Gly	Lys 160
Leu	Tyr	Ile	Trp	Glu 165	Leu	Ser	Ser	Gly	Asn 170	Leu	Leu	Cys	Val	Arg	Asp
Ala	His	Tyr 180	Gln	Gly	Ile	Thr	Thr	Ile 185	Lys	Gly	Ser	Ser	Cys	Gly	Thr
Phe	Leu	Ile 195	Thr	Gly	Gly	Glu	Asp 200	Ala	Arg	Cys	Leu	Val 205	Trp	Asn	Leu
Ala 210	Glu	Leu	Ile	Ser	Ile	Tyr 215	Asp	Lys	Ser	Asp	His 220	Gln	Val	Lys	Pro







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<210> 437
<211> 1076
<212> DNA
<213> Candida albicans
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catttttaaga	aagtattaat	cagctgaatt	aagcaattga	aacgaattga	accagctcag	300
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<210> 438  
<211> 191  
<212> PRT  
<213> *Candida albicans*

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<400> 438
Met Ser Ala Asn Asp Phe Tyr Ser Ser Gly Asp Gln Ser Asn Tyr Asp
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Pro Lys Arg Ser Ser Asn Gln Gly Ser Ser Ser Ser Asn Asp Glu Gln
      20          25          30

Gln Asp Arg Gly Leu Leu Ser Thr Val Ala Gly Gly Val Ala Gly Gly
      35          40          45

Tyr Gly Gly His Lys Leu Gly Glu Lys Ala Gln His Gly Thr Leu Gly
  50          55          60

Thr Val Leu Gly Ala Ile Gly Gly Ala Ile Gly Ala Asn Lys Leu Glu
  65          70          75          80

Asp Ala Tyr Glu Asp Arg Lys Glu His Lys Lys His Glu Gln Gln Tyr
      85          90          95

Gly Gly Ser Gly Lys His Glu Gly Gly Arg His Glu Gly Gly Phe Gly

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100 105 110  
 Gly Gly Arg Pro Asp Asp Arg Tyr Glu Gly Asp Arg Arg Asn Asp Asn  
 115 120 125  
 Tyr Gly Gly Gly Tyr Asn Asp Arg Arg Asp Asp Gly Tyr Gly Gly Gly  
 130 135 140  
 Tyr Gly Gly Gly Arg Pro Asp Asp Arg Arg His Glu Gly Gly Phe Gly  
 145 150 155 160  
 Gly Gly Arg Pro Asp Asp Arg Phe Gly Gly Gly Arg Pro Asp Asp Arg  
 165 170 175  
 Phe Gly Gly Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Trp  
 180 185 190

<210> 439  
 <211> 1745  
 <212> DNA  
 <213> Candida albicans

<400> 439  
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448

&lt;210&gt; 440

&lt;211&gt; 414

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 440

Met Lys Phe Ser Val Leu Val Leu Leu Ala Ser Tyr Leu Val Gly Val  
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Asn Ser Ser Ile Val Asp Thr Ser Glu Glu Leu Ile Cys Pro Asp Pro  
 20 25 30

Glu Asn Pro Leu Asp Cys Tyr Pro Lys Leu Phe Val Pro Thr Asn Glu  
 35 40 45

Trp Gln Thr Ile Lys Pro Gly Gln Asp Ile Pro Pro Gly Leu His Val  
 50 55 60

Arg Leu Asn Ile Asp Thr Leu Glu Lys Glu Ala Lys Leu Met Ser Ala  
 65 70 75 80

Asp Glu Lys Asp Glu Pro Val Gln Glu Val Val Val Gly Gly Glu Leu  
 85 90 95

Gln Asp His Ser Arg Glu Ala Ile Thr Glu Asn Leu Gln Lys Leu His  
 100 105 110

Glu Ser Lys His Pro Glu Val Lys Gln Glu His Ala His Arg Thr Lys  
 115 120 125

Val Ser Gln Gly Asp Leu Ser Asn Phe Asp Ala Ala Cys Ser Glu Ile  
 130 135 140

Glu Ser Phe Lys Pro His Glu Ser Asp Val Glu Arg Leu His Leu Ala  
 145 150 155 160

Leu Asp Thr Leu Glu Glu Leu Ser His Asp Ile Glu Phe Gly Val Lys  
 165 170 175

Leu Thr Ser Asp Lys Ala Ile Phe Gln Ser Phe Val Asn Ile Ala Asn  
 180 185 190

Gly Ala Ser Asp Pro Lys Ile Thr Glu Lys Val Tyr Arg Val Met Gly  
 195 200 205

Ser Ser Leu Arg Asn Asn Pro Glu Ala Ile Ser Asn Ile Leu Thr Asn  
 210 215 220

Phe Asp Lys Ser Tyr Val Asp Asn Leu Phe Glu Gln Leu Ala Asn Glu  
 225 230 235 240

Asn Asp Val Leu Gln Lys Arg Ile Leu Gly Ile Ile Gln Ala Leu Val  
 245 250 255

Gln Asn Ser His Phe Ala Arg Gln Tyr Phe Ser Phe Asp His Ser Ser  
 260 265 270

Gly Leu Asn Asp Leu Ile Ala Ile Phe Pro Lys Leu Gly Pro Asn Ser  
275 280 285

Lys Ser Arg Ala Ser Asn Ile Leu Glu Asp Leu Gln Leu Phe Pro Val  
290 295 300

Thr Asn Asp Arg Arg Ser Leu Glu Asp Gln Asp Pro Glu Ser Gln Val  
305 310 315 320

Ser Lys Phe Ile Gln Asn Ser Phe Val Gly Asn Lys Leu Asp Glu Lys  
325 330 335

Asn Phe Lys Ser Tyr Phe Asp Gln Leu Val Asn Leu His Gln Ser Asn  
340 345 350

Lys Ser Leu Arg Pro Ser Gly Asp Phe Leu Asn Trp Leu Ala Glu Glu  
355 360 365

Val Glu Ser Arg Lys Glu Asn Lys Lys Arg Asp Asp Tyr Ser Gln Glu  
370 375 380

Asp Lys Asp Phe Asp Glu Tyr Met Leu Arg Ala Arg His Glu Val Phe  
385 390 395 400

Gly Asn Pro Met Gly Leu Arg Lys Ala Ile Ala Asp Glu Leu  
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<210> 441

<211> 1244

<212> DNA

<213> Candida albicans

<400> 441

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ttgaacaaca agagaaggcc gtcacagaga atgtggccgc agctactacc accgccacag 1140
atacgaatag cgtcaatcaa caaggtctag ttatacccggt acacaatgaa ccagcaacta 1200
atatacctga ggctaccccca aaaactgcta caaataccat ctaa 1244

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450

&lt;210&gt; 442

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 442

Met Phe Ser Leu Phe Phe Pro Pro Gln Ala Ile Val Tyr Thr Leu Leu  
 1 5 10 15

Met Gly Pro Leu Gly Val Ile Gly Ala Trp Tyr Ser Leu Ile Ser Gln  
 20 25 30

Ala Ser Thr Leu Ser Ile Phe Val Val Thr Ile Ser Leu Met Pro His  
 35 40 45

Ile Gln Arg Val Ala Tyr Asp Ala Ile Leu Ser Arg Glu Cys Ala Asn  
 50 55 60

Asp Val Val Leu Met Gly Lys Leu Arg Arg Tyr Arg Lys Leu Pro Ile  
 65 70 75 80

Arg Val Arg Ala Arg Glu Tyr Leu Lys Ala Ile Pro Asp Phe Ser Ile  
 85 90 95

Phe Pro Phe Ser Leu Leu Lys Leu Leu Val Phe Phe Gly Ile Tyr Phe  
 100 105 110

Ile Pro Phe Val Gly Pro Ile Ile Val Leu Phe Phe Gln Ser Ser Lys  
 115 120 125

Arg Gly Leu Lys Ala His Ala Arg Tyr Phe Lys Leu Lys Gly Phe Ser  
 130 135 140

Arg Ser Asp Ile Arg Thr Ile His Lys Leu Asn Arg Pro Ala Tyr Met  
 145 150 155 160

Gly Tyr Gly Val Val Ala Leu Trp Leu Glu Ser Phe Pro Phe Ile Asn  
 165 170 175

Met Phe Phe Met Phe Thr Asn Thr Leu Gly Ala Ala Leu Trp Ala Val  
 180 185 190

Asp Ile Glu Gln Gln Glu Lys Ala Val Thr Glu Asn Val Ala Ala Ala  
 195 200 205

Thr Thr Thr Ala Thr Asp Thr Asn Ser Val Asn Gln Gln Gly Leu Val  
 210 215 220

Ile Pro Val His Asn Glu Pro Ala Thr Asn Ile Pro Glu Ala Thr Pro  
 225 230 235 240

Lys Thr Ala Thr Asn Thr Ile  
 245

<210> 443  
 <211> 2270  
 <212> DNA  
 <213> *Candida albicans*

<400> 443  
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 tgtattatac aatattttaa ttatagtaat catcctataa atttcaaagt caaaagacag 180  
 atcttaaggt ctaattaata actctctatg gccttctgtg tcaaatttgt gtcgtttgat 240  
 aacaagtttg gaacggtaat ggttgaaatt agaaaagaaa aaaattacac atggtagcag 300  
 ctgatgtata gaactttcta gcaaaaaaaa aaagaaagaa tttttttttc ttccattttt 360  
 caaatttgag agatcgaaat aattttcttg aattttattaa aaggggaaccc cttcccga 420  
 aatccaaaac caaaacttcc acccaaatat caaataacta acttatcatt ccaacagata 480  
 atattcccac ttcaataaca atgacaacag ctgacgaata caaagcagaa ggtaacaaat 540  
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 cacctgaacc aaaccatggt ctttattcaa atcgttctgg atcttatgcc tctttaaaag 660  
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 aagggataaa tagaattgct ggggctgaat ttgggttagg taattttgat caagccaaat 780  
 ccaattatga aaaatgtttg gagttggatc caaataatgc catggctaaa gaaggtttaa 840  
 aatcagttga atctgcttta tcatctgggt gtgggtgatga caaggattta ggatttggt 900  
 aaattttaaa tgatccta atcttatacta aattgaaaaa taatcctaaa acaagtgaat 960  
 ttatgaatga tctcaattt gttgctaaac ttgaacgtct taaaactaat ccacaattgg 1020  
 gtaatcctga tatgtttagt gatccaagat tattgacggc ttttgctgct ttaatgggt 1080  
 ttgacatgga ttaccacaa atgggattca ctgctccaaa cgaatcacaa tccaatgcat 1140  
 cagaacccaa actggaacca aaatcagtac cagaatctaa accagaacca aaagcagaac 1200  
 aaaaggaaga agaatcaacc tcagccaaag atgaagacac tccaatgact gatgcccaag 1260  
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 attataaatt gattgctaaa tcatttgcta gattaggtaa tatttatttg aaaaaagatg 1560  
 aattaccgga agcagtga aaatttgaaa aatctttaac tgaacatcgt acccctgatg 1620  
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 gaactaaaga tgttgaaatt ggtggtaaat caattcatga aattgatgaa ttaatgaata 2040  
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 gagtttctaa agatccagaa attgttcaaaa ttttacaaga tccagtaatg caaggaattt 2160  
 tagctcaagc tagagaaaat cctgctgctt tacaagatca tatgaaaaat cctgaagttt 2220  
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<210> 444  
 <211> 589  
 <212> PRT  
 <213> *Candida albicans*

<400> 444  
 Met Thr Thr Ala Asp Glu Tyr Lys Ala Glu Gly Asn Lys Tyr Phe Ala  
 1 5 10 15  
 Ala Lys Asp Phe Glu Lys Ala Ile Glu Ala Phe Thr Lys Ala Ile Glu  
 20 25 30

452



Leu Ile Ala Lys Ser Phe Ala Arg Leu Gly Asn Ile Tyr Leu Lys Lys  
 340 345 350  
 Asp Glu Leu Pro Glu Ala Val Lys Asn Phe Glu Lys Ser Leu Thr Glu  
 355 360 365  
 His Arg Thr Pro Asp Val Leu Asn Lys Leu Arg Ser Thr Gln Arg Glu  
 370 375 380  
 Ile Lys Thr Arg Glu Leu Asn Ala Tyr Ile Asp Pro Glu Lys Ala Glu  
 385 390 395 400  
 Glu Ala Arg Leu Gln Gly Lys Glu Tyr Phe Thr Lys Gly Asp Trp Pro  
 405 410 415  
 Asn Ala Val Lys Ala Tyr Thr Glu Met Ile Lys Arg Ala Pro Glu Asp  
 420 425 430  
 Ala Arg Gly Tyr Ser Asn Arg Ala Ala Ala Leu Ala Lys Leu Leu Ser  
 435 440 445  
 Phe Pro Asp Ala Ile Gln Asp Cys Asn Lys Ala Ile Glu Lys Asp Pro  
 450 455 460  
 Asn Phe Ile Arg Ala Tyr Ile Arg Lys Ala Asn Ala Gln Leu Ala Met  
 465 470 475 480  
 Lys Glu Tyr Ser His Val Met Asp Thr Leu Thr Glu Ala Arg Thr Lys  
 485 490 495  
 Asp Val Glu Leu Gly Gly Lys Ser Ile His Glu Ile Asp Glu Leu Met  
 500 505 510  
 Asn Lys Ala Thr Tyr Gln Arg Phe Gln Ala Ile Glu Gly Glu Thr Pro  
 515 520 525  
 Glu Gln Thr Met Glu Arg Val Ser Lys Asp Pro Glu Ile Val Gln Ile  
 530 535 540  
 Leu Gln Asp Pro Val Met Gln Gly Ile Leu Ala Gln Ala Arg Glu Asn  
 545 550 555 560  
 Pro Ala Ala Leu Gln Asp His Met Lys Asn Pro Glu Val Tyr Lys Lys  
 565 570 575  
 Ile Asn Met Leu Ile Ala Ala Gly Val Ile Arg Thr Arg  
 580 585

&lt;210&gt; 445

&lt;211&gt; 1019

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 445

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ccactaacaa actttttttt gactatacac cactgaaaaa aaaaaaaaaa tttttgtaaa 60
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cgttataata gaatagaata agagcatgac aacaaaggga tacaagcttg aaaaaagaaa 180
aagggtggga tatcttaaaa ttattaaaga gtttttttta taacatgtca ttgagattga 240
gattgggaat actgaattcg attttaaagt cattggatgg gagagttaat tattcgtttt 300
attattagga ttaccaatga atagtaatga agtgatggag agatagaatg aaagtattca 360
gaagagcatc aagtccttta taagtttggtg agacataata tgtctacccc cttgtcaact 420
tgtcataaat tttattgctc gtccctttaa agaaatgaat aaaaagattt actaacttaa 480
tttcaattat ttatagaaag atgtctagat taaacgaata tcaagttatt ggtcgttaatt 540
taccaactga atccgttcca gaaccaaagt tggtcagaat gagaattttt gtcctaaaca 600
ccgttggtgc caaatcaaga tattggtatt tcttgcaaaa attgcataaa gttaaaaaag 660
cttctgggtg aattgtatct gtcaacatta tttctgaagc taaaccaact aaagttaaaa 720
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acagagctag atttagaagt atccatattt tgaaagttgt tgaattagaa aaaactgatg 900
atgttaaaag acaatacgtt aaacaatttt tgactaaaga tttgaaattc ccattaccac 960
acagagtcctt aaaatctaag aaattgttcc aagctactgc tccaaccact ttctactaa 1019

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&lt;210&gt; 446

&lt;211&gt; 172

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 446

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Met Ser Arg Leu Asn Glu Tyr Gln Val Ile Gly Arg Asn Leu Pro Thr
  1             5             10             15

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```

Glu Ser Val Pro Glu Pro Lys Leu Phe Arg Met Arg Ile Phe Ala Pro
      20             25             30

```

```

Asn Thr Val Val Ala Lys Ser Arg Tyr Trp Tyr Phe Leu Gln Lys Leu
    35             40             45

```

```

His Lys Val Lys Lys Ala Ser Gly Glu Ile Val Ser Val Asn Ile Ile
    50             55             60

```

```

Ser Glu Ala Lys Pro Thr Lys Val Lys Thr Phe Gly Ile Trp Leu Arg
    65             70             75             80

```

```

Tyr Glu Ser Arg Ser Gly Ile His Asn Met Tyr Lys Glu Tyr Arg Asp
      85             90             95

```

```

Val Thr Arg Val Gly Ala Val Glu Thr Met Tyr Gln Asp Leu Ala Ala
    100            105            110

```

```

Arg His Arg Ala Arg Phe Arg Ser Ile His Ile Leu Lys Val Val Glu
    115            120            125

```

```

Leu Glu Lys Thr Asp Asp Val Lys Arg Gln Tyr Val Lys Gln Phe Leu
    130            135            140

```

```

Thr Lys Asp Leu Lys Phe Pro Leu Pro His Arg Val Gln Lys Ser Lys
    145            150            155            160

```

```

Lys Leu Phe Gln Ala Thr Ala Pro Thr Thr Phe Tyr
      165            170

```

455

<210> 447  
 <211> 932  
 <212> DNA  
 <213> Candida albicans

<400> 447  
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 tggttttttg tgtacatgtg agatatataa ttgtgtatat acagtcacgt gaatagagca 180  
 gaaaaattac gaagtagaaa tattggtagc gcgttagggc tatagcccta tttagtttgt 240  
 gcaccacacg acttacaatt tttttttttt tctttcttag aatccttgag gcactgacac 300  
 tgtactctct ctctctctct ctctctctcg taggtagtga aaaatttcca ctagtcttcc 360  
 cataaccacac ctaggttctt tcttttggaa accactgagc agtaaataca tttacttgac 420  
 gaagaagtct atacataaat ataaacttgt cccctccccc cctttttttt ttaactaact 480  
 aagaagaaaa aattaaaaaa atgtctgacg ttgaacaaga acaaattgtt gaagaagttg 540  
 ttgttgaaga acaatccggt gccatcacca ttgaagatgc tttaaaagtt gttttaagaa 600  
 cttcttttagt ccatgatggt ttagctagag gtttaagaga agcttctaaa gctttatcta 660  
 aaagagaagc tcaattatgt gttttgtgtg actctgttac tgaagaatca atcatcaaat 720  
 tgggttgaagc tttatgtaat gaaccagaag aaaaaatccc attgattaaa gtttccgatg 780  
 ctaaattatt ggggtgaatgg gctggtttat gtcaattaga tagagatggg aatgctagaa 840  
 aagttgttgg tgctcttgt gttgttgta aaaactgggg tgctgattct gatgaaagaa 900  
 acatcttggt ggaacacttt tctcaacaat aa 932

<210> 448  
 <211> 143  
 <212> PRT  
 <213> Candida albicans

<400> 448  
 Met Ser Asp Val Glu Gln Glu Gln Ile Val Glu Glu Val Val Val Glu  
 1 5 10 15  
 Glu Gln Ser Gly Ala Ile Thr Ile Glu Asp Ala Leu Lys Val Val Leu  
 20 25 30  
 Arg Thr Ser Leu Val His Asp Gly Leu Ala Arg Gly Leu Arg Glu Ala  
 35 40 45  
 Ser Lys Ala Leu Ser Lys Arg Glu Ala Gln Leu Cys Val Leu Cys Asp  
 50 55 60  
 Ser Val Thr Glu Glu Ser Ile Ile Lys Leu Val Glu Ala Leu Cys Asn  
 65 70 75 80  
 Glu Pro Glu Glu Lys Ile Pro Leu Ile Lys Val Ser Asp Ala Lys Leu  
 85 90 95  
 Leu Gly Glu Trp Ala Gly Leu Cys Gln Leu Asp Arg Asp Gly Asn Ala  
 100 105 110  
 Arg Lys Val Val Gly Ala Ser Cys Val Val Val Lys Asn Trp Gly Ala  
 115 120 125

456

Asp Ser Asp Glu Arg Asn Ile Leu Leu Glu His Phe Ser Gln Gln  
 130 135 140

<210> 449  
 <211> 881  
 <212> DNA  
 <213> Candida albicans

<400> 449  
 aaaatttcca atcttgaatt tcatcttcaa cgtcataaac ttgttctggt tgaaatttat 60  
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 acagacacac acacacacac acacacacaa ttttcagctc cttccaagtc gtgtttttttt 300  
 ggaagaaaaa aaaaacaact tggccctaaa aactctatgc tctaaccgac aacattagat 360  
 tactttgata actcacaacc tttaattaac actatctaca aaatatgaca agtacaccaa 420  
 taacgtacaa gacactagta tgaaaggcaa gcacaaactt gcaaacaaaa aacccttaac 480  
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 cattaaccag ttttaaccaat attaaagatc attcctcatt attaaattca tctaatagca 660  
 atactaatag caataccaac ggtacaattg ccagtaatgg tggaaatggg actacaagtg 720  
 atgaaaataa tgaaattgaa aattcaacaa ttcaagataa atcaaaatta aaacaattag 780  
 aaacttcaag gtatttcga tgtcttaatt gtggtagaaa tattgccggt ggaagatttg 840  
 catctcatat aagtaagtgt ttagaacgga aacggaaatg a 881

<210> 450  
 <211> 126  
 <212> PRT  
 <213> Candida albicans

<400> 450  
 Met Leu Phe Cys Phe Ile Leu Thr Lys Ile Cys Phe Phe Phe Phe Ser  
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 Lys Ala Asp Ser Ile Phe Asn Asp Leu Ile Asn Asn Ile Ile Lys Gln  
 20 25 30  
 His Thr Leu Thr Ser Leu Thr Asn Ile Lys Asp His Ser Ser Leu Leu  
 35 40 45  
 Asn Ser Ser Asn Ser Asn Thr Asn Ser Asn Thr Asn Gly Thr Ile Ala  
 50 55 60  
 Ser Asn Gly Gly Asn Gly Thr Thr Ser Asp Glu Asn Asn Glu Ile Glu  
 65 70 75 80  
 Asn Ser Thr Ile Gln Asp Lys Ser Lys Leu Lys Gln Leu Glu Thr Ser  
 85 90 95  
 Arg Tyr Phe Arg Cys Leu Asn Cys Gly Arg Asn Ile Ala Gly Gly Arg  
 100 105 110  
 Phe Ala Ser His Ile Ser Lys Cys Leu Glu Arg Lys Arg Lys  
 115 120 125

<210> 451  
 <211> 5344  
 <212> DNA  
 <213> *Candida albicans*

<400> 451  
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 gcattctact ttttttctcc ttatggaaaa cattagtact agtagtggtg gtagtagttg 180  
 ctgtttgtttg cactttgcac gtagttgttt tccccctatt ctttcatctg attattctgt 240  
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 aatgcttggg gtactttgtt gttggaaaaga gtattgcaga agtaatagtt taataaaaaga 600  
 aaagtatata acttttagtaa tcggagaaca attgaaatca atattttgaa aatatagttt 660  
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 gatgagaaac ttggaataca ctttgaagcc atctcatggc ggcaatattg aaagcaatcc 4200  
 agaaaaacca gaggatttga tgtatgatgg atcgttatta atggaaacag ctgaaaaatt 4260  
 attagttgaa atagaaaagg gtaagaaaga ggatatcaaa atgcaaagaa ttatatccga 4320  
 ttcagtattg gaaagaacaa gatcgattcg taaggatatt cacaaaacca ttgatacatt 4380  
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 ttgtttatta gatcgtctt tagaaaaatt gggtgttatg gttgaggaac atgccaacgg 4500  
 attattatta acaccaacga cctccacgga cgatctcaga agtagagcca tgtcgccatc 4560  
 ggctactggt gatacaatcc atgaaagtgc aaatgagttg attactgctg gaccaatttt 4620  
 atcaccacat gtcaatagga aagcagaaca aagctcgtat ttcccagtgt ttgccataa 4680  
 tgataatttg acccctcatc aagttgtcgt tgagtcaaat gatgaaggta gagatgttcc 4740  
 aatagataaa atgacaggac gaccagtttt gattcgatca attagtcaaa cttctgtgca 4800  
 tgcaaaagag caagaaattg aagaagggga gcttcataaa tttggattct ttattcaaca 4860  
 aaaagagaga caaaaacaac aacaacaaca acaacaaca cagaactcac accaccagca 4920  
 ccaaccggcc cagctgatcc aacaagaaaa ccagctgccg ctgccacaac aaggaaaata 4980  
 tgaagattta ccgatattaa atacattacc gtcaggacca gagttgagag atgctataat 5040  
 ggcagctaag ggagtagcaa atgttactga attaatgtat cgaattaata atcatcgtgt 5100  
 taaaatcgat gcccatcgaa caaaacacca ctaatgaattg aacaaacca attctgacaa 5160  
 agtagttgag gatgaagttg aagtttctga taatgcctct attgattcta ctaatggtga 5220  
 cgatttacat caacttggtg acggtaaaca taatggtaat ggtacggttg atcccatggt 5280  
 tagtgaagtt tatgacaagt tgttaaatga tgctgaacga gtcagactga atagagatat 5340  
 ataa 5344

<210> 452  
 <211> 1364  
 <212> PRT  
 <213> Candida albicans

<400> 452  
 Met Thr Ser Asn Ser Pro Pro Leu Gly Ser Thr Thr Asn Asp Gln Arg  
 1 5 10 15  
 Leu Pro Gln Ser Gly Val Ser Ser Ile Pro Thr Asn Lys Leu Pro Leu  
 20 25 30  
 Pro Asn Ala Asn Glu Asp Phe Ala Thr Gly Val Ser Asn Gly Asp Val

35					40					45					
Asp	Trp	Leu	Phe	Arg	Gly	Lys	Ser	Lys	Lys	Leu	Gly	Lys	Lys	Met	Ala
50						55					60				
Asn	Asn	Asn	Ala	Asn	Lys	Asp	Glu	Arg	Lys	Asn	Ser	His	Gly	Asn	Ile
65				70						75					80
Lys	Asn	Ser	Glu	Lys	Thr	Thr	Ala	Lys	Pro	Asn	Glu	Thr	Lys	His	Glu
				85					90					95	
Ser	Asn	Gly	Glu	Lys	Leu	Glu	Phe	Asn	Val	Pro	Lys	Ser	Val	Met	Pro
		100				105						110			
Thr	Lys	His	Thr	Ser	Ser	Gly	Asn	Pro	Lys	Ala	Pro	Thr	Asn	Gly	Gln
		115				120						125			
Ile	Ser	Asn	Val	Thr	Pro	Ser	Gln	Pro	Ser	Pro	Lys	Gln	Thr	Thr	Ser
130						135				140					
Gly	Ser	Thr	Asn	Ala	Asn	Asp	Ile	Pro	Pro	Ile	Ser	Pro	Lys	Gln	Pro
145				150						155				160	
Glu	Lys	Ala	Ser	Lys	Leu	Asn	Lys	Leu	Lys	Ile	Gly	Arg	Ser	Arg	Ser
				165			170						175		
Ser	Ser	Ala	Ser	Thr	Val	Val	Pro	Ser	Ser	Thr	Thr	Ala	Ser	Thr	Thr
		180						185				190			
Thr	Asn	Pro	Gly	Asp	Pro	Lys	Ser	Gln	Pro	Lys	Arg	Arg	Ser	Ser	Ser
		195				200						205			
Phe	Asn	Phe	Val	Thr	Pro	Ser	Leu	Thr	Ser	Asp	Leu	Ala	Tyr	Asp	Asp
210						215				220					
Pro	Ala	Leu	Val	Ser	Gln	Leu	Ser	Asn	Asn	Ser	Asn	Ser	Ser	Asn	Ser
225				230						235				240	
Ser	Ser	Pro	Asn	Val	Ser	Arg	Ser	Asn	Ser	Lys	Lys	Gly	Gly	Leu	Phe
				245			250						255		
Ser	Ser	Leu	Ser	Ser	Lys	Phe	Arg	Ser	Ser	Ser	Ala	Ser	Ser	Lys	Gln
		260						265				270			
Pro	Gln	Ser	His	Ser	Ser	Ser	Thr	Pro	Ser	Thr	Thr	Thr	Thr	Asn	Gly
		275				280						285			
Gly	Gly	Asn	Ser	Ser	Ala	Ala	Pro	Lys	Ser	Ser	His	His	Ser	Pro	Lys
290						295				300					
Phe	Asn	Pro	Ser	Leu	Val	Gly	Pro	Val	Ser	Lys	His	Asn	Arg	Glu	Ala
305				310						315				320	
Glu	Asp	Leu	Val	Ser	Leu	Thr	Asn	Thr	Leu	Pro	Ala	Gly	Ser	Gly	Ile
				325			330						335		
Pro	Ile	Lys	Arg	Lys	Pro	Ser	Ile	Ser	Gly	Asn	Ser	Ile	Phe	Lys	Asp

460

340	345	350
Ser Phe Leu Asp Asp Ala Ser Ser Ser Pro Ser Ser Ser Leu Asn Ser		
355	360	365
Asp Gly Gly Leu Lys Phe Phe Arg Arg Arg Ser Ser Val Ala Ser Thr		
370	375	380
Pro Ser Thr His Ala Ser Thr Pro Arg Val Ile Leu Asn Lys Asn Pro		
385	390	395
Asn Arg Arg Lys Val Pro Ile Glu Glu Ile Ser Glu Val Arg Leu Arg		
405	410	415
Arg Val Thr Phe Ser Val Asp Lys Leu Glu His Asp Pro Gln Gln Gln		
420	425	430
Ile Pro Ser Arg Arg Pro Lys Arg Gly Asn Val Leu Ile Pro Gln Asp		
435	440	445
Ile Asn Ala Pro Pro Pro Arg Leu Cys Leu Gly Ile Ser Val Asn Glu		
450	455	460
Pro Asn Asn Lys Asp Asp Gly Lys Ser His Asn His Ser Lys Tyr Ser		
465	470	475
Asp His Glu Ile Ala Leu Ala Glu Asp Ala Gln Arg Arg Ala Ile Ile		
485	490	495
Glu Ala Glu Lys His Ala Gln Glu Ala His Arg Gln Ala Lys Lys Ile		
500	505	510
Ala Gln Glu Val Ser Gly Tyr Arg Ser His Arg Phe Ile Ser Ile Lys		
515	520	525
Glu Gly Gly Ser Val Gly Asn Ser Asn Thr Asn Gly Asn Asp Asn Asp		
530	535	540
Glu Asp Asp Asp Glu Val Glu Glu Ala Val Asp Lys Lys Leu Ala Asn		
545	550	555
Asp Val Ser Val Asp Gly Pro Leu His Val His Glu Gln His Phe Glu		
565	570	575
Glu Glu Ile Glu Ser Lys Thr Gly Glu Lys Thr Ile Ser Leu Glu Thr		
580	585	590
Ile Tyr Thr Arg Cys Cys His Leu Arg Glu Ile Leu Pro Ile Pro Ala		
595	600	605
Thr Leu Lys Gln Leu Lys Asn Lys Thr Ala Pro Leu Glu Val Leu Lys		
610	615	620
Met Leu Asn Pro Lys Pro Thr Leu Ile Asp Val Leu Ser Phe Ser Asp		
625	630	635
Phe Ile Ala Ile Thr Pro Ile Asn Thr Val Ile Phe Asp Asn Val Thr		



645					650					655					
Met	Thr	Thr	Glu	Met	Leu	Lys	Asn	Phe	Leu	Gly	Ser	Leu	Thr	Tyr	Asn
			660					665					670		
Lys	Gln	Leu	Glu	Lys	Leu	Ser	Leu	Arg	Asn	Val	Ser	Ile	Asp	Glu	Leu
		675					680					685			
Gly	Trp	Lys	Tyr	Leu	Cys	Glu	Phe	Leu	Ala	Thr	Asn	Lys	Thr	Val	Lys
	690					695					700				
Lys	Leu	Asp	Ile	Ser	Gln	Gln	Arg	Ile	Lys	Pro	Asp	Thr	Pro	Asp	Thr
705					710					715					720
Ser	Ile	Arg	Gly	Asn	Met	Asn	Trp	Asp	Leu	Phe	Ile	Arg	Ser	Leu	Ile
				725					730					735	
Leu	Arg	Gly	Gly	Ile	Glu	Glu	Leu	Val	Ile	Asn	Gly	Cys	Lys	Leu	Ser
			740					745					750		
Asp	Ala	Ile	Phe	Glu	Lys	Phe	Ile	Asn	Gln	Ala	Val	Lys	Lys	Ser	Thr
	755						760					765			
Tyr	Arg	Leu	Gly	Ile	Ala	Gly	Ile	Asp	Leu	Asn	Val	Lys	Lys	Ser	Glu
	770					775					780				
Met	Val	Thr	Ser	Trp	Leu	Thr	Asp	Gly	Asn	Ser	Gln	Cys	Val	Gly	Val
785					790					795					800
Asp	Ile	Ala	Phe	Asn	Asp	Leu	Ser	Lys	Gly	Gln	Leu	Arg	Pro	Phe	Ile
				805					810					815	
Asn	Ala	Phe	Asn	Thr	Gly	Lys	Val	Asn	Asn	Leu	Val	Phe	Phe	Ser	Leu
			820					825					830		
Asn	Ser	Thr	Asn	Leu	Ser	Asn	Ile	Glu	Glu	Thr	Ser	Asp	Leu	Ile	Lys
		835					840					845			
Ser	Leu	Ile	Asn	Val	Lys	Thr	Leu	Arg	Phe	Leu	Asp	Leu	Ser	Ser	Ile
	850					855					860				
Pro	Asn	Ile	Phe	Pro	Lys	Ile	Ile	Thr	His	Leu	Asp	Lys	Tyr	Leu	Pro
865					870					875					880
Arg	Tyr	Pro	Asn	Leu	Arg	Arg	Ile	His	Phe	Asp	Leu	Asn	Glu	Leu	Thr
				885					890					895	
Ala	Gln	Ala	Ile	Gly	Ser	Leu	Ala	Gly	Cys	Leu	Ser	Lys	Met	Pro	Gln
			900					905					910		
Leu	Val	His	Val	Ser	Leu	Leu	Gly	Asn	Arg	Asn	Leu	Ser	Thr	Thr	Ser
		915					920					925			
Ala	Ala	Thr	Leu	Tyr	Gly	Ala	Val	Lys	Gln	Ser	Lys	Thr	Leu	Phe	Ala
	930					935					940				
Leu	Asp	Leu	Asp	Tyr	Asp	Leu	Ile	Pro	Asp	Gln	Leu	Ser	Gln	Arg	Ile



1250 1255 1260  
 Ala Ala Lys Gly Val Ala Asn Val Thr Glu Leu Ile Asp Arg Ile Asn  
 1265 1270 1275 1280  
 Asn His Arg Val Lys Ile Asp Ala Pro Ser Thr Lys His His His Glu  
 1285 1290 1295  
 Leu Asn Lys Pro Asn Ser Asp Lys Val Val Glu Asp Glu Val Glu Val  
 1300 1305 1310  
 Ser Asp Asn Ala Ser Ile Asp Ser Thr Asn Gly Asp Asp Leu His Gln  
 1315 1320 1325  
 Leu Gly Asp Gly Lys His Asn Gly Asn Gly Thr Val Asp Pro Met Val  
 1330 1335 1340  
 Ser Glu Val Tyr Asp Lys Leu Leu Asn Asp Ala Glu Arg Val Arg Ser  
 1345 1350 1355 1360  
 Asn Arg Asp Ile

<210> 453  
 <211> 1859  
 <212> DNA  
 <213> Candida albicans

<400> 453  
 acggaataat gttatgcgaa cagagtaact gggattatca acaagcatca gtcaattttca 60  
 aaaactcggc tgcttctttg cctagtgatg catttgatca atagaattat aattaaaaga 120  
 aaggtagaat agaattcaat gtaggtgata tcactttctg agagttctta ttacgatata 180  
 taaaatacat agccaaaatt ataatagaag aaaaacatgt aactgtgtaa ttttattcaa 240  
 gtccaaagggt attgattaat attgtagagt gttgagcatt taaaatatga aggaagaccg 300  
 ataacctaata gttttcctca ggggtgctgaa ggctaggagg aataaaatct gagtagagaa 360  
 ctttcgttta tatcagtttt ttgcaagaaa aaaaggaaaa caaaacaaaa taacaccaca 420  
 aacgaattac acaagcacat cctaaacacc actctgttgg agcaccaatc aacctgagaa 480  
 atgcaaaactt gtaataaaat atgggataca atatagcaat ggtaacagat tttttttacc 540  
 ctcaacctgg aggagtagag tttcatgtgt atcattttatc aaaaaaactc attgaactag 600  
 gacactcagt gggtatcata actcataatt attcatcaag aaatgggtgta cgagtattaa 660  
 cgaatgggtt gaaagtgtat tatgtaccac tttgggtgat ctatagaagc tcagttttcc 720  
 caactgtatt tctgtgcttc ccaatattga ggaatatctt catacgagaa aacattgaga 780  
 ttattcacgg acatgggttc ttcagcacat tatgccacga agctatatta catggccgaa 840  
 caatgggatt aaaaacagtc ttcactgatc attcactttt tggatttgcc gagattggat 900  
 caattatggg gaataaaagca ttaaagttca ctttcagtga tgttggccat gttatctgtg 960  
 tcagtcacac ctgtaaagaa aacacgggtt taagaggatc aatagacccc ataaaagtga 1020  
 gtgtgatacc gaatgcagtt attctgaaag atttcaagcc caaatcgcat tgtgttaaca 1080  
 agaactatac taaagagatc accattgttg tgatcacgag attgtttcca aataaaggag 1140  
 ccgattctatt aacggctgtt atccccaaaa tttgccagtt gaaacaaaaa gtgaaatttc 1200  
 taattgctgg tgacggcccc aagtttttag atttgaaca aatgagagaa aagtactttc 1260  
 ttcaggaaag gggtacatta gtaggcgcta taaaacacga agaagtaaga gatgtaatgg 1320  
 tccaagggtga catatactta catccttcat taacagaggc gtttggtaca gttattgtgg 1380  
 aagctgcac atgtgggtta tatgttgtca ctacaaaagt tggaggcata cccgaagtct 1440  
 taccaaacga aatgacaagc tttgctgaac cggaagaaaa ctcaattatt gatgctgcta 1500  
 tagatgctat aaataaaaatt gaaagtaatg aaatcgatac ctcaaaattt cacgatgcgg 1560

464

ttgcaaagat gtacagttgg aatgatattg caagaagaac agaaaatggt tataattcac 1620  
 ttgatttaga caaactaaac gagtcctttac ttcaccgatt acaaagatac tattgttggtg 1680  
 gtataatagc aggcaaactt tatgctttat gtgtaatagt ggatattttt attttcgtga 1740  
 tactagaatg gttgtatccc gctgatcata tcgataaagc aacaaaatgg ccactggcta 1800  
 tcaaggaaga agacgagctg gaagaagaaa catttatttt tccgaacaaa gtaaattag 1859

&lt;210&gt; 454

&lt;211&gt; 452

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 454

Met Gly Tyr Asn Ile Ala Met Val Thr Asp Phe Phe Tyr Pro Gln Pro  
 1 5 10 15

Gly Gly Val Glu Phe His Val Tyr His Leu Ser Gln Lys Leu Ile Glu  
 20 25 30

Leu Gly His Ser Val Val Ile Ile Thr His Asn Tyr Ser Ser Arg Asn  
 35 40 45

Gly Val Arg Val Leu Thr Asn Gly Leu Lys Val Tyr Tyr Val Pro Leu  
 50 55 60

Trp Val Ile Tyr Arg Ser Ser Val Phe Pro Thr Val Phe Ser Cys Phe  
 65 70 75 80

Pro Ile Leu Arg Asn Ile Phe Ile Arg Glu Asn Ile Glu Ile Ile His  
 85 90 95

Gly His Gly Ser Phe Ser Thr Leu Cys His Glu Ala Ile Leu His Gly  
 100 105 110

Arg Thr Met Gly Leu Lys Thr Val Phe Thr Asp His Ser Leu Phe Gly  
 115 120 125

Phe Ala Glu Ile Gly Ser Ile Met Gly Asn Lys Ala Leu Lys Phe Thr  
 130 135 140

Phe Ser Asp Val Gly His Val Ile Cys Val Ser His Thr Cys Lys Glu  
 145 150 155 160

Asn Thr Val Leu Arg Gly Ser Ile Asp Pro Ile Lys Val Ser Val Ile  
 165 170 175

Pro Asn Ala Val Ile Ser Lys Asp Phe Lys Pro Lys Ser His Cys Val  
 180 185 190

Asn Lys Asn Tyr Thr Lys Glu Ile Thr Ile Val Val Ile Thr Arg Leu  
 195 200 205

Phe Pro Asn Lys Gly Ala Asp Leu Leu Thr Ala Val Ile Pro Lys Ile  
 210 215 220

Cys Gln Leu Lys Pro Lys Val Lys Phe Leu Ile Ala Gly Asp Gly Pro  
 225 230 235 240

Lys	Phe	Leu	Asp	Leu	Glu	Gln	Met	Arg	Glu	Lys	Tyr	Phe	Leu	Gln	Glu	
				245					250					255		
Arg	Val	Thr	Leu	Val	Gly	Ala	Ile	Lys	His	Glu	Glu	Val	Arg	Asp	Val	
				260					265					270		
Met	Val	Gln	Gly	Asp	Ile	Tyr	Leu	His	Pro	Ser	Leu	Thr	Glu	Ala	Phe	
				275					280					285		
Gly	Thr	Val	Ile	Val	Glu	Ala	Ala	Ser	Cys	Gly	Leu	Tyr	Val	Val	Thr	
				290					295					300		
Thr	Lys	Val	Gly	Gly	Ile	Pro	Glu	Val	Leu	Pro	Asn	Glu	Met	Thr	Ser	
				305					310					315		
Phe	Ala	Glu	Pro	Glu	Glu	Asn	Ser	Leu	Ile	Asp	Ala	Ala	Ile	Asp	Ala	
				325					330					335		
Ile	Asn	Lys	Ile	Glu	Ser	Asn	Glu	Ile	Asp	Thr	Ser	Lys	Phe	His	Asp	
				340					345					350		
Ala	Val	Ala	Lys	Met	Tyr	Ser	Trp	Asn	Asp	Ile	Ala	Arg	Arg	Thr	Glu	
				355					360					365		
Asn	Val	Tyr	Asn	Ser	Leu	Asp	Leu	Asp	Lys	Leu	Asn	Glu	Ser	Leu	Leu	
				370					375					380		
His	Arg	Leu	Gln	Arg	Tyr	Tyr	Cys	Cys	Gly	Ile	Ile	Ala	Gly	Lys	Leu	
				385					390					395		
Tyr	Ala	Leu	Cys	Val	Ile	Val	Asp	Ile	Phe	Ile	Phe	Val	Ile	Leu	Glu	
				405					410					415		
Trp	Leu	Tyr	Pro	Ala	Asp	His	Ile	Asp	Lys	Ala	Thr	Lys	Trp	Pro	Ser	
				420					425					430		
Ala	Ile	Lys	Glu	Glu	Asp	Glu	Ser	Glu	Glu	Glu	Thr	Phe	Ile	Phe	Pro	
				435					440					445		
Asn	Lys	Val	Asn													
				450												

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<210> 455
<211> 1231
<212> DNA
<213> Candida albicans
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<400> 455						
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tctagaaata	attgaataat	gatataaata	taatgttgtg	aaacttggtg	aaaaatttga	120
cagcctagta	actcaagtgt	tgttacactc	ttgttattat	tattattata	tcgtttacaa	180
gtagatttct	cattttgaac	agcaaatact	gtcgttaata	ggaactcagag	gcagaaaaga	240
agagaggaga	aaaaaaaaag	gacacattta	cacgtatacc	cttaacttga	agggaaaaaa	300
caaaacaaga	gagacaaaqa	aagagacaaa	gaaataacttt	tcaacaacga	aaqatttqqa	360

Ser Gly Tyr Gly Glu Ala Phe Lys Trp Leu Ser Gln Tyr Ile

180

185

190

<210> 457  
 <211> 899  
 <212> DNA  
 <213> *Candida albicans*

<400> 457  
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 agcgcgattt taccagaact agatggcgct cgtgatcctg aaaacgggga gaaattttga 120  
 gaacaccgct ttattaggcg aagcgggtggg cacagctcac gcgtaagggtg ttcccattat 180  
 ttctcaaagt gatgcgaatt tcagagaaca cattaacctg ggggccataa acgcgacgtg 240  
 ctaccatttt cgttacgtat acttaggcca gagattacaa catgactact aatatcaaac 300  
 ataaactctat atataaggga tgaagatgta tgctttctta gaatttcaaa catgttccgt 360  
 taaagtttta cttttcgatt tcaatttcga ctgcatgatg cttttcttag gtagtttttt 420  
 gttattaaat agtatcataa attcttgtct ttttacataa gaattaggaa agtacagaac 480  
 aagagcaaatt ttaatatata atgtccgggtg gtaaagggtgg taaagctggg tcagctgcta 540  
 aagcttctca atctagatct gctaaagctg gtttaacatt cccagttggg agagtgcaca 600  
 gattgctaag aagaggtaac tacgcccaga gaattgggtc tgggtgctcca gtctatctaa 660  
 ctgctgtctt agaataattg gctgctgaaa ttttagaatt ggctggtaat gctgctagag 720  
 ataacaaaaa aaccagaatt attccaagac atttacaatt ggccatcaga aatgatgatg 780  
 aattgaacaa gctattgggt aatggtacca tcgcccaggg tgggtgtttg ccaaacattc 840  
 accaaaactt gttgccaaag aagtctgcca agactgccaa agcttctcaa gaactgtaa 899

<210> 458  
 <211> 132  
 <212> PRT  
 <213> *Candida albicans*

<400> 458  
 Met Ser Gly Gly Lys Gly Gly Lys Ala Gly Ser Ala Ala Lys Ala Ser  
 1 5 10 15  
 Gln Ser Arg Ser Ala Lys Ala Gly Leu Thr Phe Pro Val Gly Arg Val  
 20 25 30  
 His Arg Leu Leu Arg Arg Gly Asn Tyr Ala Gln Arg Ile Gly Ser Gly  
 35 40 45  
 Ala Pro Val Tyr Leu Thr Ala Val Leu Glu Tyr Leu Ala Ala Glu Ile  
 50 55 60  
 Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile  
 65 70 75 80  
 Ile Pro Arg His Leu Gln Leu Ala Ile Arg Asn Asp Asp Glu Leu Asn  
 85 90 95  
 Lys Leu Leu Gly Asn Val Thr Ile Ala Gln Gly Gly Val Leu Pro Asn  
 100 105 110  
 Ile His Gln Asn Leu Leu Pro Lys Lys Ser Ala Lys Thr Ala Lys Ala  
 115 120 125

<400> 460																
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1				5					10					15		
Ile	Asp	Glu	Glu	Val	Ala	Val	Cys	Thr	Val	Ala	Ala	Glu	Val	Leu	Ala	
			20					25					30			
Ile	Phe	Thr	Leu	Val	Cys	Thr	Arg	Val	Phe	Ile	Ile	Phe	Phe	Thr	Ala	
		35					40					45				
Arg	Ile	Cys	His	Gly	Ile	Trp	Pro	Ser	Ser	Pro	Ser	Glu	Arg	Pro	Tyr	
	50					55					60					
His	Thr	Phe	Arg	Ala	Ala	Arg	Leu	Arg	Asn	Ser	Ser	Lys	Met	Val	Ser	
65					70					75					80	
Ser	Asn	Cys	Val	Leu	Ser	Glu	Cys	Gly	Gln	Phe	Lys	Arg	Leu	Thr	Ala	
				85					90					95		
Asn	Leu	Ser	Gln	Thr	Val	Ser	Pro	Ser	His	Phe	Leu	Asn	Leu	Ile	Lys	
			100					105					110			
Ala	Pro	Leu	Leu	Ile	Ala	Gln	Arg	Cys	Cys	Glu	Cys	Ala	Ser	Gly	Asn	
		115					120					125				



Gly Cys  
130

<210> 461  
<211> 884  
<212> DNA  
<213> *Candida albicans*

<400> 461  
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gttccaagat cgcattgcaa gagtggaccg ccattgatgt taaacattaa ctccacgggg 120  
tactgtggta tgatcctcgt taaagacaga gaaaaactag agaacctcac tgaagatcct 180  
catcttgtgg acaagtcggt actgcaatgc gggttcccca acacagcagg ccaaaaaacca 240  
acagagtatc actattaagg tctattagcc atatgtacat tgtctataga tgtgtaactg 300  
cgctgtgatc ttgttttgac caatcaggag cgacgcgctt tttatcgggt caccctggcg 360  
gggggcctga caatttactt tcatagagca gtaataaaag ggaagagatg taaaagcttg 420  
gaaaaatagc agtaaagggt gttgttggac aatttatcag aatattagta actgtaatta 480  
aacgttccag aaagaacaaa atgccacagt cttttacgtc tattgcgaga attggtgact 540  
atattttgaa gtcaccgcgc ctctccaagt tatgtgttcc agttgccaat cagttcatta 600  
acctgcgagg ttacaagaag ttagggtcga aatttgacga ctttaattgca gaggaaaatc 660  
ccatcatgca gaccgcttta agaagactcc ctgaagatga atcttatgcc agagcatata 720  
gaataatcag ggctcatcaa accgagttga ctcatcattt actgccaaaga aacgaatgga 780  
tcaaagccca agaggatggt ccttacctgt tgccatacat attagaagct gaagctgcag 840  
ctaaggagaa ggacgagtta gacaacatag aggtctccaa atga 884

<210> 462  
<211> 127  
<212> PRT  
<213> *Candida albicans*

<400> 462  
Met Pro Gln Ser Phe Thr Ser Ile Ala Arg Ile Gly Asp Tyr Ile Leu  
1 5 10 15  
Lys Ser Pro Val Leu Ser Lys Leu Cys Val Pro Val Ala Asn Gln Phe  
20 25 30  
Ile Asn Leu Ala Gly Tyr Lys Lys Leu Gly Leu Lys Phe Asp Asp Leu  
35 40 45  
Ile Ala Glu Glu Asn Pro Ile Met Gln Thr Ala Leu Arg Arg Leu Pro  
50 55 60  
Glu Asp Glu Ser Tyr Ala Arg Ala Tyr Arg Ile Ile Arg Ala His Gln  
65 70 75 80  
Thr Glu Leu Thr His His Leu Leu Pro Arg Asn Glu Trp Ile Lys Ala  
85 90 95  
Gln Glu Asp Val Pro Tyr Leu Leu Pro Tyr Ile Leu Glu Ala Glu Ala  
100 105 110  
Ala Ala Lys Glu Lys Asp Glu Leu Asp Asn Ile Glu Val Ser Lys

115

120

125

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<210> 463
<211> 1025
<212> DNA
<213> Candida albicans
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<400>	463						
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gtgtagccta	atgtttaatg	cctaattttt	ttctaaaatg	cagcaaacata	catatgttga	180	
gtcgtataga	catctatata	taacaagcac	agaaccgctc	aattgggtatt	tttcaggaca	240	
ttttaaaccg	cctgtacaacg	agaacccata	cattactttt	tttaatatct	tttttgtttt	300	
caccgccttc	tttttatttt	tatccgaaga	tcttttgga	cccgcctctgc	gaatagcgaa	360	
gctaggatac	caaattgaaa	cttggaacata	actcatcatt	aaagaagtat	actgttaaga	420	
gaggcattca	tttcgtgtat	tataacgttt	agcatcagtt	acccttgaaa	gcccaacata	480	
tacaaaaata	cgcgtccaag	atgtctacta	aagcccaaaa	ccctatgcgt	gatttgaaga	540	
tcgagaaatt	ggctctgaac	atctccgctg	gtgaactctg	tcgacagatta	accaggcct	600	
ccaagggtttt	agaacaatta	tctgggtcaaa	ctccagttca	atccaaggcc	agatacactg	660	
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caaaggctga	agaaattttg	gaaagaggtt	tgaagggtcaa	ggaataccaa	ttgagagaca	780	
gaaactttctc	tgctaccggt	aacttcgggt	tcgggtattga	cgaacacatt	gacttgggta	840	
tcaagtatga	cccatccatc	ggtattttctg	gtatggattt	ctatgtcgtc	atgaacagac	900	
caggtgctag	agtcactaga	agaaagagat	gtaagggtac	tgtttggtaac	tcccacaaga	960	
caactaagga	agacaccgtc	tcttggttca	agcaaaagta	cgacgctgat	gtgctcgata	1020	
aataa						1025	

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<210> 464
<211> 174
<212> PRT
<213> Candida albicans
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<400> 464																	
Met	Ser	Thr	Lys	Ala	Gln	Asn	Pro	Met	Arg	Asp	Leu	Lys	Ile	Glu	Lys		
1				5					10					15			
Leu	Val	Leu	Asn	Ile	Ser	Val	Gly	Glu	Ser	Gly	Asp	Arg	Leu	Thr	Arg		
			20					25					30				
Ala	Ser	Lys	Val	Leu	Glu	Gln	Leu	Ser	Gly	Gln	Thr	Pro	Val	Gln	Ser		
		35					40					45					
Lys	Ala	Arg	Tyr	Thr	Val	Arg	Thr	Phe	Gly	Ile	Arg	Arg	Asn	Glu	Lys		
	50					55					60						
Ile	Ala	Val	His	Val	Thr	Val	Arg	Gly	Pro	Lys	Ala	Glu	Glu	Ile	Leu		
65					70					75					80		
Glu	Arg	Gly	Leu	Lys	Val	Lys	Glu	Tyr	Gln	Leu	Arg	Asp	Arg	Asn	Phe		
				85					90					95			
Ser	Ala	Thr	Gly	Asn	Phe	Gly	Phe	Gly	Ile	Asp	Glu	His	Ile	Asp	Leu		
			100					105					110				

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<400> 466
Met Val Phe Gly Gln Leu Tyr Ala Leu Phe Ile Phe Thr Leu Ser Cys
  1             5             10             15
Cys Ile Ser Lys Thr Val Gln Ala Asp Ser Ser Lys Glu Ser Ser Ser
      20             25             30
Phe Ile Ser Phe Asp Lys Glu Ser Asn Trp Asp Thr Ile Ser Thr Ile

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472

35	40	45
Ser Ser Thr Ala Asp Val Ile Ser Ser Val Asp Ser Ala Ile Ala Val		
50	55	60
Phe Glu Phe Asp Asn Phe Ser Leu Leu Asp Asn Leu Met Ile Asp Glu		
65	70	75
Glu Tyr Pro Phe Phe Asn Arg Phe Phe Ala Asn Asp Val Ser Leu Thr		
	85	90
Val His Asp Asp Ser Pro Leu Asn Ile Ser Gln Ser Leu Ser Pro Ile		
	100	105
Met Glu Gln Phe Thr Val Asp Glu Leu Pro Glu Ser Ala Ser Asp Leu		
	115	120
Leu Tyr Glu Tyr Ser Leu Asp Asp Lys Ser Ile Val Leu Phe Lys Phe		
	130	135
Thr Ser Asp Ala Tyr Asp Leu Lys Lys Leu Asp Glu Phe Ile Asp Ser		
	145	150
Cys Leu Ser Phe Leu Glu Asp Lys Ser Gly Asp Asn Leu Thr Val Val		
	165	170
Ile Asn Ser Leu Gly Trp Ala Phe Glu Asp Glu Asp Gly Asp Asp Glu		
	180	185
Tyr Ala Thr Glu Glu Thr Leu Ser His His Asp Asn Asn Lys Gly Lys		
	195	200
Glu Gly Asp Asp Asp Ile Leu Ser Ser Ile Trp Thr Glu Gly Leu Leu		
	210	215
Met Cys Leu Ile Val Ser Ala Leu Leu Leu Phe Ile Leu Ile Val Ala		
	225	230
Leu Ser Trp Ile Ser Asn Leu Asp Ile Thr Tyr Gly Ala Leu Glu Lys		
	245	250
Ser Thr Asn Pro Ile Lys Lys Asn Asn		
	260	265

<210> 467

<211> 854

<212> DNA

<213> Candida albicans

<400> 467

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 taacaatgca taaattatga gtagtctttt tcatcactat ataaaacctt tttcaaacga 180  
 aacgctgttt ttgttggtac tatctttgca ggtgcctttg ttttccaaac tgtatttgat 240  
 actgctatta cttcatggta cgagaatcac aacaaaggaa aattatggaa agatgtcaag 300

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gctcgaatag ctgcaggcga tggagacgac gatgatgagt aaacgctgat tatgtcacac 360
atatacgtgc aaacgctctc tctctctctc aagctatata agtggcactc gtcttattta 420
ttattttttt attttggctg gttgttcatg ttcaacccaa cctcataaag gcactcaact 480
tcataatttg acacaaatct atgtctcgcc aaagcgcatt caaatttcag aatggaaata 540
gacacgaacg agcctgtctg tcagatgttc acaaaatcct tattataatt ttatattcta 600
ctaaaggaaa aagagaatta ggaaaaagaa taactcattt tatgtatata catatatttt 660
gtacatatct ataccaagca agtatagtgc aatactgttc ttcgacgtta ttaaacgtaa 720
tagcattttc ttggtatcct ttgaatctta tatacaagta cgagtacata ctgcgcagta 780
aattgacccg gatgggtgtg ttagatttcg ccagaagcgg aggcgttctg gattctggag 840
atgtaagcct ttga 854

```

&lt;210&gt; 468

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 468

```

Met Ser Arg Gln Ser Ala Phe Lys Phe Gln Asn Gly Asn Arg His Glu
  1              5              10              15

Arg Ala Cys Leu Ser Asp Val His Lys Ile Leu Ile Ile Ile Leu Tyr
      20              25              30

Ser Thr Lys Gly Lys Arg Glu Leu Gly Lys Arg Ile Thr His Phe Met
      35              40              45

Tyr Ile His Ile Phe Cys Thr Tyr Leu Tyr Gln Ala Ser Ile Val Gln
      50              55              60

Tyr Cys Ser Ser Thr Leu Leu Asn Val Ile Ala Phe Ser Trp Tyr Pro
      65              70              75              80

Leu Asn Leu Ile Tyr Lys Tyr Glu Tyr Ile Leu Arg Ser Lys Leu Ile
      85              90              95

Leu Met Val Cys Leu Asp Phe Ala Arg Ser Gly Gly Val Leu Asp Ser
      100              105              110

Gly Asp Val Ser Leu
      115

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&lt;210&gt; 469

&lt;211&gt; 914

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;400&gt; 469

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aaatacaaat ccaagaaacc tcgatgagga tgactctgat gataatgatg actctgatga 60
gcgagagatt tggtagattc aagccctcta ctatgtttta tagttgacat atttgtatat 120
aaaaacttat acattattaa acatttgccg gtcgattgac ttttatttat tattaacaaa 180
gaagtaatac caacctaat acaaatactt cgaagtgact atcataagtt tccttatcta 240
gcgaaggcaa cttttgaact ccccagttgt taatatgtat cattatacac gacccaatca 300
aacgcgggga agtcaatgcc gaaagaattc taggacctaa aagctgctca atccttgggc 360
ctttccctaa tgacatcccc tctcaaactt tagcttagca gttgtattta atgtcctgtc 420

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<400>	471						
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cttttctcgg	tcttttcttg	ctcccacagg	ccgttaatgg	cctgaaacag	ttttgtgact	180	
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tcataaatca	tatctaaact	cacagcgcgt	agggtaggtg	tgccctggcag	tggtaaggta	360	
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gcttcaacct	tagagctgat	accttttgcc	tggtcaaagg	cgaaaacgtc	tacctcgctt	480	
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tcgctgtttca	tataatcgtc	gtcactcata	tcggcgcttt	tactgcgatgc	tgctctttga	900	
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475

<210> 472  
 <211> 167  
 <212> PRT  
 <213> Candida albicans

<400> 472  
 Met Thr Ser Phe Gln Ala Val Ser Phe Ala Leu Gly Cys Asn Thr Leu  
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 Val Ala Cys Tyr Ala Phe Thr Val Leu Glu Lys Arg Ser Leu Met Thr  
             20                    25                    30  
 Ser Cys Thr Asn Ala Leu Ser Phe Leu Phe Phe Leu Leu Thr Leu Arg  
             35                    40                    45  
 Arg Ile His Arg His Trp Tyr Lys Pro Tyr Gly Ala Phe Leu Leu Ile  
             50                    55                    60  
 Phe Val Leu Thr Leu Arg Trp Phe Arg Gly Pro Ile Ala Trp Val Val  
             65                    70                    75                    80  
 Val Asp Val Val Phe Ala Ser Cys Asn Val Val Phe Phe Ser Pro Ala  
                     85                    90                    95  
 Leu Ser Asp Glu Asn Trp Pro Tyr Val Ser Phe Phe Gly Val Val Val  
             100                    105                    110  
 Val Ile Ala Val His Ile Ile Val Val Thr His Ile Gly Ala Phe Thr  
             115                    120                    125  
 Ala Cys Cys Leu Leu Lys Arg Val Ser Leu Lys Ser Ser Glu Glu Lys  
             130                    135                    140  
 Lys Lys Lys Lys Lys Lys Lys Glu Lys Ser Leu His Thr Glu Arg  
             145                    150                    155                    160  
 Glu Lys Lys Lys Lys Lys Phe  
                     165

<210> 473  
 <211> 1343  
 <212> DNA  
 <213> Candida albicans

<400> 473  
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 gagttgcttt ctttttttgt ctcagcagtc attgtgcgcc aaaaaaagag aaaaccgtga 180  
 gccgaagtcc acgctctgga gtaggctct cccattacgg agagaagcat ttcctcagcc 240  
 tgggagcccc gttggaacag tcaggctaaa ctgggccttc ctaccactg cttgctgttt 300  
 ctactggac gcacaagggg attttctttc taccttcggc ttgcctcact gcgttggggc 360  
 ttccaatgc aacttcgttc gtatgcatac aatcttttag atattatctt ttaaaattat 420  
 tttaaaacaa ttttaaatgt atctcatatg cttttcttct gctgttgaaa aggctaaaca 480

aagaagatca ataagataaa atggctccat ctggtatgtg aactgcaata ttaatagcac 540  
gagaaaattg agaggaagat agatgggaac tagtagagtt gatattgatg agatacgaaa 600  
accacacgta aataaactat ccgacgacaa gaatagtga ttaaggactt gattaagata 660  
tggtagacaa cgtaattatc gggctcaaca gtttattagc aatcgttttg atagaagcgt 720  
tgatgctgtg gaagttgttc tttttactac caacagccat taacaaatcc attagagtgt 780  
tcgttcgttt ttctgctcag attcaagaaa attattccat cctcattata cttttttctt 840  
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tctcctatga atttactttt tgtatagcta aggtactgc cgctaagaaa gctgtcgtta 960  
agggtactaa tggtaagaag gctttgaagg tcagaacttc tgctaccttc agactaccaa 1020  
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gattggactc atacaagggtc attgagcaac caatcacttc tgaaaccgct atgaagaagg 1140  
ttgaagatgg taacattttg gttttccaag tttccatgaa agctaacaaa taccaaatca 1200  
agaaggccgt caaggaatta tacgaagttg acgtattgaa ggtaaacact ttggttagac 1260  
caaacggtac caagaaggct tacgtagat tgactgctga ctacgatgct ttggacattg 1320  
ctaacagaat cggttacatt taa 1343

&lt;210&gt; 474

&lt;211&gt; 142

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 474

Met Ala Pro Ser Ala Lys Ala Thr Ala Ala Lys Lys Ala Val Val Lys  
1 5 10 15

Gly Thr Asn Gly Lys Lys Ala Leu Lys Val Arg Thr Ser Ala Thr Phe  
20 25 30

Arg Leu Pro Lys Thr Leu Lys Leu Ala Arg Ala Pro Lys Tyr Ala Ser  
35 40 45

Lys Ala Val Pro His Tyr Asn Arg Leu Asp Ser Tyr Lys Val Ile Glu  
50 55 60

Gln Pro Ile Thr Ser Glu Thr Ala Met Lys Lys Val Glu Asp Gly Asn  
65 70 75 80

Ile Leu Val Phe Gln Val Ser Met Lys Ala Asn Lys Tyr Gln Ile Lys  
85 90 95

Lys Ala Val Lys Glu Leu Tyr Glu Val Asp Val Leu Lys Val Asn Thr  
100 105 110

Leu Val Arg Pro Asn Gly Thr Lys Lys Ala Tyr Val Arg Leu Thr Ala  
115 120 125

Asp Tyr Asp Ala Leu Asp Ile Ala Asn Arg Ile Gly Tyr Ile  
130 135 140

&lt;210&gt; 475

&lt;211&gt; 429

&lt;212&gt; DNA

<213> *Candida albicans*



477

&lt;400&gt; 475

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cttatagcaa ctactaaagc ttcagctgct aaaaaagctg ctttgaaagg tggttaacggg 60
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accagatctc caaaatacca aagaaaatca gtcccacact acaacagatt ggatgcccac 180
aaaatcattg ttgctccaat tgccactgaa actgctatga aaaaagtcga agatgggtaac 240
actttgggtt tccaagttga catcaaatcc aacaaacacc aaatcaaadc tgctgttaaa 300
gaattatacg atgttgatgc cttatacggt aacactttga tcagacctaa cggtagcaag 360
aaagcttaca tcagattaac ctctgactac gatgctttgg atattgctaa cagaatcggg 420
tacatctaa

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&lt;210&gt; 476

&lt;211&gt; 142

&lt;212&gt; PRT

<213> *Candida albicans*

&lt;400&gt; 476

```

Leu Ile Ala Thr Thr Lys Ala Ser Ala Ala Lys Lys Ala Ala Leu Lys
  1             5             10             15

Gly Val Asn Gly Lys Lys Ala Leu Lys Val Arg Thr Ser Thr Thr Phe
          20             25             30

Arg Leu Pro Lys Thr Leu Lys Leu Thr Arg Ser Pro Lys Tyr Gln Arg
      35             40             45

Lys Ser Val Pro His Tyr Asn Arg Leu Asp Ala His Lys Ile Ile Val
      50             55             60

Ala Pro Ile Ala Thr Glu Thr Ala Met Lys Lys Val Glu Asp Gly Asn
      65             70             75             80

Thr Leu Val Phe Gln Val Asp Ile Lys Ser Asn Lys His Gln Ile Lys
          85             90             95

Ser Ala Val Lys Glu Leu Tyr Asp Val Asp Ala Leu Tyr Val Asn Thr
      100            105            110

Leu Ile Arg Pro Asn Gly Thr Lys Lys Ala Tyr Ile Arg Leu Thr Ser
      115            120            125

Asp Tyr Asp Ala Leu Asp Ile Ala Asn Arg Ile Gly Tyr Ile
      130            135            140

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&lt;210&gt; 477

&lt;211&gt; 117

&lt;212&gt; DNA

<213> *Candida albicans*

&lt;400&gt; 477

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ttagataccc aacttagttc ttctccagtg tcttctttta gcattgtatc tgattttggt 60
gtcagttctc aatctgatcc attgtggcaa tggctgtgtt tgcttttgag ccttagc 117

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&lt;210&gt; 478

478

<211> 39  
 <212> PRT  
 <213> Candida albicans

<400> 478  
 Leu Asp Thr Gln Leu Ser Ser Ser Pro Val Ser Ser Phe Ser Ile Val  
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 Ser Asp Phe Val Val Ser Ser Gln Ser Asp Pro Leu Trp Gln Trp Ser  
           20                    25                    30  
 Val Leu Leu Leu Ser Leu Ser  
           35

<210> 479  
 <211> 198  
 <212> DNA  
 <213> Candida albicans

<400> 479  
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 cacaacaaag ctaaattatg gaaaaacgtc aaaggaaaat tccttgaagg tgaaggtgaa 180  
 gaagaagatg acgaataa 198

<210> 480  
 <211> 65  
 <212> PRT  
 <213> Candida albicans

<400> 480  
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     1                    5                    10                    15  
 Ala Thr Ile Phe Gly Gly Ala Phe Ala Phe Gln Gly Phe Phe Asp Val  
           20                    25                    30  
 Ala Val Asn Lys Trp Trp Glu Glu His Asn Lys Ala Lys Leu Trp Lys  
           35                    40                    45  
 Asn Val Lys Gly Lys Phe Leu Glu Gly Glu Gly Glu Glu Glu Asp Asp  
           50                    55                    60  
 Glu  
     65

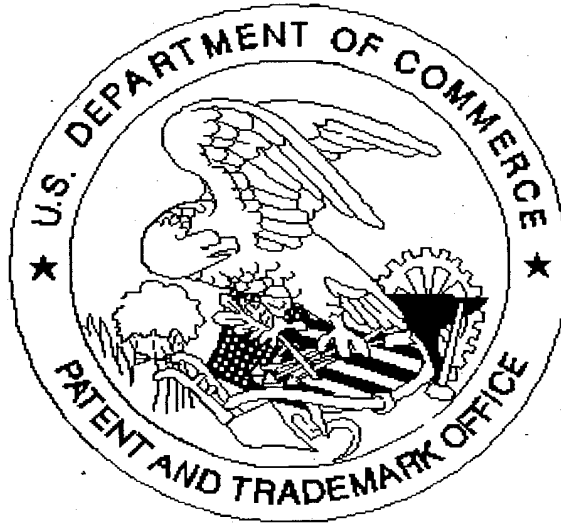
<210> 481  
 <211> 457  
 <212> DNA  
 <213> Candida albicans

<400> 481



480

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present  
for scanning. (Document title)

☒ *Scanned copy is best available. Some figures are dark.*